# Best Available Copy

F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//Hs.154326:D42087

F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-187:872:98//Hs.6162:AB018314

F-HEMBA10023481/EST//1.0e-19:285:70/Ms.121860:AA776692

F-HEMBA1002349//EST//0.011:385:59//Hs.148533:Al200996

- 5 F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//2.4e-189: 872:99//Hs.119023:AF092563
  - F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216
  - F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144
  - F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:97//Hs.25527:AC005954
- F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141
  - F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.90798:U79289
  - F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//0.11: 111:67//Hs.162154:AA528561
- 15 F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B, 6.8K [H.sapiens]//1.3e-71:346:98//Hs.136121: W26490
  - F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160
  - F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783
- F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:92//Hs.154583:D50912 F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89631:U48508 F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8e-45:331:83//Hs.6189:AB011133 F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235 F-HEMBA1002495
- 25 F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161
  - F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74//Hs.19949:X98173
  - F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:460:83//Hs.113283:AF018080
  - F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//9.Oe-159:738:98//Hs. 6764:AJ011972
- 30 F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795
  - F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:Al087951
  - F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete cds//6.1e-46:238:87//Hs. 10458:AF088219
  - F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138:655:98//Hs.68900:AF016903
- 35 F-HEMBA1002552//Human Hep27 protein mRNA, complete cds//2.8e-08:173:68//Hs.102137:U31875
  - F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.00020:603:57//Hs.20912:AB012162 F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205
  - F-HEMBA1002561//Humancione 23574 mRNA sequence//4.7e-17:268:72//Hs.79385:U90905
  - F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//4.3e-142:457:99//Hs.
- 40 151411:AF075587
  - F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//2.8e-30:156: 100//Hs.32170:AB015132
  - F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159
  - F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:Al378363
- 45 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4e-176:820:99//Hs.20141:
  - F-HEMBA1002621//EST//0.99:208:60//Hs.159127:Al384013
  - F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.2e-189:632:97//Hs.91338:
- 50 F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65//Hs.125129:AB002334 F-HEMBA1002629//Human density enhanced phosphatase 1 mRNA, complete cds//1.3e-07:473:61//Hs.1177:
  - F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390
  - F-HEMBA1002651

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- F-HEMBA1002659//Human vascular endothelial growth factor related protein VRP mRNA, complete cds//0.74: 223:60//Hs.79141:U43142
  - F-HEMBA1002661//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-122:781:85//Hs.23094: M19503

- F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497
- F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:Al351368
- F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 1 (alpha)//0.00096:418:61//Hs. 1323:S42457
- 5 F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.8e-11:541: 601/Hs.124161:AF065164
  - F-HEMBA10026961/Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e-06:345:61//Hs.155647: AC004221
  - F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.0e-12:327:62//Hs.13245: AB007924
    - F-HEMBA1002712

- F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800
- F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942: AB014521
- F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGST3) mRNA, complete cds//0.21: 157:66//Hs.111811 :AB007867
  - F-HEMBA1002742//EST//0.97:138:60//Hs.160545:71596
  - F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061:X59372
  - F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806:AA018786
- 20 F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817
  - F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834:98//Hs.74750: AB011126
  - F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:492:96//Hs.11833:Al299947
  - F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 mRNA, complete cds//3.9e-05:528:
- 25 59//Hs.128208:U63809
  - F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392
  - F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326
  - F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756
  - F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938
- 30 F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169:820:97//Hs.28307: AF071185
  - F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744
  - F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733:89//Hs.6059:AF093119
  - F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:M279904
- 35 F-HEMBA1002833
  - F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550
  - F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823
  - F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730
- 40 F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AE79429
  - F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679
  - F-HEMBA1002921
  - F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:Al088001
  - F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915
- 45 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6e-174:803:99//Hs.14687: AR011148
  - F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:GenBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA130053
  - F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1.1e-05:479:59//Hs.74019:X83703
- F-HEMBA1002944//Human putative endothelin receptor type B-like protein mRNA, complete cds//0.83:326:58// Hs.27747:U87460
  - F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.26762:AA913925
  - F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099
  - F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092
- 55 F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828
  - F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA454219
  - F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4) //1.5e-37:247:89//Hs.188:L20971

- F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.7e-05:797: 58//Hs.50758:AF092564
- F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525
- F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs.155464:AF088219
- 5 F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486
  - F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:330:78//Hs.113283:AF018080
  - F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.159425:AJ001454
  - F-HEMBA1003037//EST//0.53:59:74//Hs.148011:M268003
  - F-HEMBA1003041//ESTs, Weakly similar to F58G11.6 [C.elegans]//1.7e-64:337:95//Hs.l05907:AA186514
- F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182
  - F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438
  - F-HEMBA1003067
  - F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.5e-15:611:
- 15 59//Hs.124161:AF065164
  - F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62//Hs.48998:AB007865
  - F-HEMBA1003078//CYTOCHROME P450 IVF3//2.0e-29:452:67//Hs.106242:AB002454
  - F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:Al034461
  - F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:Al281881
- 20 F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:Al090721
  - F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M.musculus]//0.98:216:61//Hs.97865: AA405872
  - F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721
  - F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802
- F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//Hs.12432:AF070575
  F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.038:288:63//Hs.6162:AB018314
  - F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.036:286:63//Hs.6162:AB016314 F-HEMBA1003136
  - F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279
  - F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99//Hs.63931:AJ005670
- 30 F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.1e-24:171:83//Hs.l41874: AB014588
  - F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740
  - F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' region [E.coli]//4.7e-20:118:97//Hs. II8831:AA211895
- 35 F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:Al215523
  - F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135
  - F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412
  - F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:154:85//Hs.113283:AF018080
  - F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:Al076765
  - F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784
    - F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310 F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012
    - F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.00054:432:58//Hs.l32206: AF039694
- 45 F-HEMBA1003250

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- F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds//4.3e-08:426:64//Hs. 49585:AF075292
- F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991
- F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020
- 50 F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864
  - F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867
  - F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds//2.9e-146:539:97//Hs.13225:AF038662
  - F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//1.6e-167:799:98//Hs.12836: AB011109
  - F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R44912
  - F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160
  - F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.I05486:AA521012

EP 1 074 617 A2 F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//1.5e-189:865:99//Hs. 124224:AB001872 F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49:399:80//Hs.154782:X99459 F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254 F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328 F-HEMBA1003330 F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-26:256:78//Hs.146395:AB002329 F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence//0.37:187:65//Hs.80265:AD000092 F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159 F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:Al263819 F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//Hs.73919:X81637 F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58017 F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N95552 F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:Al202488 F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813 F-HEMBA1003403//Adducin 2 (beta) {alternative products }//5.0e-05:445:61//Hs.90951:U43959 F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z78309 F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//9.5e-05:541:58//Hs.89709:L35546 F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962 F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0e-149:686:99//Hs.25812:AF058696 F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:271:60//Hs.47822:AB002378 F-HEMBA1003461//Glycoprotein lb (platelet), beta polypeptide//4.8e-08:775:58//Hs.3847:U59632 F-HEMBA1003463//ESTs//3.3e-22:121:99I/Hs.130847:AA058578 F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cds//0.16:321:60//Hs.13999:AB014600 F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443 F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-51:451:78//Hs.22271:D26067 F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:Al392811 F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (islet-1)//5.0e-75:736:73//Hs.505:U07559 F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311 F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cds//3.6e-33:562:64//Hs.81469:U01833 F-HEMBA1003556 F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122 F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:Al342327 F-HEMBA1003569//Human metastasis-associated mtal mRNA, complete cds//2.0e-58:455:66//Hs.101448: U35113 F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972 F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546 F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19:108:99//Hs.18420:AA599232 F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85:487:92//Hs.57937:W68285 F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)//2.8e-06: 439:62//Hs.83532:X59405 F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827 F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916

F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]//2.4e-133:644: 97//Hs.3566:AA314782

F-HEMBA1003617//Homa sapiens mRNA for HRIHFB2157, partial cds//7.9e-171:501:97//Hs.124956:AB015344 F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//

50 4.4e-16:161:78/IHs.111323:AF077954

F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750

F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159

F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF013591

55 F-HEMBA1003640//ESTs//1.1e-11:267:661/Hs.34359:Al122791

F-HEMBA1003645

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F-HEMBA1003646

F-HEMBA1003656

- F-HEMBA1003662
- F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381
- F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906
- F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:464:61//Hs.79706:U53204
- F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//1.6e-100:478:98//Hs. 118866:AI017072
  - F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5e-74:606:77//Hs.9028:AF039691
  - F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187
  - F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.81:254:62//Hs.32316:AB011116
- F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995 10
  - F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760
  - F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:692:68//Hs.91916:AF035317
  - F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921
  - F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839
- F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6e-102:753:81//Hs.23094: 15 M19503
  - F-HEMBA1003742//Homo sapiens chromosome 19, cosmid
  - R31180//0.16:242:62//Hs.153325:AC005390
  - F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:AI198946
- F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:430:69//Hs.8136:U81984 20
  - F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920
  - F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//1.7e-24:224:81//Hs.18171:AA524327
  - F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172
  - F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L39064
- F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.13: 25 222:61//Hs.89230:AF031815
  - F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239
  - F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.119537:M88108
  - F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:Al379721
- F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3e-85:586:87//Hs.6051:AB014516 30 F-HEMBA1003836//EST//6.8e-06:98:74//Hs.I45447:AI204220
  - F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.8e-40:151:88//Hs.139007:H74314
  - F-HEMBA1003856//ESTs//8.6e-53286:95//Hs.116645:Al005167
- F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144:66//Hs.21355:AB002367 35 F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.3e-30:580:63//Hs.27621 :
  - U52840 F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//Hs.89563:D32002
  - F-HEMBA1003880
- F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cds//4.2e-18:302:67//Hs.23711:AB018295 40 F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGEN-
  - IC REGION [S.cerevisiae]//1.2e-49:295:92//Hs.114673:W72675
  - F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236
  - F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cds//0.081:345:58//Hs.78494:AB011097
- F-HEMBA1003926/IEST//2.5e-32:253 :83//Hs.132635:Al032875 45
  - F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-38:313:69//Hs.154668:AB002389
  - F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562
  - F-HEMBA1003942//EST, Weakly similar to 24 KD PROTEIN [Xenopus laevis]//0.0029:222:61//Hs.l44236:W52380
  - F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055
- F-HEMBA1003953//Zinc finger protein 7 (KOX 4, clone HF.16)//0.00014:271:66//Hs.2076:M29580 50
  - F-HEMBA1003958//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.1e-44:243:76//Hs.91146:N73230
  - F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H78567
  - F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:Al138965
- F-HEMBA1003978 55
  - F-HEMBA1003985//EST//0.32:115:69//Hs.102617:N47009
  - F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456
  - F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//

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0.022:349:58//Hs.104640:AF000561
        F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA358468
        F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493
        F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA812573
5
        F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:Al379721
        F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.2e-51:359:84//Hs.l5519:
         F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:Al239930
         F-HEMBA1004042//EST//0.00088:272:6l//Hs.155763:Al312281
10
         F-HEMBA1004045//EST//2.7e-20:408:66//Hs.I62529:AA584160
         F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.6101:M60315
         F-HEMBA1004049//ESTs//8.1e-68:430:86/JHs.146307:AA584638
         F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:457:58//Hs.82837:L13435
         F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.5e-46:199:80//Hs.
15
         46328:D87942
         F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA757426
         F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA770107
         F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.75666:M28713
         F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.3e-39:335:79//Hs.
20
         46468:U45984
         F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-24:610:61//Hs.80712:D86957
         F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA780064
         F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:Al419759
         F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1//0.00055:343:62//Hs.5923:X82260
25
         F-HEMBA1004143
         F-HEMBA1004146
         F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:Al186056
         F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete cds//1.8e-15:591:60//Hs.159277:
         AB018341
         F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:649:97//Hs.59988:AF067855
30
         F-HEMBA1004199
         F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:Al375427
         F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.2e-35:205:94//Hs.
         F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA626040
35
         F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//Hs.54515:U50748
         F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA192514
         F-HEMBA1004227//ESTs, Weakly similar to F55A11.4 [C.elegans]//0.012:156:67//Hs.l63588:Al073878
         F-HEMBA1004238
40
         F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA679571
         F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA758522
         F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) gene, complete cds//1.1e-28:295:72//Hs.
         56205:U96876
         F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:553:60//Hs.83634:U52112
         F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 protein, complete cds//4.9e-73:490:77//Hs.141874:
45
         AB014588
         F-HEMBA1004272
         F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA876444
         F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:118:65//Hs.155313:AB002331
         F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.0:364:56//Hs.118738:AB018343
50
         F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.9e-187:868:
         99//Hs.101766:AF022795
         F-HEMBA1004289
         F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA573484
         F-HEMBA1004306//ESTs//0.041:177:64//Hs.158234:Al270047
55
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F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:452:65//Hs.69740:U09367

F-HEMBA1004312//ESTs//0.83:253:59//Hs.121898:AI336314

F-HEMBA1004323//EST//0.44:134:64//Hs.145464:Al204532

- F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//0.017:209:64//Hs.43627: U35612
- F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062
- F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888
- 5 F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete cds//0.49:80:73//Hs.139648:AB014606 F-HEMBA1004341
  - F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//2.7e-39:270:86//Hs.80686: D89667
  - F-HEMBA1004354//Human CHL1 potential helicase (CHLR1), complete cds//1.3e-46:190:92//Hs.27424:U75968
  - F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:62//Hs.3022:D85376
    - F-HEMBA1004366//ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog [H.sapiens]//7.8e-10:396:61//Hs.33688:AA020928
    - F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800
    - F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//Hs.112180:AF039019
- 15 F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250
  - F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818
  - F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199
  - F-HEMBA1004408//ESTs, Weakly similar to The ha1539 protein is related to cyclophilin. [H.sapiens]/1.4e-20:144: 88//HS.121076:Al246426
- F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//4.8e-18:248:72//Hs.69747:M35531
  - F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:AF088219
  - F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080
  - F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606
- 25 F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984
  - F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450
  - F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA992600
  - F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431
  - F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-89:758:76//Hs.23094:M19503
  - F-HEMBA1004507//ESTs, Weakly similar to T19B10.6 [C.elegans]//1.4e-61:296:99//Hs.114622:AA693492
    - F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014: 265:61//Hs.43543:AF042800
    - F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//Hs.76279:X53416
    - F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381
- 35 F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.74:74:75//Hs.87497:U90552 F-HEMBA1004554
  - F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331
  - F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802
  - F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2e-17:334:67//Hs.24536:
- 40 AA479825

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- F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1 e-35:337:78//Hs.78160:AF010238
- F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661
- F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds//0.42:186: 66//Hs.84136:1170370
- F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606
  - F-HEMBA1004617//EST//0.027:188:61//Hs.l59094:Al383198
  - F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178
  - F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416
- 50 F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:Al360891
  - F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:Al346780
  - F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:Al017522
  - F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083
  - F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796
- 55 F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582
  - F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141
  - F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:Al093252
  - F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue//0.64:313:61//Hs.118578:X80821

- F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73//Hs.155174:AB007892
- F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515
- F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:244:57//Hs.99975:X55019
- F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328:60//Hs.68900:AF016903
- 5 F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.9e-32:476:70//Hs.116874: AA524909
  - F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515
  - F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004
- F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0e-61:663:71//Hs.23094:M19503 F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813
  - F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504
  - F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400: AB006626
- F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.l53563:AF011333 F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082 F-HEMBA1004758//Homosapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:
  - F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.I55657:M61120
- 20 F-HEMBA1004768//Human Line-1 repeat mRNA with.2 open reading frames//4.5e-115:909:78//Hs.23094:
  - F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139 F-HEMBA1004771
  - F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//
- 25 Hs.62004:AF039235
  - F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:Al222106
  - F-HEMBA1004795
  - F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952
  - F-HEMBA1004806//EST//0.080:142:65//Hs.160268:Al148971
- F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48: 171:92//Hs.134510:L01042
  - F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646
  - F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:Al300481
  - F-HEMBA1004847//ESTs//2.1 e-09:66:98//Hs.158161:AA312511
- 35 F-HEMBA1004850//EST//0.033:253:64//Hs.158782:A376601
  - F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150
  - F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:
  - F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077
- 40 F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633
  - F-HEMBA1004889//Growth arrest-specific I//0.20:146:68/Hs.65029:L13698
  - F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304
  - F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106
  - F-HEMBA1004918//EST//0.78:122:61//Hs.I45491:AI254348
- 45 F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172
  - F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X52947
  - F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:Al224959
  - F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds// 0.11:182:65//Hs.105932:U89331
- 50 F-HEMBA1004934
  - F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981
  - F-HEMBA1004954//ESTs//0.0i4:404:60//Hs.11177:AA417813
  - F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:Al174478
  - F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274
- 55 F-HEMBA1004972
  - F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.073:574:58//Hs.154139:
  - F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:Al361946

- F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013
- F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149I23:AI244750
- F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589
- F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:Al394026
- 5 F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429
  - F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356
  - F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:98//Hs.31921: AB014548
  - F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560
- 10 F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237
  - F-HEMBA1005039//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627 F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds//0.078:442:59//Hs. 100602:AF010193
- 15 F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802
  - F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:Al264462
  - F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds// 1.5e-59:411:85//Hs.129727:AF035587
  - F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381
- F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785
  - F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59: 631:59//Hs.27910:AF049105
  - F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170: AF080561
  - F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:Al031916
  - F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304
  - F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106
  - F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:Al032875
- 30 F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021
  - F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216
  - F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914
  - F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282197
  - F-HEMBA1005202

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- 35 F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436
  - F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547
  - F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081
  - F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302
  - F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//6.0e-54:399:79//Hs.
  - F-HEMBA1005244//ESTs//2.5e-14:85:10011Hs,128744:AI191922
  - F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896
  - F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7e-151:705:98//Hs.72660:
- 45 F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:Al261380
  - F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777
  - F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338:65//Hs.12451:U97018
  - F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:Al149232
  - F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs.155464:AF088219
- 50 F-HEMBA1005311
  - F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:Al279516
  - F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615
  - F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117
  - F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.00075:310:63//Hs.111597:U68723
- 55 F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//4.4e-153:740:97//Hs.29361:AJ007581
  - F-HEMBA1005353//EST//5.4e-09:2-22:68//Hs.119508:AA485732
  - F-HEMBA1005359//Zinc finger protein 137 (clone pHZ-30)//5.7e-100:500:88//Hs.151689:U09414
  - F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds//2.5e-70:572:73//Hs.43265:

#### AF071787

F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:Al417905

F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.1e-43:341:81//Hs. 154069:U06452

F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI93053 5

F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA804448

F-HEMBA1005394//ESTs, Weakly similar to No definition line found [C.elegans]//1.0e-130:620:98//Hs.108990: N25951

F-HEMBA1005403//ESTs, Weakly similar to No definition line found [C.elegans]//7.7e-151:727:97//Hs.17118: AI033807

F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H24513

F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347

F-HEMBA1005411

F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:

537:99//Hs.4854:AF041248 15

F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323

F-HEMBA1005443//Zinc finger protein 157 (HZF22)//9.0e-34:259:72//Hs.89897:U28687

F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783

F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107

F-HEMBA1005469//Human (clone E5.1) RNA-binding protein mRNA, complete cds//3.1e-29:155:99//Hs.75104: 20 L37368

F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-88:481:92//Hs.23094:M19503

F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs.155464:AF088219

F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414:60//Hs.132206:

25 AF039694

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10

F-HEMBA1005497//Glucocorticoid receptor alpha { alternative products}//8.7e-41:588:69//Hs.102761:U25029 F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21//1.1e-28:318:73//Hs.159530:

F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:D13635

F-HEMBA1005508//ESTs//0.45;326;59//Hs.102756;AA526911 30

F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:79//Hs.153014:AB002353 F-HEMBA1005513//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs. 22767:N99220

F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0.54:623:56// Hs.143551:AF048693

F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575

F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.1e-55:288:85//Hs.144563:

F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:76//Hs.155464:AF088219

F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//1.2e-30:166:96//Hs. 40 17035:AI080471

F-HEMBA1005530

F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18: 391:64//Hs.30250:AF055376

F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461 45

F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903

F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257

F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507

F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610:98//Hs.77738:

50 AB007932

F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:Al312873

F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64//Hs.57929:AB011538

F-HEMBA1005582

F-HEMBA1005583

F-HEMBA1005588//ESTs//1.3e-35:386:70//Hs.55855:AA621381 55

F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA

FORMS//0.54:439:591/Hs.2137:D49357

F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:57//Hs.7720:AB002323

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F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D19609
        F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982
        F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.2e-22:721:61//Hs.144563:
        AF057280
        F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//1.8e-89:454:96//Hs.19400:
5
         AA662845
         F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535
         F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734
         F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199
         F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:Al416956
10
         F-HEMBA1005666
         F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.7e-45:255:79//Hs.114293:
         AB011142
         F-HEMBA1005679//Human kpni repeat mma (cdna clone pcd-kpni-4), 3' end//1.2e-37:356:77//Hs.139107:K00629
         F-HEMBA1005680
15
         F-HEMBA1005685
         F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-
         71:497:85//Hs.26988:U66406
         F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678
         F-HEMBA1005717//EST//0.018:115:66//Hs.160541:Al270143
20
         F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstrans-
         ferase, geranyltranstransferase)//2.6e-20:151:88//Hs.77393:D14697
         F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754
         F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024
         F-HEMBA1005755//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.8e-48:425:78//Hs.103948:K00627
25
         F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs.155464:AF088219
         F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141
         F-HEMBAI0058131/ESTs//0.012:209:63//Hs.113365:R77747
         F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds//2.0e-07:439:62//Hs.6133:U94346
          F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577
30
          F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788
         F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9e-42:690:66//Hs.23094:M19503
          F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//Hs.79706:U53204
          F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150
          F-HEMBA1005884//Homosapiens mRNA, chromosome 1 specific transcript KIAA0484//1.4e-53:332:83//Hs.
35
          158095:AB007953
          F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097
          F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete cds//7.2e-45:411:77//Hs.
          46468:U45984
          F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.00054:477:59//Hs.37125:U42766
 40
          F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081
          F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//
          2.0e-46:434:78//Hs.125231:AF068006
          F-HEMBA1005931//ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]//1.2e-46:228:100//Hs.
 45
          152178:AI224880
          F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:Al291588
          F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883
          F-HEMBA1005963
          F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.
          26285:AF082516
 50
          F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:Al127530
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F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.98:197:61//Hs.5184:AA709151

F-HEMBA1006036//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080

F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526

F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.41186:R99609

F-HEMBA1006002

F-HEMBA1006031

F-HEMBA1006035

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F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.43321:AI139422
         F-HEMBA1006081
         F-HEMBA1006090//EST//1.2e-12:340:62//Hs.61195:AI418788
         F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313
         F-HEMBA1006100//ESTs//7.1 e-22:273:73//Hs.144407:AA737799
         F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273:66//Hs.8763:W30741
         F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968
         F-HEMBA1006124//EST//0.047:251:62//Hs.132257:AI027222
         F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150:62//Hs.74061:X59372
10
         F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734
         F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:Al281881
         F-HEMBA1006155
         F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:N40575
         F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627
15
         F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117
         F-HEMBA1006198//ESTs//0.017:133:67//Hs.142168:AA292540
         F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98//Hs.109268:AF070557
         F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.7647:M94046
         F-HEMBA1006252
         F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:Al140706
20
         F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.00037:158:69//Hs.159277:
         F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631
         F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140
25
         F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770
         F-HEMBA1006283
         F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:Al189964
         F-HEMBA1006291
         F-HEMBA1006293
         F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.76:416:58//
30
         Hs 46465:U45285
         F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3e-49:637:68//Hs.37656:AB011174
         F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350
         F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789
         F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:Al032142
35
         F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.
         22767:N99220
         F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287
         F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107:X59244
40
         F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:Al351026
         F-HEMBA1006377//Homo sapiens RaIBP1-interacting protein (POB1) mRNA, complete cds//0.0028:422:59//Hs.
         80667:AF010233
         F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:
         265:61//Hs.8813:AF032922
         F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:Al042531
         F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1e-49:395:80//Hs.23094:M19503
         F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:Al077477
         F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:Al281881
         F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.51048:X68830
50
         F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:Al206835
         F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264
         F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:Al209194
         F-HEMBA1006445
         F-HEMBA1006446//EST//0.14:200:59//Hs.160695:AI282889
         F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210:72//Hs.51124:AF019369
55
         F-HEMBA1006467
         F-HEMBA1006471//ESTs//1.4e-05:391:60//Hs.121282:Al091453
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F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257:

# AA875998 F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081 F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532 F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897 F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.28621:AA910431 5 F-HEMBA1006492 F-HEMBA1006494//ESTs//8.5e -24:299:72//Hs.153413:Al248625 F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389 F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470:98//Hs.153858: 10 F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]//3.9e-98:483:97// Hs.94811:AA011185 F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002 F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:Al160081 15 F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173: 654:98//Hs21301:AF093419 F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638 F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79//Hs.21490:AB007898 F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:AI198425 20 F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136 F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.44372:Al346522 F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479 F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60//Hs.106387:AF029778 F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs.155464:AF088219 25 F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6e-38:441:69//Hs.23711:AB018295 F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862 F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:Al032875 F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION [S.cerevisiae]//2.5e-75:379:97//Hs.40911:Al391502 30 F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:Al343331 F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589 F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170: 92//Hs.109818:AA411185 F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259:65//Hs.105747: 35 AA505003 F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//3.9e-28:108:93//Hs.6196: 1140282 F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87: 452:96//Hs.159574:AA190615 40 F-HEMBA1006653 F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:438:98//Hs.8173:AC005189 F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//Hs.91916:AF035317

F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:122:90//Hs.5092:Y12065

F-HEMBA1006676 45

F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575

F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145

F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:Al128198

F-HEMBA1006708

F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545 50

F-HEMBA1006717//ESTs/12.6e-31:286:78//Hs.55573:W37226

F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105

F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087

F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//

2.0e-92:817:78//Hs.129727:AF035587 55

F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0e-10:576:56//Hs.149323:AB002325

F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs141073:W72720

F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:AI252657

- F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250
- F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:Al369798
- F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-37:781:64//Hs.23094:M19503
- F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.34054:U79298
- F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMO-SOME III [C.elegans]//4.8e-110:523:98/IHs.125790:AA287723
  - F-HEMBA1006821//EST//5.1e-li:246:66//Hs.150542:AI051551
  - F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624
  - F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970
- 10 F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327
  - F-HEMBA1006865
  - F-HEMBA1006877//ESTs, Highly similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938
  - F-HEMBA1006885//ESTs, Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC
- 15 REGION [Saccharomyces cerevisiae]//9.1e-128:805:87//Hs.32376:AA758214
  - F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592
  - F-HEMBA1006914//EST//0.065:366:6211Hs.162914:AA666199
  - F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:Al376989
  - F-HEMBA1006926//Human I kappa BR mRNA, complete cds//0.90:545:59//Hs.154764:U16258
- 20 F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539
  - F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W22712
  - F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:AI150382
  - F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//4.4e-92:437:98//Hs.42644: AJ010841
- 25 F-HEMBA1006949//H.sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6940:Z48633
  - F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.8e-144:740:94//Hs. 14934:AF004828
  - F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase//1.9e-79:447:89// Hs.75268:X74570
- 30 F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968
  - F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723
  - F-HEMBA1007002
  - F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282
  - F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete cds//2.5e-78:827:
- 35 70//Hs.43003:AF035812
  - F-HEMBA1007045
  - F-HEMBA1007051//EST//0.85:65:73//Hs.158641:Al370659
  - F-HEMBA1007052
  - F-HEMBA1007062
- 40 F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212
  - F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H37845
  - F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//6.7e-75:417:91//Hs.80510: M74002
  - F-HEMBA1007080
- 45 F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-06:568:61//Hs.1974:M92432
  - F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA, complete cds//0.95:541: 57//Hs.3828:U49260
  - F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595
  - F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA196354
- 50 F-HEMBA1007121//ESTs/l3.Se-69:335:98//Hs.140519:AA643182
  - F-HEMBA1007129
  - F-HEMBA1007147//ESTs//3.2e-07:235:641/Hs.124813:W46172
  - F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136
  - F-HEMBA1007151
- 55 F-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds//6.6e-64:318:97//Hs.22396:AF062085
  - F-HEMBA1007178//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-39:248:90//Hs.157148:AA311921
  - F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965

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AB011129

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F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.6e-158:478:98//Hs.3363:
D86987
F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252
F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//1.6e-177:839:98//Hs.27197:
F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//2.7e-56:647:69//Hs.
82314:M31642
F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//Hs.79706:U53204
F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:6411Hs.12432:AF070575
F-HEMBA1007267//Human homolog of yeast mutL (hPMS1) gene, complete cds//0.99:239:60//Hs.111749:
U13695
F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836
F-HEMBA1007279//ESTs//6. 1e-36:185:78//Hs.141022:H06475
F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529
F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637
F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:Al300062
F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-09:406:61//Hs.111913:Z74615
F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506
 F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634
 F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241
F-HEMBA1007327//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens]//3.5e-09:144:76//Hs.20597:
 W58370
 F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130
 F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006
 F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561
 F-HEMBB1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568
 F-HEMBB1000008//H.sapiens mRNA for translin associated protein X//1.1e-43:370:78//Hs.96247:X95073
 F-HEMBB1000018//Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)//1.0:108:70//Hs.
 83428:M58603
 F-HEMBB1000024//EST//5.4e-07:137:70//Hs.125389:AA878307
 F-HEMBB1000025//EST//0.99:362:58//Hs.121221:AA757392
 F-HEMBB1000030//H.sapiens mRNA for cylicin II//1.3e-10:525:62//Hs.3232:Z46788
 F-HEMBB1000036
 F-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//6.2e-102:450:
 98//Hs.20815:AF084928
 F-HEMBB1000039//EST//0.0034:97:73//Hs.141684:W35358
 F-HEMBB1000044//ESTs//0.0048:218:63//Hs.123161:AA807319
 F-HEMBB1000048//EST//0.00025:222:62//Hs.122474:AA765131
 F-HEMBB1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717
 F-HEMBB1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3e-54:259:88//Hs.23094:M19503
 F-HEMBB1000055//ESTs//0.0017:289:62//Hs.125755:AA286923
 F-HEMBB1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9e-59:286:84//Hs.93121:AB018304
 F-HEMBB1000083
 F-HEMBB1000089//EST//0.0016:192:661/Hs.137093:AA917621
 F-HEMBB1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645
 F-HEMBB1000103//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//4.9e-43:418:74//Hs.103948:K00627
  F-HEMBB1000113//EST//4.6e-23:221:76//Hs.142065:AA173763
  F-HEMBB1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521
  F-HEMBB1000136//ESTs112.3e-101:507:96//Hs.12659:AA195207
  F-HEMBB1000141//ESTs//2.1e-15:283:69//Hs.126257:Al279044
  F-HEMBB1000144//EST//4.5e-52:298:91//Hs.149580:Al281881
  F-HEMBB1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs.3057:X92715
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F-HEMBB1000175//EST//1.0:101:65//Hs.162898:AA659646 F-HEMBB1000198//EST//0.99:179:56//Hs.116880:AA662457

F-HEMBB1000215//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.4e-15:139:82//Hs.101414:

F-HEMBB1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X69962

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F-HEMBB1000240//H.sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y08612
        F-HEMBB1000244//ESTs//3.2e-15:139:81//HS.134549:Al078483
        F-HEMBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds//2.1e-156:735:981/Hs.
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        151411:AF075587
         F-HEMBB1000258//EST//0.0091:325:60//Hs.97533:AA435884
        F-HEMBB1000264//Human CHL1 potential helicase (CHLR1), complete cds//1.4e-33:100:100//Hs.27424:U75968
        F-HEMBB1000266//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.0019:373:60//Hs.
         16533:D87930
        F-HEMBB1000272//ESTs//1.3e-93:440:99//Hs.I09224:N46684
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        F-HEMBB1000274//ESTs//0.41:221:65//Hs.71990:AA151796
        F-HEMBB1000284//EST//0.00024:108:73//Hs.100725:F13689
        F-HEMBB1000307//EST//3.6e-10:149:73//Hs.140415:AA778574
         F-HEMBB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.00092:252:65//Hs.41153:
15
         AB018326
         F-HEMBB1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787
         F-HEMBB1000318//EST//0.014:184:61//Hs.155758:Al311870
         F-HEMBB1000335//EST//0.99:187:63//Hs.137424:AA243729
         F-HEMBB1000336//EST//1.0:209:63//Hs.150410:Al003611
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         F-HEMBB1000337//EST//0.086:133:66//Hs.128207:AA972330
         F-HEMBB1000338//EST//7.1e-07:129:72//Hs.140488:AA767127
         F-HEMBB1000339//Small inducible cytokine A5 (RANTES)//1.2e-36:336:7611Hs.155464:AF088219
         F-HEMBB1000341
         F-HEMBB1000343//EST//0.66:163:63//Hs.150822:Al302729
         F-HEMBB1000354//ESTs//7.e-61:292:100//Hs.152266:AA926874
25
         F-HEMBB1000369//ESTs, Highly similar to t-BOP [M.musculus]/10.013:157:64//Hs.129982:Al420970
         F-HEMBB1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934
         F-HEMBB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348
         F-HEMBB1000391//ESTs//0.033:237:64//Hs.135289:Al092963
         F-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//9.4e-165:762:98//Hs.16184:AJ001642
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         F-HEMBB1000402//EST//0.013:291:59//Hs.149191:Al246155
         F-HEMBB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194
         F-HEMBB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925
         F-HEMBB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//9.4e-73:364:83//Hs.
35
         129735AF010144
         F-HEMBB1000438//ESTs//0.073:446:58//Hs.134632:AI223429
         F-HEMBB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627
         F-HEMBB1000449//EST//5.5e-21:356:671/Hs.157848:AI362501
         F-HEMBB1000455//ESTs//0.092:147:65//Hs.106446:N93227
         F-HFMBB1000472
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         F-HEMBB1000480//EST//0.98:83:71//Hs.146462:Al124898
         F-HEMBB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206
         F-HEMBB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI057560
         F-HEMBB1000491
         F-HEMBB1000493//ESTs//0.019:103:69//Hs.138358:T66178
45
         F-HEMBB1000510//Glucocorticoid receptor alpha {alternative products}//1.6e-46:409:77//Hs.102761:U25029
         F-HEMBB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413
         F-HEMBB1000523//ESTs//0.69:332:59//Hg.106845:W19543
         F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus//2.1e-38:138:
         96//Hs.36131:Y11710
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         F-HEMBB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//7.7e-31:
         554:67//Hs.157142:U85996
         F-HEMBB1000554//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-27:282:75//Hs.
         158095:AB007953
         F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds//2.0e-33:537:65//Hs.5444:
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         AB018293
         F-HEMBB1000564
         F-HEMBB1000573//H.sapiens HCG II mRNA//7.5e-27:197:76//Hs.146333:X81001
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F-HEMBB1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.78160:AF010238
        F-HEMBB1000586//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164,
        DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:M18533
        F-HEMBB10005891/PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79//Hs.73734:Z23091
        F-HEMBB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71990
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        F-HEMBB1000592//EST//0.0038:51:88//Hs.148022:Al269323
        F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:503:99//Hs.3386:AF053356
        F-HEMBB1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U66589
        F-HEMBB1000623//H.sapiens mRNA for GAIP protein//0.89:376:59//Hs.22698:X91809
        F-HEMBB1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:168:61//Hs.105850:AB007864
10
        F-HEMBB1000631//ESTs//1.7e-06:247:64//Hs.156864:Al346481
        F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-50:811:65//Hs.29963:AB002349
        F-HEMBB1000637//Sialophorin (gpL115, leukosialin, CD43)//2.4e-79:304:85//Hs.80738:X52075
         F-HEMBB1000638//EST//0.0076:92:75//Hs.125496:AA883735
        F-HEMBB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:74//Hs.51048:X68830
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         F-HEMBB1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.4e-52:533:75//Hs.51011:L19778
         F-HEMBB1000652//ESTs//1.6e-49:345:84//Hs.132722;AA618531
         F-HEMBB1000665//EST//0.44:152:63//Hs.149534:Al280924
         F-HEMBB1000671//Human Line-1 repeat mRNA with 2 open reading frames//2.2e-79:280:85//Hs.23094:M19503
         F-HEMBB1000673//ESTs//0.99:177:59//Hs.149864:N80474
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         F-HEMBB1000684//Protein kinase, interferon-inducible double stranded RNA-dependent//2.6e-31:220:87//Hs.
         73821:M35663
         F-HEMBB1000693//Homo sapiens neuroanl mRNA, complete cds//5.3e-120:575:97//Hs.158300:AF040723
         F-HEMBB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125
         F-HEMBB1000706//EST//8.6e-14:373:61//Hs.138281:RS5703
25
         F-HEMBB1000709//EST//0.99:110:651/Hs.162437:AA577510
         F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.123109:X56741
         F-HEMBB1000726//EST//1.3e-43:257:84//Hs.162197:AA535216
         F-HEMBB1000738//EST//5.9e-13:259:64//Hs.159699:Al417328
         F-HEMBB1000749//EST//3.1e-42:271:871/Hs.162197:AA535216
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         F-HEMBB1000763
         F-HEMBB1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOLOG [D.melanogaster]//0.021:111:
         72//Hs.38178:AA921830
         F-HEMBB1000774//ESTs, Weakly similar to mTERF [H.sapiens]//2.5 e-116:580:97//Hs.5009:AA081390
         F-HEMBB1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:426:74//Hs.86201:U78876
35
         F-HEMBB1000789//Homosapiens mRNA for KIAA0677 protein, complete cds//3.0e-65:672:71//Hs.155983:
         AB014577
         F-HEMBB1000790//ESTs//1.2e-52:344:86//Hs.35254:Al133727
         F-HEMBB1000794//ESTs//0.00098:289:59//Hs.138782:N73572
         F-HEMBB1000807//ESTs//2.1e-91:434:99//Hs.61334:Al298375
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          F-HEMBB1000810//ESTs//0.038:92:71//Hs.148763:AA66887
          F-HEMBB1000821//EST//0.94:129:62//Hs.162299:AA555154
          F-HEMBB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421
          F-HEMBB1000826//ESTs//4.8e-13:343:65//Hs.153429:Al283069
          F-HEMBB1000827
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          F-HEMBB1000831
          F-HEMBB1000835//EST//4.3e-27:201:851/Hs.141451:N29915
          F-HEMBB1000840//EST//6.3e-75:380:96//Hs.142557:AA464948
         F-HEMBB1000848//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-135:875:85//Hs.23094:
 50
          F-HEMBB1000852//Phosphoribosyl pyrophosphate amidotransferase//0.12:292:61//Hs.311:U00238
          F-HEMBB1000870//EST//0.00091:246:62//Hs.126502:AA913831
          F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:200:94//Hs.128434:AF085351
          F-HEMBB1000883//ESTs//0.42:107:67//Hs.154173:Al379823
          F-HEMBB1000887
 55
          F-HEMBB1000888//ESTs//1.0:137:67//Hs.8121:AA521290
          F-HEMBB1000890//ESTs//1.0:116:65//Hs.7105:T23433
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F-HEMBB1000893//EST//0.0079:408:58//Hs.146504:AI129834

- EP 1 074 617 A2 F-HEMBB1000908//EST//9.2e-21:205:79//Hs.132635:Al032875 F-HEMBB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:327:60//Hs.7938:D86984 F-HEMBB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049 F-HEMBB1000915//ESTs//2.5e-90:423:99//Hs.135254:Al095468 F-HEMBB1000917//EST//2.8e-49:241:100//Hs.162216:AA548089 F-HEMBB1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593 F-HEMBB1000947 F-HEMBB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//9.3e-48:572:72//Hs.2379:U23942 F-HEMBB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938 F-HEMBB1000975//ESTs//0.78:180:66//Hs.104789:AA417124 F-HEMBB1000981 F-HEMBB1000985//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.7e-07:308:62//Hs. 122967:AF059569 F-HEMBB1000991//EST//0.12:125:66//Hs.22945:R43713 F-HEMBB1000996//ESTs//6.9e-05:273:63//Hs.133116:AI054055 F-HEMBB1001004//Homo sapiens mRNA for KIAA0665 protein, complete cds//0.62:193:62//Hs.119004: F-HEMBB1001008//EST//4.7e-09:203:65//Hs.105221:AA489025 F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//2.4e-17:384:67//Hs.108604: F-HEMBB1001014//EST, Weakly similar to putative p150 [H.sapiens]//0.21:284:60//Hs.161547:W04991 F-HEMBB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247 F-HEMBB1001024//ESTs, Highly similar to t-BOP [M.musculus]//0.11:242:61//Hs.129982:Al420970 F-HEMBB1001037//EST//0.0057:192:66//Hs.149987:AI291177 F-HEMBB1001047//ESTs//1.6e-22:360:70//Hs.120734:W58721 F-HEMBB1001051//H.sapiens mRNA for FAN protein//3.8e-29:160:98//Hs.78687:X96586 F-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.0e-42:149:96//Hs.15832: AB014518 F-HEMBB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349:82//Hs.155464:AF088219 F-HEMBB1001060//ESTs//1.6e-62:464:81//Hs.138663:N24942 F-HEMBB1001063 F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-148:736:95//Hs.12953:AF034803 F-HEMBB1001096//EST//0.017:154:66//Hs.130403:AA909272 F-HEMBB1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293 F-HEMBB1001105//Human BRCA2 region, mRNA sequence CG016//0.30:84:75//Hs.112434:U50529 F-HEMBB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//9.3e-38:341:77//Hs.14038:R06800 F-HEMBB1001114//EST//6.4e-07:296:62//Hs.128420:AA975062 F-HEMBB1001117//EST//1.6e-99:464:99//Hs.130493:AA928139 F-HEMBR1001119 F-HEMBB1001126 F-HEMBB1001133//H.sapiens mRNA for translin associated protein X//1.2e-28:739:61//Hs.96247:X95073 F-HEMBB1001137
- F-HEMBB1001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23:340:69//Hs.146395:AB002329 45
- F-HEMBB1001151//ESTs//2.6e-30:252:79//Hs.6880:W26854

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- F-HEMBB1001153//ESTs//7.6e-16:97:96//Hs.113307:H16716
- F-HEMBB1001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863
- F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:66//Hs.73073:D78334
- F-HEMBB1001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN 50 HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:100//Hs.86878:AA599183
  - F-HEMBB1001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:199:64//Hs.74047:X71129 F-HEMBB1001199
  - F-HEMBB1001208//ESTs//0.12:120:69//Hs.130093:AA928802
- F-HEMBB1001209//EST//0.00028:215:65//Hs.118276:W15258 55
  - F-HEMBB1001210//EST//2.9e-05:297:60//Hs.88840:AA281452
  - F-HEMBB1001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5e-37:260:76//Hs.72660:AB011157 F-HEMBB1001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//0.00046:650:58//Hs.

- 158241:AB007976
- F-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Mus musculus]//6.7e-103:477: 100//Hs.127835:AI378790
- F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds//1.2e-31:458:67//Hs.129918:AB005754
- 5 F-HEMBB1001249//EST//0.26:203:63//Hs.140791:AA935909
  - F-HEMBB1001253//ESTs//4.0e-91:433:98//Hs.120636:AA325219
  - F-HEMBB1001254//ESTs//2.0e-24:180:85//Hs.136391:H04977
  - F-HEMBB1001267//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//6.1e-24:146: 78//Hs.51187:U82828
- 10 F-HEMBB1001271//ESTs//2.5e-05:686:58//Hs.115423:Al359248
  - F-HEMBB1001282//GA-binding protein transcription factor, beta subunit 2 (47kD)//0.39:531:57//Hs.78915: U13045
  - F-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//4.9e-10:91:89//Hs.16606:W81021
- 15 F-HEMBB1001289//ESTs//6.4e-100:467:99//Hs.151720:Al287890
  - F-HEMBB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.3e-135:654:98//Hs. 124217:AA020848
  - F-HEMBB1001302
  - F-HEMBB1001304//ESTs//0.98:109:68//Hs.138972:AA047725
- 20 F-HEMBB1001314//ESTs//7.4e-39:285:77//Hs.144749:Al217339
  - F-HEMBB1001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs.155464:AF088219
  - F-HEMBB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98:625:85//Hs.23094:M19503 F-HEMBB1001326//ESTs//0.00030:257:63//Hs.62208:H12380
  - F-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//1.0e-48:332:87//Hs.43071:AA206222
- 25 F-HEMBB1001335
  - F-HEMBB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56:282:87//Hs.15731: AB011135
  - F-HEMBB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694 F-HEMBB1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878
- 30 F-HEMBB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293: AB011142
  - F-HEMBB1001356//EST//0.32:292:59//Hs.135771:Al005648
  - F-HEMBB1001364
  - F-HEMBB1001366//EST//7.8e-24:367:69//Hs.138765:N70347
- 35 F-HEMBB1001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs.155464:AF088219
  - F-HEMBB1001369//EST//0.17:211:63//Hs.120066:AA707973
  - F-HEMBB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36:225:79//Hs.129748: AB011099
  - F-HEMBB1001384
- 40 F-HEMBB1001387//ESTs//0.61:215:60//Hs.145915:Al342230
  - F-HEMBB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94:568:83//Hs.23094:M19503
  - F-HEMBB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750: AF065988
  - F-HEMBB1001424//EST//0.20:307:58//Hs.135336:AI049827
- 45 F-HEMBB1001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//Hs.83466:AF038174
  - F-HEMBB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]//5.5e-153:729:96//Hs. 21679:AF034175
  - F-HEMBB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345 F-HEMBB1001443
- 50 F-HEMBB1001449//Homo sapiens sodium bicarbonate cotransporter (HNBC1) mRNA, complete cds//0.033:478: 58//Hs.5462:AF007216
  - F-HEMBB1001454//ESTs//1.4e-46:279:93//HS.104866:AA426038
  - F-HEMBB1001458//EST//1.7e-09:106:83//Hs.141422:N20920
  - F-HEMBB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220
- 55 F-HEMBB1001464//Homo sapiens Coch-5B2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740
  - F-HEMBB1001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27:292:74//Hs.137168: AB018303
  - F-HEMBB1001500//ESTs//8.1e-28:312:74//Hs.18498:N52088

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F-HEMBB1001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.
46328:D87942
F-HEMBB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815
F-HEMBB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735
F-HEMBB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093
F-HEMBB1001536//ESTs//0.0047:120:68//Hs.144858:R67748
F-HEMBB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-
20:297:73//Hs.42457:AA523306
F-HEMBB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//
Hs.102877:U41315
F-HEMBB1001562//ESTs//0.95:161:61//Hs.145075:Al208240
F-HEMBB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.
158095:AB007953
F-HEMBB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080
F-HEMBB1001585
F-HEMBB1001586//EST//0.84:132:64//Hs.145264:Al218708
F-HEMBB1001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.90798:U79289
F-HEMBB1001603//ESTs//1.3e-12:84:96//Hs.13380:R60414
F-HEMBB1001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680
F-HEMBB1001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314
F-HEMBB1001630//EST//1.4e-07:334:62//Hs.145698:AI266713
F-HEMBB1001635//ESTs//0.92:282:60//Hs.126980:AA934077
F-HEMBB1001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.116549:AL009172
F-HEMBB1001641//EST//0.11:53:81//Hs.112445:AA594279
F-HEMBB1001653//EST//0.91:124:64//Hs.144213:T40480
F-HEMBB1001665//Human mRNA for apolipoprotein E receptor 2, complete cds//7.0e-13:473:63//Hs.54481:
F-HEMBB1001668//ESTs//0.94:83:69//Hs.146202:AI252519
F-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.3e-172:803:98//Hs.24439:
F-HEMBB1001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:100//Hs.106104:AA599496
F-HEMBB1001685//EST//2.2e-05:112:73//Hs.130984:Al015430
F-HEMBB1001695//Human novel homeobox mRNA for a DNA binding protein//1.6e-08:425:62//Hs.37035:U07664
F-HEMBB1001704//EST//5.8e-20:295:69//Hs.140231:AI054398
F-HEMBB1001706
F-HEMBB1001707//EST//0.091:241:60//Hs.136830:AA769219
F-HEMBB1001717//ESTs//2.9e-06:325:60//Hs.150063:AI298064
F-HEMBB1001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs.155464:AF088219
F-HEMBB1001736//ESTs, Weakly similar to E04D5.1 [C.elegans]//5.4e-99:485:97//Hs.120581:W25578
F-HEMBB1001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244
F-HEMBB1001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.5e-75:315:83//Hs.
 129735:AF010144
 F-HEMBB1001753//ESTs//0.00013:35:100//Hs.139643:H06263
 F-HEMBB1001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077
 F-HEMBB1001760//ESTs//6.5e-06:503:58//Hs.21766:Al357639
 F-HEMBB1001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//2.9e-13:498:60//Hs.
 158241:AB007976
 F-HEMBB1001785//EST//0.16:262:60//Hs.162526:AA584102
 F-HEMBB1001797//ESTs//0.37:201:63//Hs.91559:AA806370
 F-HEMBB1001802//ESTs//1.6e-06:447:58//Hs.134672:AI087951
 F-HEMBB1001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.3e-54:311:81//Hs.
 92381:AB007956
 F-HEMBB1001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017
 F-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//7.6e-
 164:763:98//Hs.159396:AF056209
 F-HEMBB1001834//TRICHOHYALIN//7.1e-05:548:60//Hs.82276:L09190
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F-HEMBB1001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:86//Hs.22271:D26067

F-HEMBB1001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370

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F-HEMBB1001850//EST//0.0035:204:61//Hs.7311:T23858
        F-HEMBB1001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357:82//Hs.155464:AF088219
        F-HEMBB1001867//ESTs//2.2e-40:265:88//Hs.146323:Al251752
        F-HEMBB1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371
        F-HEMBB1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503
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        F-HEMBB1001872
        F-HEMBB1001874//H.sapiens mRNA for CHD5 protein//0.0033:388:60//Hs.19923:Y12478
        F-HEMBB1001875//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//0.32:346:60//Hs.
        F-HEMBB1001880//EST//4.0e-28:171:92//Hs.151194:AI125868
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        F-HEMBB1001899//ESTs//0.17:242:62//Hs.136969:AA830918
         F-HEMBB1001905
         F-HEMBB1001906//ESTs//5.6e-49:290:92//Hs.127298:H09155
         F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//1.2e-83:672:
15
         81//Hs.82210:U47742
         F-HEMBB1001910//EST, Weakly similar to albumin [H.sapiens]//0.047:206:62//Hs.159777:Z19955
         F-HEMBB1001911
         F-HEMBB1001915//ESTs//0.92:136:71//Hs.144465:R68882
         F-HEMBB1001921//EST//2.0e-19:398:67//Hs.44789:N36113
         F-HEMBB1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245
20
         F-HEMBB1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398
         F-HEMBB1001930//EST//0.043:157:63//Hs.161927:AA483904
         F-HEMBB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:80//Hs.154326:D42087
         F-HEMBB1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875
         F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:66//Hs.40100:AB002390
25
         F-HEMBB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:384:60//Hs.8546:U97669
         F-HEMBB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101
         F-HEMBB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//Hs.96:D90070
         F-HEMBB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418
         F-HEMBB1001962//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//2.3e-31:390:
30
         70//Hs.1361:M55053
         F-HEMBB1001967//H.sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969
         F-HEMBB1001973//Myelin oligodendrocyte glycoprotein {alternative products}//2.1e-48:426:78//Hs.53217:
         F-HEMBB1001983
35
         F-HEMBB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051
         F-HEMBB1001990//ESTs//0.25:171:64//Hs.7961:AA401205
         F-HEMBB1001996//ESTs//1.8e-19:436:65//Hs.125539:Al339103
         F-HEMBB1001997//EST//5.3e-33:294:76//Hs.161041:H82636
         F-HEMBB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964
40
         F-HEMBB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093
         F-HEMBB1002009//ESTs//0.066:441:58//Hs.125313:Al201685
         F-HEMBB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951
         F-HEMBB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699
         F-HEMBB1002043//ESTs, Weakly similar to T06E6.d [C.elegans]//1.0:217:60//Hs.3487:AA425553
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         F-HEMBB1002044
         F-HEMBB1002045
         F-HEMBB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.082:201:61//Hs.88756:AB018256
         F-HEMBB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2557:Y00661
         F-HEMBB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1e-07:402:61//Hs.112499:
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         AB014512
         F-HEMBB1002069
         F-HEMBB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239
          F-HEMBB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625
          F-HEMBB1002115//EST//0.0083:244:64//Hs.125353:AA877080
55
         F-HEMBB1002134//ESTs//1.7e-69:398:91//Hs.157492:Al361027
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F-HEMBB1002139//ESTs//0.64:145:71//Hs.157821:Al362013 F-HEMBB1002142//ESTs//0.013:311:59//Hs.150037:Al292214

- F-HEMBB1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254
- F-HEMBB1002189//EST//0.26:81:70//Hs.147726:AI220208
- F-HEMBB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.16:608:58//Hs.4:X03350
- F-HEMBB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//Hs.301:U18934
- F-HEMBB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:405:67//Hs.104115:X52332
  - F-HEMBB1002218//EST//0.015:241:61//Hs.105298:AA489813
  - F-HEMBB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs.155464:AF088219
  - F-HEMBB1002247
  - F-HEMBB1002249//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//
- 10 6.8e-47:418:77//Hs.125231:AF068006
  - F-HEMBB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0e-47:437:77//Hs.154872: AB011166
  - F-HEMBB1002255//ESTs//0.017:255:61//Hs.126786:U74314
  - F-HEMBB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA, complete cds//0.17:511:57//
- 15 Hs.58169:AF017790
  - F-HEMBB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998
  - F-HEMBB1002300
  - F-HEMBB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.3e-14:228:72//Hs. 46468:U45984
- 20 F-HEMBB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083
  - F-HEMBB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:399:96//Hs.105837:AA536054
  - F-HEMBB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188
  - F-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//1.4e-155:724:98//Hs.42644: AJ010841
- 25 F-HEMBB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991
  - F-HEMBB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//1.7e-06:66:96//Hs.154762:
  - F-HEMBB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838
  - F-HEMBB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796
- 30 F-HEMBB1002381

- F-HEMBB1002383//vasoactive intestinal peptide receptor 2//0.98:190:63//Hs.2126:L36566
- F-HEMBB1002387//EST//2.1e-07:253:61//Hs.145993:Al277784
- F-HEMBB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456
- F-HEMBB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.0e-32:371:73//Hs. 159897:AB007970
  - F-HEMBB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.54486:X54150
    - F-HEMBB1002442
    - F-HEMBB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:77//Hs.154326:D42087
    - F-HEMBB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101
- 40 F-HEMBB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274
  - F-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds//6.0e-89:493:92//Hs.159605:U43885
  - F-HEMBB1002489//Homo sapiens 195 kDa comified envelope precursor mRNA, complete cds//0.019:228:63// Hs.74304;AF001691
  - F-HEMBB1002492//EST//0.24:149:62//Hs.146790:Al149051
- F-HEMBB1002495//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//1.3e-22:331:71//Hs.30:
  - F-HEMBB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494
  - F-HEMBB1002509//ESTs//0.017:220:63//Hs.155263:Al273725
  - F-HEMBB1002510//ESTs//6.4e-102:476:99//Hs.152289:Al247354
- 50 F-HEMBB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-50:580:72//Hs.23094:M19503
  - F-HEMBB1002522//EST//0.010:172:62//Hs.147224:Al205719
  - F-HEMBB1002531
  - F-HEMBB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs.155464:AF088219
  - F-HEMBB1002545//ESTs//3.9e-24:181:86//Hs.13753:Al088102
- 55 F-HEMBB1002550//Syntaxin 5A//0.27:354:59//Hs.154546:U26648
  - F-HEMBB1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191
  - F-HEMBB1002579//EST//1.0:77:68//Hs.147935:Al250286
  - F-HEMBB1002582//ESTs//0.00032:178:68//Hs.139163:AA226095

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F-HEMBB1002590//ESTs//0.64:132:63//Hs.155688:AI003657
        F-HEMBB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336
        F-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-152:710:98//Hs.129826:
        AF089749
        F-HEMBB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817
5
        F-HEMBB1002603//EST//0.10:144:63//Hs.158180:Al367945
        F-HEMBB1002607//ESTs//0.024:345:62//Hs.143304:Al084058
        F-HEMBB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323
        F-HEMBB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711
        F-HEMBB1002614//ESTs//0.0048:136:71//Hs.106280:R13901
10
        F-HEMBB1002617//EST//0.034:320:59//Hs.41223:H89127
        F-HEMBB1002623//ESTs//0.88:222:60//Hs.129920:AA167217
        F-HEMBB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs.151051:U07620
         F-HEMBB1002664//EST//0.00013:203:61//Hs.117141:AA678811
        F-HEMBB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680
15
        F-HEMBB1002683//ESTs//0.23:224:61//Hs.128883:Al026679
        F-HEMBB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124
        F-HEMBB1002686//EST//0.25:189:62//Hs.132431:AA909674
         F-HEMBB1002692//ESTs//0.00020:162:66//Hs.118180:N68504
         F-HEMBB1002697//EST//7.2e-17:219:74//Hs.100459:T61992
20
         F-HEMBB1002699//Homo sapiens transmembrane activator and CAML interactor (TACI) mRNA, complete cds//
         0.059:297:62//Hs.158341:AF023614
         F-HEMBB1002702//ESTs//0.26:284:61//Hs.41250:H89588
         F-HEMBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SUI2-TDH2 INTERGENIC
         REGION [Saccharomyces cerevisiae]//0.0048:84:83//Hs.20814:Al242922
25
         F-HEMBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729
         F-MAMMA1000009//Human c-yes-1mRNA//1.0e-48:447:77//Hs.75680:M15990
         F-MAMMA1000019
         F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750
         F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945
30
         F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739
         F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461
         F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//2.7e-18:330:63//Hs.59906:
         AA001281
         F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.2e-
35
         50:367:75//Hs.133089:AF064019
         F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:Al336840
         F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067
         F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:
40
         F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//
         Hs.90357:U40705
         F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:
         AB011792
         F-MAMMA1000117
45
         F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508
         F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402
         F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319
         F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:Al383843
         F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:
50
         AB014585
         F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:
         219:87//Hs.129724:AF031924
         F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050
         F-MAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695
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F-MAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:65//Hs.89434:D17530

F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763

F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657

- F-MAMMA1000198//ESTs//0.0092;235;62//Hs.98783;AI091739
- F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035
- F-MAMMA1000227//ESTs//0.010:268:60//Hs.16412:AA506926
- F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913
- 5 F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873
  - F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:Al247587
  - F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:Al003543
  - F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015
  - F-MAMMA1000266//EST//0.14:270:60//Hs.132593:Al031874
- 10 F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087
  - F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726
  - F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:Al347361
  - F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505 F-MAMMA1000284
- 15 F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087
  - F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641
  - F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243
  - F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529
  - F-MAMMA1000312//EST//0.042:183:63//Hs.158928:Al379519
- 20 F-MAMMA1000313
  - F-MAMMA1000331
  - F-MAMMA1000339
  - F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//Hs.13096:AA180963
- 25 F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892
  - F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs. 158095:AB007953
  - F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-75:498:85//Hs.23094:M19503
  - F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:85//Hs.154326:D42087
- 30 F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569
  - F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344
  - F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710: 98//Hs.32170:AB015132
  - F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590
- 35 F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-58:834:68//Hs.23094:M19503
  - F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08: 117:84//Hs.83916:U53468
  - F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:Al200725
  - F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092
- F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111
  - F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532
  - F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:
- 45 F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459
  - F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:Al377641
  - F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102: AF034546
  - F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830
- 50 F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872: AB011166
  - F-MAMMA1000446
  - F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [C.elegans]//5.1e-08:58: 93//Hs.9043:W21827
- F-MAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, complete cds//0.58:311:63//Hs.66721:D49818
  - F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830
  - F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080

- F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830 F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948 F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482 F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219 F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878 5 F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352 F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497 F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352 F-MAMMA1000565 F-MAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete 10 cds//5.8e-51:404:80//Hs.125231:AF068006 F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045 F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:Al276780 F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//8.8e-45:390:78//Hs.159523:AF001622 15 F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744 F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886 F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519 F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300:60//Hs.29207:AF071494 F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478 20 F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605 F-MAMMA1000623 F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.98614:AF006751 F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//0.092:365:59//Hs.75474: 25 F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353 F-MAMMA1000669//Human kpni repeat mma (cdna clone pcd-kpni-4),3' end//9.0e-30:531:64//Hs.139107: F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:Al244490 F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4316:U80743 30 F-MAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//3.3e-07:249:62//Hs.44481: F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627 F-MAMMA1000707//ESTs//1.4e-09:225:65//Hs.138722:N51081 F-MAMMA1000713//Acetylcholinesterase {I4-E5 doman} [human, tumor cell lines, Genomic, 847 nt]//0.16:84:72// 35 Hs.157124:S71129 F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263:6//Hs.27414:U79275 F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210:66//Hs.71148:AA854648 F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247 F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288:72//Hs.114685: 40 AA700024 F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs.22670:AF006513 F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-40:288:78//Hs. 158095:AB007953 F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//Hs.1742:L33075 45 F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802:98//Hs.31575: AF100141 F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580 F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323:88//Hs.153468: 50 F-MAMMA1000746//ESTs//2.3e-42:409:76//Hs.61199:AA024494
  - F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285:68//Hs.162011:AA513663
  - F-MAMMA1000760//Myelin oligodendrocyte glycoprotein {alternative products}//6.2e-47:341:82//Hs.53217: Z48051
- 55 F-MAMMA1000761//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]// 9.8e-19:131:76//Hs.118972:AA761369
  - F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288
  - F-MAMMA1000776//ESTs//5.5e-43:154:84//Hs.141581:AA315361

- F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114
- F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137
- F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575
- F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849
- 5 F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130
  - F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:Al298089
  - F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e48:241:74//Hs.155464:AF088219

F-MAMMA1000841

- F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//0.18:483:59//
- 10 Hs.82210:U47742

- F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696
- F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877
- F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022
- F-MAMMA1000855
- 15 F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:320:59//Hs.71388:AF032906
  - F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135
  - F-MAMMA1000862//EST//1.0:92:66//Hs.157599:Al357342
  - F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172
  - F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812
- 20 F-MAMMA1000867//EST//0.027:236:60//Hs.147156:Al191777
  - F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59//Hs.75850:D87459
  - F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147
  - F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-91: 484:94//Hs.138938;AA012894
- 25 F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812
  - F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465
  - F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3//2.6e-06:211:63//Hs.76716:
  - F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683
- 30 F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506
  - F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081
  - F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628
  - F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:Al125239
  - F-MAMMA1000931//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.0e-25:312:66//Hs. 116007:S79267
  - F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968
    - F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785
    - F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734
- 40 F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63//Hs.83790:AB002303
  - F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:64//Hs.25640:AB000714
  - F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474
  - F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-56:310:85// Hs.129735:AF010144
- 45 F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814
  - F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096
  - F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802
  - F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062
  - F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007
- 50 F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:Al003724
  - F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711
  - F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451: Y15718
  - F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968
- F-MAMMA1001030//Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete cds//3.6e-32:753: 61//Hs.98384:AF062006
  - F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857
  - F-MAMMA1001038

- F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//Hs.119000:M95178
- F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:Al419882
- F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs. 135623:AA134719
- F-MAMMA1001067//EST//0.30:166:60//Hs.148441:AI198503 5
  - F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585
  - F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116
  - F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs. 135251:L09749
- F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503 10 F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420
  - F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896
  - F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333: AB018254
- F-MAMMA1001092//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948: 15
  - F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66// Hs.97905:AF016045
  - F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915
- F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219 20
  - F-MAMMA1001133
  - F-MAMMA1001139
  - F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:Al091534
  - F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217
- F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741 25
  - F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468: AB011147
  - F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:AI014299
  - F-MAMMA1001181
- F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47: 30 313:81//Hs.97203:U83171
  - F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083
  - F-MAMMA1001198
  - F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348
- F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974 35
  - F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.5e-25: 275:75//Hs.105292:AA504776
  - F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200
  - F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:84//Hs.154326:D42087
- F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898: 40 AB014534
  - F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587
  - F-MAMMA1001244

- F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:AI220476
- F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:AI160121
  - F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149
  - F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:
  - F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503
- F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747 50
  - F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522
  - F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832
  - F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998
  - F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA757426
- F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305 55
  - F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat// 1.9e-58:295:97//Hs.102336:Z83838

- F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087
- F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:745:73//Hs.93174:X57147
- F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806
- F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197
- 5 F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267
  - F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cds//0.94:89:75//Hs.109358:AB018258
  - F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.3e-49:273:80//Hs.42674:U61981
  - F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR//4.6e-09:415:58//Hs.839:M86826
- 10 F-MAMMA1001397//Prostaglandin I2 (prostacyclin) synthase //1.3e-26:358:67//Hs.61333:D83402
  - F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763
  - F-MAMMA1001411//Autosomal dominant polycystic kidney disease type II//1.0:176:64//Hs.82001:U50928
  - F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:409:80//Hs.43681:AL022394
  - F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//0.00042:125:75//Hs.
- 15 46328:D87942
  - F-MAMMA1001435//Human HsLIM15 mRNA for HsLim15, complete cds//8.2e-43:543:71//Hs.37181:D64108
  - F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321
  - F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590
  - F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:Al424040
- 20 F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053
  - F-MAMMA1001476//Human mRNA for 5'-terminal region of UMK, complete cds//2.0e-24:273:72//Hs.75939: D78335
  - F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//3.2e-25:397:68//Hs.116874: AA524909
- 25 F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366
  - F-MAMMA1001502//Human p120E4F transcription factor mRNA, complete cds//0.99:258:61//Hs.154196:U87269
  - F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795
  - F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:Al018506
  - F-MAMMA1001547
- F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds//7.5e-130:614:98//Hs.129937: AB007931
  - F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//0.71:181:62//Hs.118866: AI017072
  - F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150785:M61764
- 35 F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339
  - F-MAMMA1001600//EST/1.0e-08:81:87//Hs.149220:Al247132
  - F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375
  - F-MAMMA1001606//Human clone 23627 mRNA, complete cds//0.64:336:58//Hs.23642:U79266
  - F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152
- 40 F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58//Hs.158229:U28727
  - F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of antigen Kl-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a protein gene. Contains a DXS1003 and SSTs, STSs and GSSs and genomic markers DXS1003 and
- 45 DXS1055//1.4e-40:447:73//Hs.154353:AL022165
  - F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds//3.6e-44:611:67//Hs.57679:U57796 F-MAMMA1001635
  - F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524
  - F-MAMMA1001654//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.00069:140: 68//Hs.59829:AB014602
  - F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.015:135:71//Hs.27349: AR007917
  - F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sapiens]//0.064:472:60//Hs.110819: Al027548
- 55 F-MAMMA1001671

- F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA573317
- F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA036889
- F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:Al138765

F-MAMMA1001692//ESTs//0.97:104:70//Hs.27596:AI188549

F-MAMMA1001711//Human G protein-coupled receptor (STRL22) mRNA, complete cds//8.0e-45:323:83//Hs. 46468-Ll45984

F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs.130815:AA936548

5 F-MAMMA1001730//ESTs//0.048:198:65//Hs.116412:AA506926

F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//1.5e-111:725:84//Hs. 159154:U47634

F-MAMMA1001740//EST//0.77:119:65//Hs.148140:AA887098

F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs.163688:H48768

10 F-MAMMA1001744//EST//0.00019:134:70//Hs.146863:Al161245

F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-67:822:69//Hs.23094:M19503 F-MAMMA1001751//Homo sapiens two P domain potassium channel subunit (HOHO1) mRNA, complete cds//1.0e-36:583:65//Hs.79351:U33632

F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs.157928:AA775822

15 F-MAMMA1001757//EST//0.042:177:63//Hs.144436:R07109

F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense transcript, partial//6.6e-41:309:84//Hs. 102576:AJ010230

F-MAMMA1001764//ESTs//0.057:290:60//Hs.68647:AA524072

F-MAMMA1001768//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds// 2.2e-05:504:60//Hs.96028:AF042832

F-MAMMA1001769//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-85:686:79//Hs.113283:AF018080 F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete cds//0.00071:392:60//Hs.32981: L138276

F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs.142524:H02940

25 F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs.61809:AA503549

F-MAMMA1001788//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//6.7e-21:212:77//Hs.103948: K00627

F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:139:72//Hs.5158:AB007869

F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs.105665:H78987

30 F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs.98613:D83884

F-MAMMA1001815//EST//2.1e-56:374:85//Hs.141488:N47096

F-MAMMA1001817//EST//8.6e-39:336:78//Hs.162236:AA551582

F-MAMMA1001818//EST//0.32:375:58//Hs.72729:AA167589

F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA, complete cds//0.082:153:66//

35 Hs.114948:AF059293

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F-MAMMA1001824//EST//0.0013:195:63//Hs.129275:AA992742

F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs.92290:R78691

F-MAMMA1001837/Homo sapiens mRNA for zinc finger protein FPM315, complete cds//2.0e-29:641:62//Hs. 56808:D88827

40 F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs.116430:AA644665

F-MAMMA1001851//ESTs//0.00050:251:64//Hs.163776:Al393028

F-MAMMA1001854

F-MAMMA1001858//EST//1.0:113:68//Hs.132482:AA922218

F-MAMMA1001864//EST//1.3e-06:399:60//Hs.161500:N68060

F-MAMMA1001868//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.084:672:58//
Hs.152455:AF044209

F-MAMMA1001874//ESTs//0.97:292:58//Hs.24553:AI150687

F-MAMMA1001878

F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs.15776:T91944

50 F-MAMMA1001890//EST//1.7e-85:440:97//Hs.128842:AA977576

F-MAMMA1001907//EST//2.7e-26:294:74//Hs.98794:AA434078

F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs.146145:Al391521

F-MAMMA1001931//ESTs//1.0:108:67//Hs.126624:AA768874

F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs.76260:M12529

55 F-MAMMA1001963//ESTs//0.84:320:60//Hs.6523:AA218859

F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:423:81//Hs.91916:AF035317

F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs.2820:X64878

F-MAMMA1001992//EST, Weakly similar to reverse transcriptase [H.sapiens]//7.9e-09:150:72//Hs.118222:

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F-MAMMA1002009//ESTs//2.2e-18:234:69//Hs.21978:AA009633

F-MAMMA1002011//ESTs//0.91:276:59//Hs.141196:AA704826

F-MAMMA1002032//ESTs//7.8e-40:344:77//Hs.141658:N77915

5 F-MAMMA1002033//ESTs//2.5e-30:293:76//Hs.139158:AA226159

F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.2e-54:455:70//Hs. 158095:AB007953

F-MAMMA1002042//ESTs//1.4e-20:199:79//Hs.140913:R44580

F-MAMMA1002047//EST//4.2e-14:170:75//Hs.124348:AA830225

F-MAMMA1002056//EST//2.1e-49:414:80//Hs.162335:AA564256

F-MAMMA1002058//EST//4.7e-26:268:78//Hs.140520:AA809305

F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-36:382:75//Hs.23094:M19503 F-MAMMA1002078

F-MAMMA1002082

15 F-MAMMA1002084//EST//0.37:351:59//Hs.46576:N46012

F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//0.54:388:57//Hs.99423: AJ010840

F-MAMMA1002108//Loricrin//0.00066:410:56//Hs.155657:M61120

F-MAMMA1002118//EST//0.50:202:64//Hs.126872:AA932932

20 F-MAMMA1002125//Small inducible cytokine A5 (RANTES)//2.4e-39:272:86//Hs.155464:AF088219

F-MAMMA1002132//EST//6.4e-05:245:60//Hs.149361:Al272963

F-MAMMA1002140//ESTs//5.8e-33:212:77//Hs.141203:H52638

F-MAMMA1002143//SERUM PROTEIN MSE55//1.9e-12:192:70//Hs.148101:M88338

F-MAMMA1002145//EST//0.12:204:60//Hs.160983:Al392837

25 F-MAMMA1002153

F-MAMMA1002155//ESTs, Weakly similar to p40 [H.sapiens]//3.6e-67:335:97//Hs.88424:AA281385

F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)//0.99:310:58//Hs.87149:M35999

F-MAMMA1002158//EST//0.015:278:58//Hs.162666:AA605196

F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573:82//Hs.119389:X17206

30 F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375:78//Hs.75859:U39400

F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:121:98//Hs.146354:Z22548

F-MAMMA1002209//ESTs//1.1e-84:409:98//Hs.139235:AA278362

F-MAMMA1002215//Loricrin//0.0024:369:57//Hs.155657:M61120

F-MAMMA1002219//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:

100//Hs.118849:AA215645

F-MAMMA1002230//ESTs//0.92:253:60//Hs.4222:Al024063

F-MAMMA1002236//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//4.6e-69: 344:90//Hs.76822:AI359536

F-MAMMA1002243//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//0.99:454:56//Hs.

40 122755:AF032986

F-MAMMA1002250//Human involucrin mRNA//0.0037:396:62//Hs.157091:M13903

F-MAMMA1002267//ESTs//2.0e-12:296:62//Hs.155686:Al308841

F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//1.2e-06:427:61//Hs. 69949:M94172

45 F-MAMMA1002269

F-MAMMA1002282//ESTs//5.9e-65:342:95//Hs.13962:T72715

F-MAMMA1002292//EST//0.0050:346:58//Hs.97639:AA398440

F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.8e-60:387:75//Hs.133089:AF064019

50 F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//4.3e-07:349:64//Hs. 92614:M62302

F-MAMMA1002297//EST//0.98:98:68//Hs.148207:AA897460

F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471:57//Hs.77234:AB001914

F-MAMMA1002299//ESTs//1.0:162:68//Hs.134132:AA205935

55 F-MAMMA1002308//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-41: 293:83//Hs.105292:AA504776

F-MAMMA1002310//Homo sapiens serine protease-like protease (nes1) mRNA, complete cds//0.0037:173:67// Hs.69423:AF055481

- F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-41:473:65//Hs. 92381:AB007956
- F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA806291
- F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908
- 5 F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:68//Hs.133342:AF070536
  - F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515
  - F-MAMMA1002329//Homo sapiens clone 24444 RaP2 interacting protein 8 (RPIP8) mRNA, complete cds//0.0079: 143:67//Hs.6755:AF055026
  - F-MAMMA1002332//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//1.2e-26:342:72//Hs.103948: K00627
    - F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.8e-07:669:58//Hs.5333: AB018254
    - F-MAMMA1002339//H.sapiens mRNA for retrotransposon//3.2e-40:348:73//Hs.6940:Z48633
    - F-MAMMA1002347//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-14:146:81//Hs.163073:R02591
      - F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907
      - F-MAMMA1002352//EST//1.7e-09:198:68//Hs.149218:Al247086
      - F-MAMMA1002353//ESTs//7.4e-15:163:77//Hs.157253:AI357539
      - F-MAMMA1002355//Homo sapiens KIAA0441 mRNA, complete cds//7.7e-47:307:78//Hs.32511:AB007901
- 20 F-MAMMA1002356//ESTs//0.012:380:58//Hs.105349:AA779733
  - F-MAMMA1002359//EST//1.1e-44:264:77//Hs.141095:H23818
  - F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830
  - F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923
  - F-MAMMA1002362//EST//0.25:304:58//Hs.1.62427:AA576345
- 25 F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34677
  - F-MAMMA1002384//ESTs//1.1 e-05:220:65//Hs.141388:R52022
  - F-MAMMA1002385//ESTs, Moderately similar to T11G6.8 [C.elegans]//8.4e-118:578:97//Hs.25516:Al086362
  - F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624
  - F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:AI142632
- 30 F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W85737
  - F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745
  - F-MAMMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788
  - F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030
  - F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:83//Hs.154326:D42087
- 35 F-MAMMA1002446

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- F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809
- F-MAMMA1002461//Human diacylglycerol kinase (DAGK) mRNA, complete cds//6.3e-06:595:59//Hs.99932: L38707
- F-MAMMA1002470
- F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, complete cds//0.018:417:58//Hs.
  - F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:N67059
  - F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//9.4e-120:560:98//Hs.155223: AF055460
- 45 F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628
  - F-MAMMA1002498//ESTs, Weakly similar to hypothetical protein [H.sapiens]//4.0e-07:257:63//Hs.133013: AA604920
  - F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391:L12392
  - F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//
- 50 4.5e-162:775:97//Hs.18858:AF065214
  - F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788
  - F-MAMMA1002554
  - F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:187:62//Hs.62354:M83822
  - F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421
- 55 F-MAMMA1002571//EST//0.28:115:66//Hs.156768:Al351368
  - F-MAMMA1002573//ESTs//2.1e-4.8:265:94//Hs.155128:Al224516
  - F-MAMMA1002585
  - F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831

F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:Al334107

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F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:100//Hs.153:X57958 F-MAMMA1002603//EST//0.070:99:71//Hs.122387:AA789220 F-MAMMA1002612//ESTs, Moderately similar to hCDC10 protein [H.sapiens]//8.3e-18:353:65//Hs.60895: F-MAMMA1002617//B94 PROTEIN//0.0097:229:62//Hs.75522:M92357 F-MAMMA1002618 F-MAMMA1002619 F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//4.7e-22:157:90//Hs.47344:AF041449 F-MAMMA1002623//EST//1.5e-33:168:81//Hs.141526:N52300 10 F-MAMMA1002625 F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//1.1e-35:355:76//Hs. 158241:AB007976 F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.9e-05:439:61//Hs.91400: 15 F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47:367:72//Hs.117977:L04733 F-MAMMA1002646//EST//1.2e-32:302:78//Hs.112540:AA601385 F-MAMMA1002650//TRICHOHYALIN//1.2e-08:570:63//Hs.82276:L09190 F-MAMMA1002655//EST//8.8e-40:198:100//Hs.159724:Al393335 F-MAMMA1002662//EST//0.99:95:63//Hs.144074:Al005489 20 F-MAMMA1002665//Lysosomal-associated membrane protein 2//1.8e-35:722:64//Hs.8262:U36336 F-MAMMA1002671//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//8.6e-06:272:64//Hs.106070:U22398 F-MAMMA1002673 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.2e-162:752:99//Hs.3363: 25 D86987 F-MAMMA1002685//ESTs//7.5e-40:373:78//Hs.163937:N69915 F-MAMMA1002698//ESTs//2.5e-09:190:68//Hs.138292:AI220397 F-MAMMA1002699//Homo sapiens epsin 2b mRNA, complete cds//4.7e-56:398:81//Hs.22396:AF062085 F-MAMMA1002701//ESTs//4.3e-10:110:80//Hs.156041:Al274697 F-MAMMA1002708//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.1e-51:307:79//Hs. 30 46328:D87942 F-MAMMA1002711//EST//3.6e-38:186:77//Hs.139715:N25041 F-MAMMA1002721//EST//3.9e-06:110:71//Hs.136758:AA714692 F-MAMMA1002727//EST//0.97:137:63//Hs.145153:AI150165 F-MAMMA1002728//ESTs, Highly similar to PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE [Saccha-35 romyces cerevisiae]//2.6e-12:129:81//Hs.154181:AA193502 F-MAMMA1002744//ESTs//0.0026:420:58//Hs.95793:AA617853 F-MAMMA1002746//ESTs//0.28:117:69//Hs.12925:T66312 F-MAMMA1002748 F-MAMMA1002754//ESTs//1.1e-34:340:77//Hs.163641:R61848 40 F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//1.1e-27:151:98//Hs.32168:AB007902 F-MAMMA1002764//ESTs//1.7e-45:323:84//Hs.155243:N70293 F-MAMMA1002765//EST//3.2e-11:145:73//Hs.162551:AA584782 F-MAMMA1002769 F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene// 45 7.6e-84:417:97//Hs.77705:U07563 F-MAMMA1002780//EST//0.78:210:63//Hs.149413:AI273988 F-MAMMA1002782 F-MAMMA1002796//ESTs//0.021:122:65//Hs.132221:Al380710 50 F-MAMMA1002807//EST//1.0e-31:184:71//Hs.161497:N66919 F-MAMMA1002820//ESTs//0.21:292:59//Hs.132513:AI778514 F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-57:286:88//Hs.15731: AB011135 F-MAMMA1002833//Human mRNA for KIAA0033 gene, partial cds//9.1e-52:583:72//Hs.22271:D26067 F-MAMMA1002835 55 F-MAMMA1002838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 [Locusta migratoria]//7.7e-38:179:78//Hs.141344:H29951 F-MAMMA1002842//ESTs//1.7e-19:134:89//Hs.111583:AA463590

- F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//5.4e-137:635:99//Hs.7531: AB018353
- F-MAMMA1002844//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.6e-07:329:58//Hs.107747:Al357868 F-MAMMA1002858
- 5 F-MAMMA1002868//EST//4.1e-23:180:77//Hs.163196:AA767643
  - F-MAMMA1002869//Human PINCH protein mRNA, complete cds//7.0e-88:696:78//Hs.83987:U09284
  - F-MAMMA1002871//ESTs//3.4e-93:466:96//Hs.11873:T68423
  - F-MAMMA1002880//EST//2.0e-09:364:59//Hs.145181:AI183632
  - F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds//3.8e-30:680:61//Hs.129732:
- 10 D45027
  - F-MAMMA1002886//Long (electrocardiographic) QT syndrome 2//0.00075:504:60//Hs.19944:U04270
  - F-MAMMA1002887//ESTs//0.044:144:68//Hs.133152:H91657
  - F-MAMMA1002890//EST//1.7e-05:74:86//Hs.116013:AA612666
  - F-MAMMA1002892//EST//2.1e-67:383:93//Hs.22815:R44265
- 15 F-MAMMA1002895//Human transcription factor ERF-1 mRNA, complete cds//0.00053:382:57//Hs.61796:U85658
  - F-MAMMA1002908//EST//0.0022:132:68//Hs.161697:AA224952
  - F-MAMMA1002909//ESTs//9.1e-21:343:70//Hs.142068:AA176125
  - F-MAMMA1002930//ESTs//0.55:72:72//Hs.132440:AA923730
  - F-MAMMA1002937//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.9e-103:485:99//Hs.
- 20 102928:AI346344
  - F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//1.6e-194:910:98//Hs.31720: AB014598
  - F-MAMMA1002941//ESTs//9.5e-19:196:67//Hs.137945:AI423389
  - F-MAMMA1002947//ESTs//1.2e-96:460:99//Hs.156001:Al313418
- 25 F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial cds//0.48:250:60//Hs.54697:AB007884
  - F-MAMMA1002970//EST//2.0e-16:132:84//Hs.136518:AA601400
  - F-MAMMA1002972
  - F-MAMMA1002973//ESTs//3.2e-43:225:74//Hs.155179:AA223932
  - F-MAMMA1002982//ESTs//0.0017:162:66//Hs.152669:AA604944
- 30 F-MAMMA1002987//EST//0.044:254:59//Hs.135014:AI095645
  - F-MAMMA1003003//Coagulation factor III (thromboplastin, tissue factor)//3.9e-22:185:83//Hs.62192:J02931
  - F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.0e-16:343:61//Hs. 159897:AB007970
  - F-MAMMA1003007//EST//6.6e-10:265:66//Hs.144389:AA530979
- F-MAMMA1003011//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.2e-51:620:69//Hs.75258: AF054174
  - F-MAMMA1003013//Human HOX4C mRNA for a homeobox protein//0.73:347:58//Hs.74061:X59372
  - F-MAMMA1003015//EST//2.5e-11:137:77//Hs.141312:H73062
  - F-MAMMA1003019//ESTs//0.0099:182:65//Hs.60787:Al374951
- 40 F-MAMMA1003026//EST//1.0:136:67//Hs.9123:T50137
  - F-MAMMA1003031//EST//1.3e-11:244:67//Hs.136611:AA669549
  - F-MAMMA1003035
  - F-MAMMA1003039//ESTs//1.4e-23:265:74//Hs.33393:R83391
  - F-MAMMA1003040//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.5e-93:339:85//Hs.5247:AF029750
- 45 F-MAMMA1003044//Cyclin D2//1.0:234:61//Hs.75586:D13639
  - F-MAMMA1003047//H.sapiens mRNA for F25B3.3 kinase like protein from C.elegans//1.0:209:60//Hs.99491: Y12336
  - F-MAMMA1003049//EST//0.99:126:67//Hs.162634:AA601742
  - F-MAMMA1003055//ESTs//0.00011:130:70//Hs.130539:R68518
- 50 F-MAMMA1003056
  - F-MAMMA1003057//ESTs, Moderately similar to hypothetical protein MD6 [M.musculus]//1.3e-88:334:97//Hs. 96500:Al206781
  - F-MAMMA1003066//ESTs//0.77:88:71//Hs.143618:AI022618
  - F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 protein, partial cds//4.5e-51:329:71//Hs.75154:
- 55 AB014531
  - F-MAMMA1003099//Homo sapiens actin-binding protein homolog ABP-278 mRNA, complete cds//8.5e-44:288: 88//Hs.81008:AF043045
  - F-MAMMA1003104//H.sapiens mRNA for ASM-like phosphodiesterase 3a//1.0:213:60//Hs.42945:Y08136

- F-MAMMA1003113//Homo sapiens mRNA for hair keratin acidic 3-II//0.99:200:64//Hs.32950:X82634 F-MAMMA1003127//Homo sapiens brush border myosin I (BBMI) mRNA, complete cds//5.4e-27:421:66//Hs.5394: AF105424
- F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786
- 5 F-MAMMA1003140
  - F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein//7.2e-82:397:97//Hs.151344:Y15062
  - F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cds//0.00019:297:61//Hs.108945: AB011087
  - F-MAMMA1003166//Glycoprotein lb (platelet), beta polypeptide//1.2e-31:487:65//Hs.3847:U59632
- F-NT2RM1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:244:63//Hs.79706:U53204 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-66:385:92//Hs.82510:D31886 F-NT2RM1000032
  - F-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-110:849:81//Hs.78442:D83782
  - F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.5e-108:542:95//Hs.60103:
- 15 AB014590

- F-NT2RM1000039//Human plectin (PLEC1) mRNA, complete cds//0.11:545:57//Hs.79706:U53204
- F-NT2RM1000055//ESTs, Highly similar to TIP120 [R.norvegicus]//3.2e-69:353:96//Hs.154980:AA948067
- F-NT2RM1000059//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.029:281:59// Hs.46465:U45285
- 20 F-NT2RM1000062//ESTs//0.30:368:59//Hs.131675:AA843210
  - F-NT2RM1000080//Homo sapiens chromosome 9, P1 clone 11659//2.8e-102:493:97//Hs.3439:AC004472
  - F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//5.8e-116:550:97//Hs.65238: AB014561
  - F-NT2RM1000092//Murine leukemia viral (bmi-1) oncogene homolog//0.42:190:63//Hs.431:L13689
- 25 F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00086:126:70//Hs.92693: AF007155
  - F-NT2RM1000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:Z48054
  - F-NT2RM1000127
  - F-NT2RM1000131
- F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds//3.7e-92:448:97//Hs.49767:AF044959
  - F-NT2RM1000153//Homo sapiens mRNA for MTG8-related protein MTG16a, complete cds//1.0:546:58//Hs. 110099:AB010419
  - F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00081:126:70//Hs.92693: AF007155
  - F-NT2RM1000187//ESTs//3.4e-79:400:96//Hs.54971:Al424382
    - F-NT2RM1000199//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.87:454:59//Hs.47061:AF045458 F-NT2RM1000242
    - F-NT2RM1000244//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.97:
- 40 135:66//Hs.27910:AF049105 F-NT2RM1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L09190
  - F-NT2RM1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-13:248:69//Hs.1674:M90516
  - F-NT2RM1000257//ESTs, Highly similar to similar to mago nashi [H.sapiens]//2.9e-98:530:93//Hs.104650: Al037879
- 45 F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-58:460:80//Hs.23106:D50920
  - F-NT2RM1000271//ESTs//0.93:224:60//Hs.91226:AA649047
  - F-NT2RM1000272
  - F-NT2RM1000280//ESTs, Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]//1.3e-21:308: 73//Hs.15071:AA781144
- 50 F-NT2RM1000300
  - F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-128:708:92//Hs.5719:D63880
  - F-NT2RM1000318//Human mRNA for ribosomal protein L39, complete cds//1.8e-35:182:99//Hs.9837:D79205
  - F-NT2RM1000341//ESTs//2.3e-72:381:95//Hs.23070:AA631976
  - F-NT2RM1000354//EST//5.2e-27:202:84//Hs.151186:AI125798
- 55 F-NT2RM1000355//ESTs, Weakly similar to putative [M.musculus]//7.7e-75:387:95//Hs.108619:W28608
  - F-NT2RM1000365//ESTs//1.7e-99:495:97//Hs.103926:AA165691
  - F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase [H.sapiens]//7.4e-91:481:95//Hs. 163707:AA137181

- F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.8939:X80507
- F-NT2RM1000394//HISTONE H3.3//8.5e-91:474:93//Hs.118838:M11353
- F-NT2RM1000399
- F-NT2RM1000421
- F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.2e-85:418:97// Hs.20815:AF084928
  - F-NT2RM1000499//ESTs, Weakly similar to KIAA0167 protein [H.sapiens]//1.6e-38:201:97//Hs.106262:AI052382 F-NT2RM1000539//EST//0.070:145:62//Hs.149711:AI284660
  - F-NT2RM1000553//EST//2.2e-48:265:95//Hs.99230:AA449847
- 10 F-NT2RM1000555//ESTs//0.82:193:61//Hs.96944:AI359957
  - F-NT2RM1000563//Human plectin (PLEC1) mRNA, complete cds//1.0:336:58//Hs.79706:U53204
  - F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gene, partial cds//0.98:226:61//Hs.17931:AB006625
  - F-NT2RM1000648//ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]//6.2e-51:254:98//Hs.132096:AA314601
- F-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds//8.5e-55:276:97//Hs.19122: AF038957
  - F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete cds//0.87:274:60//Hs.113936:AB005297
  - F-NT2RM1000669//ESTs//5.5e-63:481:85//Hs.90527:Al188279
  - F-NT2RM1000672
- 20 F-NT2RM1000691//Homa sapiens mRNA for HRIHFB2060, partial cds//7.0e-121:582:98//Hs.146282:AB015348 F-NT2RM1000699//ESTs//1.1e-89:435:97//Hs.28964:AA715101
  - F-NT2RM1000702//ESTs//5.4e-90:429:99//Hs.151001:AA564706
  - F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase//1.5e-66:435:85//Hs.5038:AJ004832
  - F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds//2.6e-127:690:92//Hs.147946:
- 25 AB011139
  - F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds//8.2e-68:524:83//Hs.112360:AF027208 F-NT2RM1000746//ESTs//2.6e-37:231:89//Hs.94446:AA845465
  - F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, complete cds//3.3e-09:321:63//Hs.150390:AB007885
  - F-NT2RM1000772//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.053:271:60//Hs.139745:
- 30 U39067
  - F-NT2RM1000780//Human Line-1 repeat mRNA with 2 open reading frames//6.9e-20:128:94//Hs.23094:M19503 F-NT2RM1000781//ESTs//4.4e-60:346:92//Hs.35089:N50845
  - F-NT2RM1000800
  - F-NT2RM1000802
- F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds//1.2e-64:490:84//Hs.112360:AF027208 F-NT2RM1000826//ESTs//0.82:193:61//Hs.96944:Al359957
  - F-NT2RM1000829//Mannose-binding lectin, soluble (opsonic defect)//0.92:283:58//Hs.2314:X15422
  - F-NT2RM1000833//Hydroxysteroid (11-beta) dehydrogenase 2//0.022:178:67//Hs.1376:U26726
  - F-NT2RM1000850//Human protein tyrosine kinase related mRNA sequence//3.8e-06:384:59//Hs.90314:L05148
- F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//3.0e-149:726:97//Hs.99423:
  AJ010840
  - F-NT2RM1000857//ESTs//0.52:274:60//Hs.112095:AA447643
  - F-NT2RM1000867//ESTs, Highly similar to signal peptidase:SUBUNIT//5.3e-54:277:96//Hs.11125:Al015619
  - F-NT2RM1000874//ESTs//0.032:185:64//Hs.97713:AA442239
- F-NT2RM1000882//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.0e-155:750:97//Hs.132898:AC004770
  - F-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//8.8e-158:762:97//Hs. 26285:AF082516
  - F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds//6.3e-19:310:67//Hs.65238:
- 50 AB014561
  - F-NT2RM1000894
  - F-NT2RM1000898
  - F-NT2RM1000905//EST//4.8e-07:77:84//Hs.148017:Al268701
  - F-NT2RM1000924//HOMEOBOX PROTEIN HOX-A5//0.00051:458:59//Hs.37034:M26679
- F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 protein, partial cds//0.084:386:58//Hs.101474:AB018350 F-NT2RM1000962//Human mRNA for KIAA0252 gene, partial cds//0.98:299:59//Hs.83419:D87440
  - F-NT2RM1000978
  - F-NT2RM1001003//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.3e-161:760:98//

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Hs.58488:U97067
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F-NT2RM1001008//ESTs//1.3e-12:144:75//Hs.133122:AI025200

F-NT2RM1001043//EST//0.24:117:64//Hs.161536:N80395

F-NT2RM1001044//ESTs, Weakly similar to C43E11.9[C.elegans]//3.0e-98:491:96//Hs.102173:AA045270

F-NT2RM1001059//Human plectin (PLEC1) mRNA, complete cds//0.52:533:57//Hs.79706:U53204

F-NT2RM1001066//ESTs//1.2e-114:538:99//Hs.129020:Al380703

F-NT2RM1001072//Human beige-like protein (BGL) mRNA, partial cds//0.69:586:56//Hs.62354:M83822

F-NT2RM1001074//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.0019:294:64//Hs.30223:X90846

F-NT2RM1001082//Archain//3.9e-37:290:81//Hs.33642:X81198

10 F-NT2RM1001085

5

F-NT2RM1001092//Zinc finger protein 43 (HTF6)//1.9e-57:770:68//Hs.74107:X59244

F-NT2RM1001102//ESTs//1.2e-35:638:63//Hs.131737:Al343331

F-NT2RM1001105//WEE1-LIKE PROTEIN KINASE//0.0024:246:63//Hs.75188:U10564

F-NT2RM1001112//ESTs//8.9e-82:437:93//Hs.6330:H38495

15 F-NT2RM1001115

F-NT2RM1001139//Keratin 9//1.5e-05:518:59//Hs.2783:Z29074

F-NT2RM2000006//ESTs//3.9e-16:96:98//Hs.101117:AA576113

F-NT2RM2000013//RNA polymerase II polypeptide B (140 kD)//6.3e-13:640:59//Hs.148027:X63563

F-NT2RM2000030

20 F-NT2RM2000032//ESTs//7.1 e-18:138:68//Hs.114031:AA700958

F-NT2RM2000042//ESTs//0.0091:241:61//Hs.147895:Al286243

F-NT2RM2000092

F-NT2RM2000093//ESTs//2.6e-40:226:94//Hs.163521:H42085

F-NT2RM2000101//ESTs//1.0:235:61//Hs.48860:N27428

25 F-NT2RM2000124//Protein kinase, cAMP-dependent, catalytic, alpha//5.8e-46:287:88//Hs.77271:X07767

F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//3.0e-139:566: 97//Hs.18953:AF067223

F-NT2RM2000192//EST//3.5e-07:168:65//Hs.163122:AA756999

F-NT2RM2000239//ESTs, Weakly similar to K04G2.6 [C.elegans]//3.6e-93:489:95//Hs.143499:R72672

30 F-nnnnnnnnn//ESTs//1.0e-70:269:97//Hs.156175:Al334328

F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.0e-129:615:98//Hs.111862: AB011162

F-NT2RM2000259//ESTs//6.1e-30:172:85//Hs.116406:AA209520

F-NT2RM2000260//ESTs//2.5e-25:133:93//Hs.14169:AA203500

35 F-NT2RM2000287//ESTs//6.2e-13:97:83//Hs.118523:H98981

F-NT2RM2000322//Interferon regulatory factor 5//0.84:208:61//Hs.54434:U51127

F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds//2.8e-176:805:99//Hs.129952:

F-NT2RM2000363//ESTs//1.2e-24:139:96//Hs.48818:N63543

40 F-NT2RM2000368//Horno sapiens protein kinase C-binding protein RACK7 mRNA, partial cds//3.7e-96:599:86// Hs.75871:U48251

F-NT2RM2000371

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F-NT2RM2000374//ESTs//3.2e-13:98:91//Hs.65853:AI050866

F-NT2RM2000395//Growth arrest-specific 1//0.80:129:67//Hs.65029:L13698

F-NT2RM2000402//Human p76 mRNA, complete cds//7.2e-23:714:59//Hs.28757:U81006

F-NT2RM2000407//ESTs//9.4e-92:458:96//Hs.148873:T33582

F-NT2RM2000420//EST//1.8e-61:296:99//Hs.147186:AI193053

F-NT2RM2000422//Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4//1.5e-06:260:61// Hs.553:L05568

50 F-NT2RM2000452//ESTs//1.0:132:62//Hs.110004:Al097379

F-NT2RM2000469//ESTs//0.34:249:60//Hs.149575:Al281807

F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.4e-16:386:63//Hs.8309:AB018290 F-NT2RM2000502//Human nicotinamide N-methyltransferase (NNMT) mRNA, complete cds//0.99:272:61//Hs.

76669:U08021

55 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//1.6e-172:824:97//Hs.4812: AF061243

F-NT2RM2000522//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.18:313:60//Hs.129725:AF047487

F-NT2RM2000540//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.7e-41:231:94//Hs.7049:

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- F-NT2RM2000556//ESTs//3.1e-33:183:96//Hs.136990:AA769220
- F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751:97//Hs.74369:AF032108
- F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.89631:U48508
- 5 F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128
  - F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214:92//Hs.55609:W37993
  - F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.8e-175:820:98//Hs.3363: D86987
- 10 F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs.136990:AA769220
  - F-NT2RM2000594
  - F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.017:253:65//Hs.102402: AF040963
  - F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313
- 15 F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217:AA846548
  - F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.024:326:59//Hs.6150:AB011093 F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258
  - F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0e-143:664:98//Hs.19542: AB018272
- 20 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4e-139:664:98//Hs.7278:AB014558 F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:AI189702
  - F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4e-169:518:99//Hs.115763: AB014576
  - F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs.156342:Al337371
- 25 F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds//6.7e-86:746:74//Hs. 5321:AF006083
  - F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:64//Hs.7938:D86984
  - F-NT2RM2000718//Homa sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:594:98//Hs.136058:AB015342 F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756:82//Hs.74107:X59244
- F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION [Saccharomyces cerevisiae]//4.2e-85:464:91//Hs.161551:W24286 F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-82:640:81//Hs.5247:AF029750

F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//Hs.105919:AB002338

- F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:Al346701
- F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//2.8e-185:847:99//Hs.137580: AB015046
  - F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//6.2e-94:441:99//Hs.59075: AI023761
  - F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//Hs.84753:D87433
- 40 F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831
  - F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//2.9e-48:282:93//Hs. 17035:Al080471
  - F-NT2RM2001065

- F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449:
- 62//Hs.75111:D87258
  F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds// 0.00079;274:59//Hs.102732:U88153
- F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190
- F-NT2RM2001141
- 50 F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042
  - F-NT2RM2001177
  - F-NT2RM2001194//ESTs, Weakly similar to T28H10.2 [C.elegans]//2.4e-23:149:93//Hs.10618:Al288739
  - F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959
  - F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:69//Hs.155291:D13630
- 55 F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165:64//Hs.24279:AB018349 F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:AI004766
  - F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:64//Hs.75889:U65928
  - F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321:61//Hs.132206:

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F-NT2RM2001256

F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845

F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601

5 F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615

F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.elegans]//5.2e-30:277:77//Hs.25347: Al138605

F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567 F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706

10 F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905

F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61//Hs.82925:U70322

F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:U68382

F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378

F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-97:453:99//Hs.155218:

15 AJ007509

F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X57303

F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328:60//Hs.68900:AF016903

F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969

F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459

20 F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262

F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//6.9e-28:582: 64//Hs.1042:M62800

F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:57:89//Hs.114722:AA448077

F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65//Hs.32168:AB007902

25 F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:Al391729

F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//Hs.76272:S66431

F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:Al016073

F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:Al393918

30 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.0e-154:740:98//Hs.15832: AB014518

F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952

F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]//3.5e-13:94:92// Hs.22142:AA814725

F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:Al016073

F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301

F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287

F-NT2RM2001664//Homo sapiens lkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-

40 173:802:99//Hs.31323:AF044195

F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATSCH REPAIR PROTEIN MSH6 [H.sapiens]//1.1e-136: 671:97//Hs.27721:U17907

F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414: AB011129

45 F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:Al365356

F-NT2RM2001675

F-NT2RM20016811/ESTs//0.16:197:63//Hs.20585:R10305

F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211

F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216

50 F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//5.8e-16:144:84//Hs.14671:T79937

F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:Al277415

F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:Al003817

F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds// 0.95:270:61//Hs.15791:AF027826

55 F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788

F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650

F-NT2RM2001718

F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//Hs.12457:AF052123

- F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0e-112:530:98//Hs.129937:
- F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269:58//Hs.129952: AB011132
- 5 F-NT2RM2001743
  - F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:AB011399
  - F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:Al016073
  - F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:Al222742
- 10 F-NT2RM2001771//Zinc finger protein 10 (KOX 1)//1.1e-66:669:71//Hs.2479:X78933
  - F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698
  - F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:Al193595
  - F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770
- 15 F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481:72//Hs.70617:D31763
  - F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142:66//Hs.78202: U29175
  - F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195
- 20 F-NT2RM2001805//EST//1.0:45:80//Hs.159007:Al381341
  - F-NT2RM2001813//EST//0.41:268:58//Hs.150031:Al292068
  - F-NT2RM2001823//H.sapiens mRNA for 218kD Mi-2 protein//9.7e-21:554:60//Hs.74441:X86691
  - F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//1.2e-132:738:90//Hs.7753:AF013759
  - F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:329:86//Hs.113283:AF018080
- 25 F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M57567
  - F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-28:421:66//Hs.8763:W30741
  - F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723
  - F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.1e-189:866:97//Hs.4198: AB014610
- F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892
  - F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4e-178:859:97//Hs.129937: AB007931
  - F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.2e-08:481:59//Hs.27621:
- 35 U52840

- F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//0.37;424:60//Hs.118634:U66688
- F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//2.2e-139:653:98//Hs.21811: AF091080
- 40 F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392
  - F-NT2RM2001982
  - F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds//1.2e-21:123:98//Hs.6454: AF089816
  - F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//Hs.104135:AJ006778
- 45 F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538
  - F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//0.99:271:60//Hs.63888:AA203398
  - F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5e-37:509:65//Hs.6214:AB018274
  - F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:429:58//Hs.79090:D89729
  - F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822:73//Hs.1674:M90516
- 50 F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427
  - F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:Al382154
  - F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:Al198377
  - F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//Hs.89631:U48508
  - F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.5e-165:776:98//Hs.99423: AJ010840
  - F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435
  - F-NT2RM2002128

- F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274
- F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.4e-144:800: 92//Hs.20815:AF084928
- F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds//1.7e-165:787:97//Hs.11147:
- 5 AB007936
  - F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//0.064:291:61//Hs. 99936:X14487
  - F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:610:59//Hs.148027:X63563
  - F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074
- 10 F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:Al391464
  - F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:Al094674
  - F-NT2RM4000061//ESTs//0.89:207:60//Hs.98445:AI038511
  - F-NT2RM4000085//ESTs, Weakly similar to The KIAA0134 gene product is related to human RNA helicase A. [H. sapiens]//1.6e-30:369:70//Hs.114623:Al204280
- 15 F-NT2RM4000086
  - F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds// 1.3e-24:345:69//Hs.13128:AF060865
  - F-NT2RM4000139
  - F-NT2RM4000155
- 20 F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632
  - F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, complete cds//9.8e-30:676:61// Hs.159228:AF041853
  - F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044
  - F-NT2RM4000191//TRICHOHYALIN//0.011:324:60//Hs.82276:L09190
- 25 F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744
  - F-NT2RM4000199//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.13:322: 61//Hs.145088:Al221147
  - F-NT2RM4000200
  - F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.0027:424:60//HS.91400:
- 30 AB006626

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- F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//4.4e-184:856:98//Hs.111138: AB018255
- F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//0.0013:358:60//Hs.75055:M93651
- F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.65:572:60//Hs.47061:AF045458
- 35 F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582
  - F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439
  - F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTEIN [Schizosaccharomyces pombe]//1.1e-16:112:92//Hs. 93841:AA442297
  - F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//1.8e-48:229:83//Hs. 46328:D87942
  - F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds//2.5e-154:609:93//Hs. 31305:M99438
  - F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complete cds//0.070:460:59//Hs.5372:
- 45 F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:AI240707
  - F-NT2RM4000344//ESTs, Highly similar to YME1 PROTEIN [Saccharomyces cerevisiae]//2.7e-83:432:95//Hs. 12796:W27884
  - F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-53:666:68//Hs.155291:D13630
  - F-NT2RM4000354//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//0.0078:55:92//Hs.59075:
    - F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:Al418425
    - $F-NT2RM4000366//Homo\ sapiens\ mRNA\ for\ KlAA0642\ protein,\ partial\ cds//5.3e-135:628:99//Hs.8152:AB014542\ F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745$
- F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//2.0e-72: 843:68//Hs.23796:AL022718
  - F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)//0.63:166:65//Hs.946:X73029

F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds//4.9e-17:114:94//Hs.137580: AB015046

F-NT2RM4000421

F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42:432:74//Hs.154872:

5 AB011166

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F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.023:543:58//Hs.2175:M59820 F-NT2RM4000457

F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:178:631/Hs. 66369:U95040

10 F-NT2RM4000486//ESTs//9.2e-48:237:99//Hs.160685:Al280004

F-NT2RM4000496//ESTs//0.069:252:61//Hs.155958:AA573632

F-NT2RM4000511//EST//0.92:191:58//Hs.61517:AA028915

F-NT2RM4000514

F-NT2RM4000515//ESTs//7.3e-93:450:98//Hs.120975:AA034409

F-NT2RM4000520//ESTs//0.13:183:65//Hs.144828:Al221305

F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.8e-153:756:96// Hs.125870:Al364967

F-NT2RM4000532//ESTs//7.7e-43:388:78//Hs.105665:H78987

F-NT2RM4000534

20 F-NT2RM4000585

F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593:62//Hs.7764: AB007938

F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//3.1e-104:532:96//Hs.6092:T75227

25 F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305:68//Hs.40100:AB002390

F-NT2RM4000611//EST//0.76:268:58//Hs.150031:Al292068

F-NT2RM4000616

F-NT2RM4000674

F-NT2RM4000689

30 F-NT2RM4000698//Apolipoprotein E//1.0:290:59//Hs.76260:M12529

F-NT2RM4000700

F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.5e-91:744:77//Hs. 42400:AF022789

F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus] //2.6e-163:771:97//Hs.6823:W18181

F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257:60//Hs.957:M84605

F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-159:743:98//Hs.137168: AB018303

F-NT2RM4000741

40 F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.1e-75:388:96//Hs. 112361:R99396

F-NT2RM4000764//ESTs//3.8e-104:539:95//Hs.24739:H67815

F-NT-2RM4000778//ESTs//1.5e-85:419:97//Hs.99838:AA204731

F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.8e-173:810:98//Hs.18586:

45 AB007920

F-NT2RM4000787//EST//0.011:182:65//Hs.159928:AA969186

F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736:98//Hs.25817:AC005306

F-NT2RM4000795//ESTs, Highly Similar to LIVER CARBOXYLESTERASE PRECURSOR [Homo sapiens]//6.7e-19:160:80//Hs.124902:Al337820

50 F-NT2RM4000796//Human K+ channel subunit gene, complete cds//0.96:292:62//Hs.124212:M64676

F-NT2RM4000798//ESTs//1.9e-34:271:82//Hs.128203:AA972301

F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//0.052:238:64//Hs:113265:AF032387

F-NT2RM4000820//ESTs//0.053:274:61//Hs.23748:H16568

55 F-NT2RM4000833

F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:374:61//Hs.7841:AB002322

F-NT2RM4000852//EST//1.0:222:60//Hs.120354:AA718934

F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 [Homo sapi-

	ens]//4.4e-29:164:95//Hs.115095:Al392943
	F-NT2RM4000887
	F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete
	cds//6.8e-22:407:64//Hs.21293:AB011004
_	
5	F-NT2RM4000950
	F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:AI014546
	F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-63:571:77//Hs.7289:AB007875
	F-NT2RM4000996//Zinc finger protein 3 (A8-51)//8.7e-34:381:67//Hs.2481:X78926
	F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.6e-171:803:98//Hs.19542:
10	AB018272
	F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//1.1e-126:584:99//Hs.15711:
	AB014539
	F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete cds//4.8e-05:469:58//Hs.5333:
	AB018254
15	F-NT2RM4001047//ESTs, Moderately similar to MO25 PROTEIN [M.musculus]//7.0e-56:340:92//Hs.87310:
	Al247543
	F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM" PRECURSOR//
	0.79:142:69//Hs.77424:M63835
	F-NT2RM4001084
20	F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045:235:62//Hs.108947:D30758
	F-NT2RM4001116
	F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.00029:225:61//Hs.134989:L12701
	F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730
	F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:Al004145
25	F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351
	F-NT2RM4001187
	F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220
	F-NT2RM4001200//Zinc finger protein 10 (KOX 1)//4.0e-68:799:69//Hs.2479:X78933
	F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.4e-153:707:99//Hs
30	14934;AF004828
	F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME
	III [Caenorhabditis elegans]//0.19:291:62//Hs.31582:AA877205
	F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds//7.0e-63:715:70/
	Hs.104925:AF059611
35	F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-67:208:96//Hs
	26676:AA033997
	F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete cds//0.0019:435:59//Hs.6360
	AB007950
	F-NT2RM4001309//Human Chromosome 16 BAC clone CIT987SK-254P9//0.019:356:59//Hs.26971:AC003003
40	F-NT2RM4001313//H.sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-79:474:89//Hs.32971:Z46973
	F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335
	F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-43:642:66//Hs.87435:D89016
	F-NT2RM4001340//EST//0.40:135:70//Hs.161198:Al418988
	F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTER
45	GENIC REGION [Saccharomyces cerevisiae]//0.0096:284:58//Hs.120997:R56714
	F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf
	protein [C.elegans]//3.7e-52:252:100//Hs.15301:AA167818
	F-NT2RM4001371//EST//0.52:262:59//Hs.145991:Al277656
	F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-169:790:98//Hs.5151
50	AF098799
	F-NT2RM4001384
	F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575
	F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:475:64//Hs.105052:AB000520
	F-NT2RM4001412
55	F-NT2RM4001414//ESTs, Moderately similar to 18547_1 [H.sapiens]//5.2e-18:133:87//Hs.28209:Al073817
	F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:70//Hs.154326:D42087

F-NT2RM4001444

F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658

- F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914
- F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sapiens]//1.1e-71:313:99//Hs. 163754:AA587784
- F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.9e-157:724:99//Hs.153121:
- 5 AB014585
  - F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619
  - F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.cerevisiae]//1.3e-114:536:99//Hs.88820: AA456247
  - F-NT2RM4001557
- 10 F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487
  - F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//1.0: 255:60//Hs.14207:U86453
  - F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:Al198859
  - F-NT2RM4001582
- 15 F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566
  - F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0072:484:60//Hs.129892:
  - F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus]//2.3e-72:387:95//Hs.114722:AA448077
  - F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.1e-163:750:99//Hs.23255:
- 20 AB018334
  - F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans]//8.6e-05:91:79//Hs.24647:W19739
  - F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEMBRANE PROTEIN [Homo sapiens] //0.0042:153:68//Hs.114832:Al147946
  - F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339
- 25 F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320
  - F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323
  - F-NT2RM4001682//EST//0.027:145:70//Hs.133253:Al052638
  - F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384
  - F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957
- 30 F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:Al332905
  - F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903
  - F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318
  - F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306
  - F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]// 2.0e-27:205:83//Hs.110601:AA206719
- 2.0e-27:205:83//Hs.110601:AA206719
   F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:
  - F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4e-175:803:99//Hs.39871: AB018270
- F-NT2RM4001783//ESTs, Weakly similar to T12D8.i [C.elegans]//3.1e-71:376:95//Hs.108396:AA160677
  F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.99:
  446:58//Hs.27910:AF049105
  - F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547 F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712
- 45 F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.3e-40:252:90//Hs.119294:
  - F-NT2RM4001828//Zinc fmger protein 157 (HZF22)//1.8e-75:688:72//Hs.89897:U28687
  - F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953:M96824
  - F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:Al214204
- 50 F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814
  - F-NT2RM4001856

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X97630

- F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250
- F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.3e-150:704:98//Hs.61628:
- F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:66//Hs.7938:D86984 F-NT2RM4001880
- F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:Al204212

- F-NT2RM4001922//ESTs//2.5e-51:291:93//Hs.26660:Al312633
- F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, partial cds//0.98:359:57//Hs.155356: AJ224875
- F-NT2RM4001938
- 5 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808:98//Hs.118631: AF098162
  - F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:83//Hs.154326:D42087
  - F-NT2RM4001965//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//1.8e-65:337:96//Hs. 130135:AA905493
- 10 F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:Al312862
  - F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527:76//Hs.159277: AB018341
  - F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082
  - F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181:65//Hs.11147:AB007936
- 15 F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:Al302271
  - F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601
  - F-NT2RM4002034
  - F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048
  - F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912
- 20 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:
  - F-NT2RM4002062//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus] //7.0e-94:396:94//Hs.59346:AI126802
  - F-NT2RM4002063
- 25 F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313: AF071309
  - F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040
  - F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302
  - F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.
- 30 122967:AF059569
  - F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//9.2e-34:532:65//Hs. 146459:X66975
  - F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs. 69360:U63743
- 35 F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542
  - F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877
  - F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158
  - F-NT2RM4002146//ESTs, Highly similar to similar to mago nashi [H.sapiens]//1.6e-135:646:97//Hs.104650: AI037879
- F-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535
  - F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L21998
  - F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454:60//Hs.32981: U38276
- 45 F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454
  - F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313:61//Hs.118087:AB011182 F-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster] //8.4e-125:588:98//Hs.23900:U82984
  - F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966
- 50 F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:Al205764
  - F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502:57//Hs.77783:AF014118
  - F-NT2RM4002278//EST//0.33:138:63//Hs.144096:AI032180
  - F-NT2RM4002281
  - F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979
- 55 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:72//Hs.31463:D87457 F-NT2RM4002301
  - F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:Al343331
  - F-NT2RM4002339

- F-NT2RM4002344//EST//0.16:166:64//Hs.128600:AA906454
- F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.1e-151:708:98//Hs.26163: AR014549
- F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0040:303:63//Hs.23741:AB018263
- 5 F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:N70293
  - F-NT2RM4002390
  - F-NT2RM4002398
  - F-NT2RM4002409
  - F-NT2RM4002438//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//1.1e-55:282:96//Hs.
- 10 26676:AA033997
  - F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339:60//Hs.18686:AF052151 F-NT2RM4002452
  - F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228:81//Hs.115263:D30783 F-NT2RM4002460//EST//1.0:142:65//Hs.145370:Al252780
- F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//8.9e-165:777:98//Hs. 8765:AF083255
  - F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464:97//Hs.94781: AB014591
  - F-NT2RM4002493
- 20 F-NT2RM4002499//ESTs//1.3e-44:653:67//Hs.23790:N99347
  - F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225:83//Hs.155464:AF088219
  - F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290:60//Hs.154968: U02020
  - F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232:61//Hs.82042:D87075
- F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor All/AVP mRNA, complete cds//1.0:100:70// Hs.159483:AF054176
  - F-NT2RM4002558//Homo sapiens amphiphysin II mRNA, complete cds//0.17:393:61//Hs.6619:U84004
  - F-NT2RM4002565//Horno sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226:60//Hs.84043: D84273
- F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C.elegans]//3.3e-88:484:93//Hs.105837:AA536054 F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase [H.sapiens]//0.059:121:70//Hs.155413:AA429394
  - F-NT2RM4002593//ESTs//1.0e-15:103:95//Hs.108920:W28151
  - F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06: 499:59//Hs.79357:D78275
- 35 499:59//Hs.79357:D78275 F-NT2RM4002623//ESTs//1.2e-11:92:92//Hs.164046:T97402
  - F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746:81//Hs.3628:AB014587 F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747:96//Hs.159597: A.I012449
- 40 F-NT2RP1000040//ESTs//1.3e-58:338:92//Hs.17534:H16907
  - F-NT2RP1000063//ESTs//0.0013:72:83//Hs.108196:W81647
  - F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548:91//Hs.79971:X98834
  - F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247:61//Hs.30792: AF044924
- 45 F-NT2RP1000111
  - F-NT2RP1000112//TTK protein kinase//3.2e-40:324:81//Hs.2052:M86699
  - F-NT2RP1000124//ESTs//2.4e-42:268:89//Hs.146078:AI084025
  - F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens]//1.4e-71: 382:94//Hs.127842:W38901
- F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77:90// Hs.3760:AF011792
  - F-NT2RP1000170//EST//0.68:130:63//Hs.146994:Al184430
  - F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679:97//Hs.78019:AF070535
  - F-NT2RP1000191//ESTs//1.3e-71:405:93//Hs.24054:N46499
- 55 F-NT2RP1000202//H.sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591:58//Hs.74019:X83703 F-NT2RP1000243
  - F-NT2RP1000259
  - F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528:97//Hs.

- 4214:AF067730
- F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:N41661
- F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551
- 5 F-NT2RP1000333//Homo sapiens monocyte/macrophage lg-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231
  - F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:U53204 F-NT2RP1000357
  - F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07807
- F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497:86//Hs.77864: AB014538
  - F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178:877: 96//Hs.120360:AF064594
  - F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA828031
- 15 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.0e-179:710:98//Hs.21862: AB011159
  - F-NT2RP1000416//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus] //7.3e-177:857:97//Hs.6823:W18181
  - F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.46:222:
- 20 60//Hs.89230:AF031815

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- F-NT2RP1000439//EST//0.98:339:56//Hs.137377:AA101603
- F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356:59//Hs.58435:AF001862 F-NT2RP1000460
- F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence//3.7e-134: 665:96//Hs.143187:AC002985
  - F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440:80//Hs. 159154:U47634
  - F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA535102
  - F-NT2RP1000493
- 30 F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA480977
  - F-NT2RP1000522//Homo sapiens clone DT1P1A11 mRNA, CAG repeat region//0.21:255:62//Hs.98834:U92992 F-NT2RP1000547//H.sapiens mRNA for transmembrane protein rnp24//1.9e-06:337:63//Hs.75914:X92098 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82:295:92//Hs. 104105:AF017418
- F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213
  F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223:89//Hs.110802:X04385
  F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//2.2e-49:506:73//Hs.132898:AC004770
  - F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556:62//Hs. 152936:D63475
    - F-NT2RP1000630
    - F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389:59//Hs.3844: U24576
  - F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553
- 45 F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:
  - F-NT2RP1000701//Myogenic factor 3//0.81:186:63//Hs.2834:AF027148
  - F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.0e-33:278:78//Hs.58167:D30612
  - F-NT2RP1000730//ESTs, Weakly similar to putative p150 [H.sapiens]//6.2e-40:297:84//Hs.18122:Al338045
- 50 F-NT2RP1000733//G1 to S phase transition 1//1.4e-31:286:78//Hs.2707:X17644
  - F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//2.6e-123:604:96//Hs.21771:AF101434
  - F-NT2RP1000746
  - F-NT2RP1000767
- 55 F-NT2RP1000782//Human globin gene//3.6e-21:140:91//Hs.100090:M69023
  - F-NT2RP1000796//H.sapiens mRNA for ROX protein//0.17:404:57//Hs.25497:X96401
  - F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//

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2.7e-23:147:91//Hs.102336:Z83838
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F-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143:424: 96//Hs.18953:AF067223

F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:Al332903

5 F-NT2RP1000836//EST//0.60:103:66//Hs.145708:Al267990

F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:Al288838

F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875

F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023

F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//Hs.125156:AF064094

10 F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:Al218683

F-NT2RP1000915//ESTs//8.8e-11:102:81//Hs.163740:Al248847

F-NT2RP1000916//ESTs, Weakly similar to coded for by C. elegans cDNA cm04e9 [C.elegans]//2.2e-27:159:94// Hs.122153:AA780270

F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U76248

15 F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400

F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//2.7e-26: 185:87//Hs.108332:U39317

F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.154276:AB002803

F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:AI248847

20 F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M17885

F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858

F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:N28866

F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//Hs.82837:L13435

F-NT2RP1001011

25 F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:Al089163

F-NT2RP1001014

F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M61764

F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901

F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:Al360531

F-NT2RP1001080//Homo sapiens forkhead protein (FKHRL1) mRNA, complete cds//0.57:215:64//Hs.14845: AF032886

F-NT2RP1001113//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//1.4e-65:293: 95//Hs.32751:H38087

F-NT2RP1001173

35 F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-26:259:74//Hs.75258: AF054174

F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524

F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:AI022150

F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.

40 25195:U81523

F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:Al337094

F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:

F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724

45 F-NT2RP1001294

50

F-NT2RP1001302

F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341 F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:H67815

F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//3.1e-87:437:97//Hs.132898:AC004770

F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos taurus]//6.8e-101:480:94//Hs.75017:AA166853

F-NT2RP1001385//EST//0.86:127:65//Hs.156304:AI336859

F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673

55 F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081

F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700

F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700

F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:AF052149

- F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104
- F-NT2RP1001466
- F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742
- F-NT2RP1001482
- 5 F-NT2RP1001494
  - F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI016400
  - F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:254:64//Hs.75814:AB000277 F-NT2RP1001569
  - F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds//2.5e-41:496:74//Hs.12956:U90913
- 10 F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420
  - F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//4.7e-137:685:96//Hs.93677: AF091081
  - F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C .elegans]//8.2e-47:300:89//Hs.6473:AA853955
  - F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:68//Hs.40100:AB002390
- F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:66//Hs.70617:D31763 F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]// 2.0e-26:214:82//Hs.140385:AA773359
  - F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:AI038867
  - F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1e-78:383:97//Hs.8309:AB018290
- 20 F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds// 7.8e-97:467:97//Hs.6216:AF061749
  - F-NT2RP2000054//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:L20433
  - F-NT2RP2000056//Hurnan HPTP epsilon mRNA for protein tyrosine phosphatase epsilon//1.2e-27:146:100//Hs. 155991:X54134
- F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//8.1e-41: 767:61//Hs.23796:AL022718 F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609
- 30 F-NT2RP2000076//H.sapiens mRNA for TFIIAI/0.00023:356:62//Hs.121686:D14887
  - F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs. 54877:AF050078
  - F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879
  - F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:
- 35 AB018338
  - F-NT2RP2000091
  - F-NT2RP2000097
  - F-NT2RP2000098//ESTs//0.086;92;69//Hs.159389;Al371963
  - F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390
- 40 F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-115:551:97//Hs.17706: AB018356
  - F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22670
  - F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:
- 45 607:96//Hs.159273:AF054177
  - F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195
  - F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs. 152936:D63475
  - F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910
- 50 F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291
  - F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:Al188190
  - F-NT2RP2000173
  - F-NT2RP2000175
  - F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.0018:324:58//
- 55 Hs. 100058-AB006713
  - F-NT2RP2000195//ESTs, Weakly similar to C37E2.2 [C.elegans]//3.6e-37:233:90//Hs.56750:Al148761
  - F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050
  - F-NT2RP2000208

F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.0071: 243:61//Hs.143641:AB009462 F-NT2RP2000232//EST//0.0087:187:62//Hs.151024:Z39990 F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:342:59//Hs.8546:U97669 F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227:60//Hs.47822:AB002378 F-NT2RP2000248//EST//0.49:117:70//Hs.61016:AA019719 F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.51:227:60//Hs.30223:X90846 F-NT2RP2000258//ESTs//3.1e-48:261:94//Hs.128230:AA972691 F-NT2RP2000270//ESTs//2.9e-38:357:75//Hs.140329:AA714011 F-NT2RP2000274//ESTs//1.1e-106:508:98//Hs.47646:AA307599 F-NT2RP2000283//EST//1.0:139:63//Hs.128256:AA972910 F-NT2RP2000288 F-NT2RP2000289 F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.2e-60:744:70//Hs. 15 F-NT2RP2000298//ESTs//6.1e-46:322:85//Hs.159490:AI123467 F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//4.3e-13:140: 80//Hs.58218:U82381 F-NT2RP2000327//ESTs//4.3e-18:108:98//Hs.126212:AI417006 20 F-NT2RP2000328//ESTs//6.3e-88:437:96//Hs.127336:Al332905 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607:66//Hs.101642: X60673 F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:126:69//Hs.153706:AF026547 F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.2e-130:627: 25 97//Hs.76556:U83981 F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.56:464:57//Hs.12259:AB014530 F-NT2RP2000412//ESTs//1.0:214:60//Hs.91226:AA649047 F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67:375:93//Hs.808:L28010 F-NT2RP2000420//ESTs, Moderately similar to zinc finger protein [H.sapiens]//3.9e-75:413:92//Hs.36779: 30 AA626790 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//6.7e-128:609: 96//Hs.5819:AF102265 F-NT2RP2000438//ESTs//1.3e-05:50:98//Hs.156532:AA913381 F-NT2RP2000448//EST//1.1e-24:136:98//Hs.160402;Al393918 35 F-NT2RP2000459//H.sapiens mRNA for imagen 38//1.9e-22:158:87//Hs.154655:Z68747 F-NT2RP2000498//ESTs//1.0e-17:181:79//Hs.155243:N70293 F-NT2RP2000503//ESTs//4.5e-41:205:100//Hs.62751:AA765702 F-NT2RP2000510 F-NT2RP2000516 F-NT2RP2000523//ESTs, Highly similar to APOLIPOPROTEIN B MRNA EDITING PROTEIN [Rattus norvegicus] 40 //3.2e-15:167:75//Hs.10984:AA806768 F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6e-38:196:98//Hs.14409:AB011144 F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//1.0: 242:57//Hs.114001:Z20656 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2e-151:732:97//Hs.7314:AB014514 45 F-NT2RP2000644//ESTs//0.035;276;60//Hs.43660;N33174 F-NT2RP2000656 F-NT2RP2000658//ESTs//0.032:281:59//Hs.124853:AA420602 F-NT2RP2000668

50 F-NT2RP2000678//ESTs//2.9e-16:310:65//Hs.126867:AI093453 F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//2.4e-31:233:78//Hs.114905:AA088442 F-NT2RP2000710 F-NT2RP2000715

55 F-NT2RP2000731

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10

F-NT2RP2000758//EST//1.0e-14:199:71//Hs.162409;AA573242

F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.6e-74: 445:89//Hs.21421:AA911739

- F-NT2RP2000809//ESTs//1.2e-36:235:89//Hs.154580:N34101
- F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351:58//Hs.159275:AF030880 F-NT2RP2000814
- F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.0:311:61//Hs.118087:AB011182
- F-NT2RP2000819
  - F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390:70//Hs.20695:AB002292
  - F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds//9.5e-29:167:94//Hs. 75794:U80811
  - F-NT2RP2000845//ESTs//1.0e-83:403:98//Hs.156828:Al336850
- F-NT2RP2000863//ESTs, Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]//6.4e-34:207:92//Hs.135235:Al081880
  - F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.7e-142:732:94//Hs.3615: AB018284
  - F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.50:189:65// Hs.46146:AA418097
  - F-NT2RP2000931//MATRIN3//1.1e-130:610:98//Hs.78825:AB018266
  - F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21//5.5e-66:326:97//Hs.15144:AC005014
  - F-NT2RP2000938//ESTs//1.8e-28:296:75//Hs.22822:H06408
  - F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.9e-113:533:98//Hs.19822:
- 20 AB018298

- F-NT2RP2000965//ESTs//5.3e-59:328:94//Hs.35575:R96494
- F-NT2RP2000970
- F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [Saccharomyces cerevisiae]//7.3e-76:385:96//Hs.21875:AA243700
- 25 F-NT2RP2000987//ESTs//5.6e-11:177:72//Hs.15776:T91944
  - F-NT2RP2001036//ESTs//2.0e-55:352:88//Hs.122131:AA789292
  - F-NT2RP2001044//EST//0.069:267:60//Hs.102808:N67117
  - F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-145:696:97//Hs. 67619:AB007957
- 30 F-NT2RP2001065
  - F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313
  - F-NT2RP2001081
  - F-NT2RP2001094//ESTs//0.0071:262:64//Hs.128115:Al356560
  - F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs.155464:AF088219
- F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519:63//Hs.80358:U52191 F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR ALPHA [Bos taurus]//6.4e-34: 201:91//Hs.118470:Al336362
  - F-NT2RP2001149//EST//3.9e-27:244:78//Hs.162236:AA551582
  - F-NT2RP2001168//ESTs//0.0023:216:62//Hs.134938:Al091361
- 40 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567:96//Hs.26247: AB007949
  - F-NT2RP2001174//H.sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011
  - F-NT2RP2001196
  - F-NT2RP2001218//ESTs//1.1e-65:337:96//Hs.115710:AA524598
- 45 F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.2685:Z50053
  - F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656:70//Hs.69740:U09367
  - F-NT2RP2001245//EST//0.018:228:62//Hs.116798:AA633813
  - F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514:97//Hs.7531:AB018353
  - F-NT2RP2001277//EST//0.42:127:66//Hs.42834:N20277
- 50 F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-62:527:76//Hs.75848:U39412
  - F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287
  - F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:AI146387
  - F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359:71//Hs.76090:M80783
  - F-NT2RP2001328//ESTs//5.2e-103:532:94//Hs.69476:AA628522
- 55 F-NT2RP2001347//ESTs//4.3e-28:217:82//Hs.31775:H41883
  - F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:418:91//Hs.107039:W27244
  - F-NT2RP2001378
  - F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:Al377558

F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//0.28: 225:62//Hs.159402:AC005609

F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:AI189767

F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088

5 F-NT2RP2001420

F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H.sapiens]//0.030:443:59//Hs.140506:AA308018 F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:Al032875

F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966

F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide//

10 9.8e-56:603:72//Hs.75544:Z82248

F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218

F-NT2RP2001449

F-NT2RP2001450

F-NT2RP2001467

15 F-NT2RP2001506

F-NT2RP2001511//ESTs, Weakly similar to F48F7.1 [C.elegans]//3.2e-83:409:98//Hs.156161:Al333779

F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.4e-138:657:97//Hs.4277: Y14494

F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134

F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds// 5.2e-105:384:94//Hs.99742:AF035586

F-NT2RP2001560

F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.4e-124:590:98//Hs. 67619:AB007957

25 F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:521:60//Hs.75936:U28389 F-NT2RP2001581//EST//1.0:28:96//Hs.148002:Al264876

F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:165:65//Hs.82201:M55268

F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-138:647:98//Hs.27197: AB018340

30 F-NT2RP2001613

F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:Al082229

F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//4.9e-124:604:96// Hs.58488:U97067

F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-

35 NA. complete cds//1.3e-145:687:97//Hs.159558:AF058718

F-NT2RP2001663//Enolase 1. (alpha)//4.2e-38:372:74//Hs.675:M14328

F-NT2RP2001675//X-LINKED HELICASE II//0.040:454:58//Hs.96264:U72936

F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.028:285:63//Hs.6162:AB018314

F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.7e-34:328:76//Hs.27621:

40 U52840

F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091

F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.musculus]//1.0:173:62//Hs.107361: AI197870

F-NT2RP2001721

45 F-NT2RP2001740//Homo sapiens Rigui (RIGUI) mRNA, complete cds//0.58:403:57//Hs.8114:AF022991

F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)//1.2e-19:151:86//Hs.77393:D14697

F-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete\_cds//5.2e-34:191:96//Hs.47504: AF091754

50 F-NT2RP2001813//EST//0.46:183:57//Hs.144096:Al032180

F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:Al052250

F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610

F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//0.0013:174:62//Hs.9443: AF027219

55 F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768

F-NT2RP2001883

F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR//3.0e-113:633: 90//Hs.142189:M74161

- F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650
- F-NT2RP2001907//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//0.37:263:62//Hs.106377:H29757
- F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:Al393754
- F-NT2RP2001936
- 5 F-NT2RP2001943
  - F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797
  - F-NT2RP2001947
  - F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489
  - F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//Hs.155174:AB007892
- 10 F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4e-05:235:62//Hs.129943:
  - F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196
  - F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314:97//Hs.116604: AB018299
- 15 F-NT2RP2002032
  - F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:AI003543
  - F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336
  - F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R51509
  - F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:Al284198
- F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137:71//Hs.3615:AB018284 F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509: 66//Hs.44553:AF055634
  - F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241
  - F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:96//Hs.11039:AF052183
- 25 F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014
  - F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:Al313156
  - F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//3.2e-112:533:97//Hs.155218: AJ007509
  - F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//6.1e-07:408:60//Hs.
- 30 122755:AF032986
  - F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286
  - F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319:59//Hs.995:M83363
  - F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.100217:AJ008112
  - F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:AI085314
- 35 F-NT2RP2002185//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//6.8e-61:354:91//Hs.109966:
  - F-NT2RP2002192//Human 75-kD autoantigen (PM-Sc1) mRNA, complete cds//3.7e-37:194:97//Hs.91728:
  - F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds// 6.8e-15:228:67//Hs.111323:AF077954
  - F-NT2RP2002208

- F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628
- F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:Al394318
- F-NT2RP2002235//H.sapiens mRNA for PHAPI2b protein//0.86:67:82//Hs.84264:U70439
- F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cds//0.79:264:59//Hs.129748:AB011099 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//2.1e-51:315:89//Hs.150595: AF005418
  - F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:343:71//Hs.92137:M19720
  - F-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//1.3e-31:206:88//Hs.4029:Z78373
- 50 F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23079
  - F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//5.0e-95:467:96//Hs.
  - F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445
  - F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.3e-124:640:
- 95//Hs.31034:AB015594
  - F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257:60//Hs.75516:X54637
  - F-NT2RP2002373
  - F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//3.1e-139:673:

97//Hs.109051:AF038958

F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.90798:U79289

F-NT2RP2002408//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//0.00069:265:65//Hs.74095:L20433

F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:AI269098

5 F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326

F-NT2RP2002442//ESTs, Weakly similar to similar to molybdoterin biosynthesis MOEB proteins [C.elegans]//5.6e-26:169:89//Hs.25198:AA904265

F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:AI091436

F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013:207:63//Hs.1560:D42045

10 F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:Al139929

F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//7.6e-125:607:96//Hs. 125856:AB005289

F-NT2RP2002498

F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.2e-89:314:87//Hs.102681:U95044

F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.8e-159:761:97//Hs.23255: AB018334

F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs.107563:M28212

F-NT2RP2002537

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F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096

F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979

F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.9e-33:285:78//Hs.159277: AB018341

F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:Z35309

F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4e-24:144:95//Hs.23094:M19503

F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1) mRNA, complete cds//1.0:120:68//Hs.334: U02082

F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp//4.3e-28:460:63//Hs. 20521:Y10805

F-NT2RP2002621

F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0022:210:64//Hs. 155302:U57317

F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs.94694:W52493

F-NT2RP2002701//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:278:97//Hs.109857:AA088385

35 F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58583

F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.0e-42:631:65//Hs.6336: AB014572

F-NT2RP2002727

F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217

F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:AI150297

F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30:628:62//Hs.87435:D89016

F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29:285:75//Hs.146395:AB002329

F-NT2RP2002752//EST//2.2e-06:126:74//Hs.159913:AA862709

F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705

45 F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:507:57//Hs.79706:U53204

F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:AI216407

F-NT2RP2002800

F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763

F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:Al382142

50 F-NT2RP2002862

F-NT2RP2002880

F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0:237:62//Hs.106487:AB014573

F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:W22606

F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds//3.9e-136:623:99//Hs.

55 116674:AF038392

F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24:158:65//Hs.108447:AJ000517

F-NT2RP2002939

F-NT2RP2002954

F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//6.4e-21: 135:91//Hs.108332:U39317

F-NT2RP2002979

F-NT2RP2002980

F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272:61//Hs. 122967:AF059569

F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965:Al004740

F-NT2RP2002993

F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:81//Hs.155464:AF088219

10 F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048:AA811741

F-NT2RP2003073//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.6e-43:381: 78//Hs.159176:U92019

F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190

F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:67//Hs.153704:U11050

15 F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408:AA416633

F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998:AI291379

F-NT2RP2003125//Serum response factor (c-fos serum response element-binding transcription factor)//4.5e-06: 556:57//Hs.155321:J03161

F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836:AA121544

20 F-NT2RP2003137

F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.40:227:61//Hs.105958:AB014520 F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds//5.7e-113:581:93//Hs.9736: D67025

F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532:Al424170

25 F-NT2RP2003164//EST//0.11:179:63//Hs.163299:AA853944

F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342:79//Hs.153014:AB002353

F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767:N91123

F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531:Al393223

F-NT2RP2003206//EST//0.095:182:60//Hs.88461:AA278594

30 F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726:93//Hs.154443:X74794

F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720:AA526947

F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543:77//Hs.108966:U48696

F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.52:

35 200:62//Hs.102732:U88153

F-NT2RP2003265

F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//5.8e-57:313:93//Hs.109966:

F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9e-147:714:96//Hs.154919:

40 AB014525

F-NT2RP2003280

F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.0097:243:65//Hs.21862:

F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227:Al269334

F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds//2.0e-86:416:97//Hs. 7943:AB006572

F-NT2RP2003297//EST//0.99:240:60//Hs.133228:AI052312

F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020:AA442752

F-NT2RP2003308

50 F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//1.8e-102:532:95//Hs.6092:T75227

F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649:Al346765

F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003:H85963

F-NT2RP2003367//Human HsLIM15 mRNA for HsLim15, complete cds//0.99:243:60//Hs.37181:D64108

55 F-NT2RP2003391

F-NT2RP2003393

F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416:57//Hs.4976:AF039023 F-NT2RP2003401

F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//3.7e-33:303:77//Hs.14038:R06800

F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893

F-NT2RP2003446//Prostaglandin receptor, ep1 subtype//0.81:273:61//Hs.159360:L22647

5 F-NT2RP2003456//EST//0.17:95:65//Hs.147190:Al193320

F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//4.3e-53:339:78//Hs.132874:AC004770

F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04106

F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481:60//Hs.80220:U96136

10 F-NT2RP2003506

F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.107164:M96803

F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403:94//Hs.78482:Y16270

F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//1.3e-24:151:95//Hs.1976:M12783

15 F-NT2RP2003522//Zinc finger protein 148 (pHZ-52)//1.1e-17:512:60//Hs.112180:AF039019

F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:AI138765

F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010

F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:Al356513

F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28:664:

20 63//Hs.1042:M62800

F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114:541:98//Hs.129937: AB007931

F-NT2RP2003581//EST//1.0:59:76//Hs.158575:Al368947

F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//1.3e-63:224:95//Hs.34627:

25 AA126463

35

F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124:585:98// Hs.58488:U97067

F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166

F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M97252

30 F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds// 9.4e-47:371:80//Hs.125231:AF068006

F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:Al032875

F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247

F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61//Hs.18366:L09561

F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]//5.1e-44:269:91//Hs.139757:N95271 F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494: AB011097

F-NT2RP2003713

F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:

40 252:83//Hs.86371:AF054180

F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879

F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds//4.0e-55: 584:71//Hs.118797:U39318

F-NT2RP2003751

45 F-NT2RP2003760

F-NT2RP2003764

F-NT2RP2003769

F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:U47677

F-NT2RP2003777

50 F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]//3.7e-63:356:92//Hs.16131:AA568689

F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955

F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742

F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300:59//Hs.77768:X63368

F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425

55 F-NT2RP2003859

F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780

F-NT2RP2003885

F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA [Emericella nidulans]//2.2e-

- 113:632:92//Hs.50072:Al378221
- F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H.sapiens]//1.0:146:67//Hs. 156920:AA489296
- F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//6.8e-30:165:96//Hs.
- 5 35086;AB014458
  - F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.9e-116:610:94//Hs.7302:
  - F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2e-161:783:96//Hs.7316:AB018347 F-NT2RP2003984
- 10 F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:Al050036
  - F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124:AF019369
  - F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//7.0e-104:556:93// Hs.111081:Al380378
  - F-NT2RP2004014
- 15 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs.10116:AC004780
  - F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147: AF011573
  - F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:AI217942
- F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2) mRNA, complete cds//0.15:199: 60//Hs.104315:AF054828
  - F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:AJ007292
  - F-NT2RP2004142
  - F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872
- 25 F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs.78353:U88666 F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:Al419966
  - F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:Al343501
  - F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.7e-16:276:67//Hs.36779:
- F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs.155302: U57317
  - F-NT2RP2004196
  - F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756
  - F-NT2RP2004226//ESTs, Weakly Similar to teg292 protein [M.musculus]//1.8e-80:386:98//Hs.68791:AA527270
- 35 F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756
  - F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680
  - F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536
  - F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs.129725:AF047487
  - F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.elegans]//8.2e-51:474:74//Hs.108990:
- 40 N25951

- F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:60//Hs.12432:AC005263 F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35: 157:67//Hs.37121:Z37544
- F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs.61152: AF000416
- F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735
- F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510
- F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632
- F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202
- 50 F-NT2RP2004365
  - F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.60:295:57//Hs.39163: AF000986
  - F-NT2RP2004373
  - F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III
- 55 [Caenorhabditis elegans]//3.3e-97:477:98//Hs.30490:AA146916
  - F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588
  - F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21//1.4e-174:875:95//Hs.152759:AC005164
  - F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans]//1.2e-92:519:91//Hs.13275:AI341468

F-NT2RP2004400//EST//0.018:150:65//Hs.158739:Al375367

F-NT2RP2004412

F-NT2RP2004425//EST//0.049:145:64/Hs.160759:R36944

F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687

F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//0.45: 208:61//Hs.24040:AF006823

F-NT2RP2004490

F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:AI091203

F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.3e-29:270:79// Hs.73614:U83460

F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6e-139:687:96//Hs.129908: AB011163

F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:Al346891

F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-06:291:61//Hs.132206:

15 AF039694

10

F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:82//Hs.155464:AF088219

F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.98:136:64//Hs.28020:AB018309

F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.0:104:68//Hs.125729:N99898

F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:60//Hs.24756:U43895

20 F-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-59: 273:93//Hs.12845:N28835

F-NT2RP2004614//EST//0.99:103:68//Hs.148738:AI224908

F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496:98//Hs.5198:AJ006291

F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2e-155:728:98//Hs.29956:

25 AB007929

F-NT2RP2004675//EST//0.65:151:62//Hs.130504:AI003839

F-NT2RP2004681

F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1e-61:327:94//Hs.154919: AB014525

30 F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942

F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780

F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.1e-118:582:96//Hs.4236: AB007947

F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609242

35 F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183

F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]// 3.7e-110:548:96//Hs.85768:W16504

F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA, complete cds//0.025:547:57//Hs. 107474:AF045451

F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete cds//0.99:121:64//Hs.2864: L40157

F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds// 4.9e-118:594:95//Hs.40820:AF058953

F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043

45 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495:97//Hs.67052: AF054179

F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83//Hs.84775:M23161

F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:AI290258

F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111

50 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418:95//Hs.25619:AB007144 F-NT2RP2004936

F-NT2RP2004959

F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456:66//Hs.70617:D31763

F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:AI149478

55 F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:Al239735

F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218:61//Hs.7414:AB007927

F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260:60//Hs. 41723:U37426

- F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478 F-NT2RP2004999
- F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58// Hs.124161:AF065164
- 5 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972: AB014515
  - F-NT2RP2005003//H.sapiens Staf50 mRNA//9.9e-44:430:75//Hs.68054:X82200
  - F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5e-100:501:96//Hs.31575:AF100141 F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:J03600
- 10 F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA527433
  - F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.095:271:60//Hs.139745:U39067 F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:338:61//Hs.112743:D67035
  - F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial cds//0.098:217:60//Hs.58167:D30612
  - F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, complete cds//0.22:498:59//Hs.137574:
- 15 AF055917

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- F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838
- F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//6.4e-105:495:98//Hs.22616: AR014564
- F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//9.2e-29:157:98//Hs. 100555:X98743
- F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803
- F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947
- F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds//8.3e-91:447:96//Hs.132226: AF045583
- 25 F-NT2RP2005147
  - F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:Al357582
  - F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.97:80:73//Hs.107747:Al357868
  - F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//4.4e-127:633:96//Hs.155218: AJ007509
- 30 F-NT2RP2005204//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.0034:187:66//Hs.82128:AJ012159 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-66:340:95//Hs.8173:AC005189
  - F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783
  - F-NT2RP2005254//H.sapiens mRNA for PHAPI2b protein//1.0:101:71//Hs.84264:U70439
  - F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete cds//0.56:114:68//Hs.154503:U36341
- F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, complete cds//1.2e-40:594:65//Hs. 81452:AF030555
  - F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:Al383932
  - F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.3e-123:604:96//
- 40 F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:98//Hs.44766:AJ007590
  - F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833
  - F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.6e-97:483:96//Hs.115763: AB014576
  - F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.6e-23:166:90//Hs. 1569:U11701
    - F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds//0.016:353:62//Hs.113265:AF032387
    - F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds//2.8e-30:456:66//Hs.44697:AB011138 F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958
- 50 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-100: 489:96//Hs.107254:AC005943
  - F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122
  - F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mRNA, complete cds//0.87:244:59//Hs. 113252:U80761
- 55 F-NT2RP2005407
  - F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cds//0.28:338:57//Hs.6189:AB011133
  - F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068
  - F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI091164

- F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos taurus]//8.5e-48:295:90//Hs.75017:AA166853
- F-NT2RP2005464//ESTs//2.0e-99:495:96//Hs.3530:AA808243
- F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog//0.032:176:64//Hs.16:D10656
- 5 F-NT2RP2005472//ESTs//1.4e-34:180:98//Hs.158892:AD78412
  - F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds//9.9e-48:432:77//Hs.15519: AB018315
  - F-NT2RP2005490//ESTs//4.5e-19:165:84//Hs.134382:AA083573
  - F-NT2RP2005491
- 10 F-NT2RP2005495//ESTs//5.6e-96:452:99//Hs.145417:Al084164
  - F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds//4.4e-48:621:68//Hs.6833:AB002324
  - F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, complete cds//1.6e-63:503:78//Hs.7688:
  - F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.56:139:66//Hs.8546:U97669
- F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//1.0: 291:59//Hs.89709:L35546
  - F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//1.2e-82: 444:92//Hs.119023:AF092563
  - F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds//2.2e-19:112:99//Hs.6232:
- 20 AB018307
  - F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1 [H.sapiens]//3.5e-50:366:83//Hs. 61833:AA036735
  - F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//9.4e-155:747:97//Hs.159597: AJ012449
- 25 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.9e-131:618:98//Hs.62515: AB007963
  - F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III [C.elegans]//2.5e-51:292:93//Hs.105684:H24407
  - F-NT2RP2005555//EST//0.046:308:57//Hs.145962:Al276822
- 30 F-NT2RP2005557//ESTs//4.6e-48:382:79//Hs.125014:Al422839
  - F-NT2RP2005581//ESTs//6.3e-28:166:93//Hs.87803:AA034436
  - F-NT2RP2005600//ESTs//1.6e-40:228:93//Hs.160085:Al218627
  - F-NT2RP2005605//ESTs//5.7e-13:115:86//Hs.37718:H60071
  - F-NT2RP2005620//Homo sapiens epsin 2b mRNA, complete cds//3.1e-92:447:97//Hs.22396:AF062085
- 35 F-NT2RP2005622//ESTs//0.16:242:63//Hs.136395:AA523702
  - F-NT2RP2005635
  - F-NT2RP2005637//ESTs//0.055:96:69//Hs.105998:R90905
  - F-NT2RP2005640//ESTs//4.5e-16:107:92//Hs.150823:Al292145
  - F-NT2RP2005645//ESTs//2.7e-29:181:90//Hs.121653:Al375440
- 40 F-NT2RP2005651//Oxysterol binding protein//0.00011:122:69//Hs.1433065:M86917
  - F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.5e-08:351:62//Hs.91400: AR006626
  - F-NT2RP2005669//ESTs//0.016:185:64//Hs.97713:AA442239
  - F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//7.7e-96:462:98// Hs.25664:AF089814
  - F-NT2RP2005683//ESTs//0.83:242:62//Hs.136395:AA523702
  - F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.5e-11:328:61//Hs.79217:M77836
  - F-NT2RP2005694

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- F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA, complete cds//0.15:496: 55//Hs.79326:L76703
- F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//5.1e-126:599:97//Hs.61638:
  - F-NT2RP2005719//ESTs//0.58:326:60//Hs.157209:N57527
  - F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)//8.2e-46:415:77//Hs.69740:U09367
- 55 F-NT2RP2005723//ESTs//1.0e-15:141:81//Hs.163747:AA174017
  - F-NT2RP2005726//EST//3.4e-15:96:95//Hs.156170:Al334191
  - F-NT2RP2005732//ESTs//0.99:162:62//Hs.154914:AA721086
  - F-NT2RP2005741//Homo sapiens chondroadherin gene, 5'flanking region and//0.80:362:58//Hs.97220:U96769

F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688

F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96// Hs.159651:AF068868

F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs. 26285:AF082516

F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425:56//Hs.79768:D21853 F-NT2RP2005767//Homolog 2 of Drosophila large discs//0.085:262:61//Hs.23205:X82895

F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:M77836

F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:

10 Z50115

F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556

F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs. 34853:U28368

F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820

15 F-NT2RP2005812

5

F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595

F-NT2RP2005835

F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K exchanger (NCKX1) mRNA, complete cds//0.94:148:65// Hs.59829:AB014602

20 F-NT2RP2005853

F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//5.4e-176:829: 98//Hs 50758:AF092564

F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567

F-NT2RP2005868

25 F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.240: L16782

F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943

F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360

F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399

30 F-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//7.9e-90:326:98//Hs.156882: AA292186

F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770

F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339

F-NT2RP2006023

35 F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382

F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.51:271:59//Hs.37035:U07664 F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093

F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58//Hs.57652:D87469

F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:Al337416

40 F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970

F-NT2RP2006100

F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135

F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349

F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240

45 F-NT2RP2006166

F-NT2RP2006184//H.sapiens p63 mRNA for transmembrane protein//1.0:94:73//Hs.74368:X69910

F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-114:567:96//Hs.109299: AB014554

F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-23:187:85//Hs.15519:

50 AB018315

F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503

F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//4.4e-118:618:93//Hs.153910:X96484

F-NT2RP2006237

F-NT2RP2006238

55 F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI269970

F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK//0.019:111:71//Hs.157199:X97630 F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//2.4e-05:388: 60//Hs.75111:D87258

F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:598:97//Hs.3404:AF035262 F-NT2RP2006320//ESTs, Moderately similar to maternal transcript Maid [M.musculus]//1.9e-29:151:100//Hs.36794:Al038407

F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371

5 F-NT2RP2006323//Homo sapiens mRNA for NBPhox, complete cds//4.7e-06:170:70//Hs.87202:D82344 F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0.11:43:100//Hs.6892: AF076974

F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1e-05:233:65//Hs.37656:AB011174 F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501

10 F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341

F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs. 95838:AF059734

F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:Al221934

F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:Al360509

15 F-NT2RP2006456

F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein/1.1e-149:545:98//Hs.72160:AJ006266

F-NT2RP2006467

F-NT2RP2006472

F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048

20 F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134

F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds//2.1e-115:669:90//Hs.31218:AF038966

F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs. 73864:U22029

25 F-NT2RP2006573

F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223

F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180

F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-137:637:98//Hs.6764:

30 F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531: AF000560

F-NT2RP3000047

F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs. 37138:U35376

35 F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961

F-NT2RP3000068

F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769

F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353:78//Hs.108287:L27670

F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//Hs.80741:X14608

40 F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:Al253140

F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595

F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:438:100//Hs.8173:AC005189 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9e-182:849:98//Hs.13273:

F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-20:133:94//Hs.23094:M19503 F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//6.6e-08:152:71//Hs. 127338:AB007961

F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779

F-NT2RP3000207

50 F-NT2RP3000220

F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.6e-20:509:58//Hs. 122967:AF059569

F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740

F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691:86//Hs.75863:D86972

55 F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733

F-NT2RP3000252

F-NT2RP3000255

F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568

EP 1 074 617 A2 F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//1.7e-13:214:67//Hs. 80261:L43821 F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863 F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds// 0.0088:236:63//Hs.102732:U88153 F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:Al091242 F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.57:189:65// Hs.46146:AA418097 F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:78//Hs.40100:AB002390 F-NT2RP3000348 F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.78582:X80754 F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66//Hs.101642: X60673 F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921 F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Lymnaea stagnalis]//4.0e-116: 596:95//Hs.21094:Al337016 F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639 F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.6e-175:841:97//Hs.28307: F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-33:610:65//Hs.23094:M19503 F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948 F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487 F-NT2RP3000441 F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:Al051562 F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315:58//Hs.75562:U48705 F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068 F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:Al289822 F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:AI084058 F-NT2RP3000512//Homeo box B3//3.1e-18:109:97//Hs.49931:X16667 F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:N21379 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:63//Hs.79347:D86966 F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:H08308 F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA486412 F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404 F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723 F-NT2RP3000578 F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277 F-NT2RP3000584 F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904 F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:57//Hs.77234:AB001914 F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.118741:AA179811 F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [C.elegans]//9.3e-61:355:92//Hs.114622:AA693492 F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553:59//Hs.79170:D86980 F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.127152:Al421203 F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683 F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162 F-NT2RP3000628//ESTs//0.96:221:61//Hs.131161:AI017333 F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs.155464:AF088219

F-NT2RP3000685 F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001

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F-NT2RP3000661

13063:AF017789

F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884

F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854

F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:Al369426

F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305:59//Hs.

- F-NT2RP3000753//ESTs//2.6e-63:318:97//Hs.153000:AA777765
- F-NT2RP3000759//Homo sapiens mRNA for follistain-related protein (FRP), complete cds//1.6e-38:245:91//Hs. 2427:D89937

F-NT2RP3000815

- 5 F-NT2RP3000825//EST//1.0:220:61//Hs.135944:N45132
  - F-NT2RP3000826//Homo sapiens deltex (Dx) mRNA, complete cds//0.00040:263:65//Hs.124024:AF053700 F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 [H.sapi-

ens]//1.1e-71:363:96//Hs.23803:AA126476 F-NT2RP3000841//EST//0.36:224:60//Hs.162094:AA524012

- 10 F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593:68//Hs.157199:
  - F-NT2RP3000847//ESTs//0.0028:56:92//Hs.116406:AA209520
  - F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323:86//Hs.155464:AF088219 F-NT2RP3000852
- 15 F-NT2RP3000859//ESTs//0.39;169:62//Hs.148948:AA699918
  - F-NT2RP3000865//EST//0.15:236:62//Hs.123366:AA811476
  - F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//6.4e-31:766:60//HS.15432:U53445
  - F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701:60//Hs.79706:U53204
- 20 F-NT2RP3000875
  - F-NT2RP3000901//ESTs//8.2e-26:191:87//Hs.18793:R99101
  - F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:Al348374
  - F-NT2RP3000917
  - F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:340:60//Hs.109895:X68277
- 25 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351:83//Hs.2953:X84407
  - F-NT2RP3000980//ESTs//6.5e-10:102:81//Hs.86950:Al204212
  - F-NT2RP3000994//ESTs//4.1e-120:571:98//Hs.127295:AA918411
  - F-NT2RP3001004//ESTs//1.1e-76:438:88//Hs.144554:N92198
  - F-NT2RP3001007
- F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]// 2.9e-121:588:98//Hs.128781:AA160707
  - F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-54:282:97//Hs. 30303:Al244662
  - F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.7e-51:534:74//
- 35 Hs.27007;AF060219
  - F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474:60//Hs.21264:AB018325 F-NT2RP3001096//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.4e-16:428:60//Hs.155481: A.I006470
  - F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712:64//Hs.82292:D86969
- 40 F-NT2RP3001109//ESTs//1.2e-67:323:99//Hs.134734:Al337050
  - F-NT2RP3001111
  - F-NT2RP3001113//EST//1.1e-33:173:99//Hs.112640:AA609088
  - F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA688023
  - F-NT2RP3001116//ESTs//1.1e-15:93:98//Hs.58412:W74779
- 45 F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258:61//Hs.12107:AF042384
  - F-NT2RP3001120//Zinc finger protein 136 (clone pHZ-20)//2.4e-77:687:75//Hs.69740:U09367
  - F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341:60//Hs.94790:
  - F-NT2RP3001133//Homeo box A4//0.00011:484:59//Hs.77637:M74297
- 50 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851:98//Hs.5378:AB018305 F-NT2RP3001147
  - F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257:59//Hs.957:M84605
  - F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//1.7e-191:891:98//Hs.72160:AJ006266 F-NT2RP3001176
- 55 F-NT2RP3001214//EST//0.88:218:60//Hs.161147:Al417859
  - F-NT2RP3001216//ESTs//1.5e-66:340:96//Hs.105994:W19981
  - F-NT2RP3001221//ESTs, Weakly similar to M05D6.7 [C.elegans]//1.7e-97:512:95//Hs.103816:AA130866
  - F-NT2RP3001232//EST//0.0016:116:71//Hs.136498:AA594010

- F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:Al362756
- F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62//Hs.103042:L06237
- F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA743132
- F-NT2RP3001253//Human prepromultimerin mRNA, complete cds//0.99:293:60//Hs.32934:U27109
- 5 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds//1.2e-48:761:64//Hs.107809:
  - F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.2e-42:454: 72//Hs.41728:L75847
  - F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566
- 10 F-NT2RP3001274
  - F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811
  - F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds//2.4e-48:544:69//Hs.31463:D87457
  - F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0.72:151:68//Hs.159437: U44060
- F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.012:522:56//Hs.904:U84010
  - F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731
  - F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-30:345:73//Hs.79347:D86966
  - F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//6.3e-67:559:80//Hs.18586:
- 20 AB007920
  - F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.00019:473: 61//Hs.124161:AF065164
  - F-NT2RP3001355//ESTs, Weakly similar to ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 [H.sapiens]// 1.1e-81:421:96//Hs.32508:H29831
- 25 F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.15:313:60//Hs.129725:AF047487 F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022
  - F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.30965:AB001451
  - F-NT2RP3001384//Homa sapiens mRNA for HRIHFB2018, partial cds//2.1e-158:743:98//Hs.146214:AB015332 F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595
- 30 F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783
  - F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide)//1.0e-05:189: 66//Hs.41728:L75847
  - F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CTP) mRNA, 3' end//0.77:132:66//Hs. 111024:L77567
- 35 F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658
  - F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047
  - F-NT2RP3001426
  - F-NT2RP3001427
  - F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.8e-73:431:91//Hs.85844:X66397
- 40 F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//6.9e-05:195:65//Hs.115868:AA568393
  - F-NT2RP3001447
  - F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:68//Hs.89631:U48508 F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212
- 45 F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323
  - F-NT2RP3001459
  - F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds//4.2e-10:168:70//Hs.32317: AF072836
  - F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877
- 50 F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231
  - F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds// 2.8e-172:804:98//Hs.28285:AF064801
  - F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds//9.4e-139:743: 91//Hs.85283:U36500
- F-NT2RP3001529//ESTs, Moderately similar to topoisomerase IC-terminal fragment [H.sapiens]//0.28:224:65//Hs. 105912:Al431328
  - F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074
  - F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//Hs.147918:U38291

- F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302
- F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)//0.049:185:65//Hs.1686: M69013
- F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.6e-51:345:82//Hs.144563:
- 5 AF057280

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- F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688
- F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:Al091349
- F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435
- F-NT2RP3001629
- F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4e-62:276:97//Hs.9899:AF099149 F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173
  - F-NT2RP3001646
  - F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.1e-172:816:98//Hs.159597: AJ012449
- 15 F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027
  - F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//9.0e-53: 375:85//Hs.41127:AA555184
  - F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65//Hs.79077:D87071
  - F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III
- 20 [Caenorhabditis elegans]//4.0e-111:518:99//Hs.20364:Al420022
  - F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63//Hs.7486:D83198
  - F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329
  - F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219
  - F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRECURSOR [D.melanogaster]//1.4e-31:191:94//Hs.131279:AA486291
  - F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41:259:59//Hs.58435:AF001862 F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus] //7.6e-159:747:98//Hs.6823:W18181
  - F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//4.4e-161:
- 30 565:97//Hs.159273:AF054177
  - F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.5e-116:554:98//Hs.144332:AA046836
  - F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:78//Hs.90998:D50918 F-NT2RP3001739
- 35 F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.116549:AL009172
  - F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//0.10:528:56//Hs.22138:U49250
  - F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2.4e-47:725:64//Hs.41688: 1127193
- F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds//0.42:198:61//Hs. 57783:U78525
  - F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1e-153:710:98//Hs.28169: AB007928
  - F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.79024:L03532
- 45 F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361
  - F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.53563:L41162
  - F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-II//0.90:379:58//Hs.32950:X82634
  - F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729
  - F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.8e-35:481:67//Hs.158225:
    - F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706
    - F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [C.elegans]//2.9e-94:452:98//Hs.54952: AA872675
    - F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6139:AL022326
- 55 F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896
  - F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185
  - F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247
  - F-NT2RP3001931

F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//0.0022:268:61//Hs.106070:U22398 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.8e-167:815:96//Hs.15869: AB014575

F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:Al339335

5 F-NT2RP3001969

F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180

F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:83//Hs.155464:AF088219

F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//Hs.75087:X86779

F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946

10 F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821

F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67//Hs.147189:D88153

F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]//3.8e-48:353:81//Hs.127507:

F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0e-25:212:83//Hs.71622:AA195155

15 F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PROTEIN 1 [Homo sapiens]//4.2e-82: 407:97//Hs.131888:AI091806

F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-21:168:85//Hs.23094:M19503 F-NT2RP3002062//EST//0.46:198:62//Hs.157711:Al359710

F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//

20 0.91:194:65//Hs.1298:J03779

F-NT2RP3002081

F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA partial cds//0.073: 297:61//Hs.102732:U88153

F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256

25 F-NT2RP3002108

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F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018

F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260

F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative

CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009

F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644

F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985 F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus] //3.0e-61:340:93//Hs.11379:AA594140

35 F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046

F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141429:AA631915

F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA30643

F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic1)//0.98:

40 242:57//Hs.114001:Z20656

F-NT2RP3002248

F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261

F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds//0.42:189:62//Hs. 110637:AC004080

45 F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139

F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386

F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//1.3e-05:496:60//Hs.21537:X80910 F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871

F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:462:56//Hs.143624:AF033383

F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1.6e-65: 588:75//Hs.154672:X16396

F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//4.2e-166:770:98//Hs.6483: Y16355

F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5e-161:911:89//Hs.2397:Z70200

F-NT2RP3002399
F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233:94//Hs.22880:AA056274

F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9e-140:649:99//Hs.12707: AB014578

- F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:Al291310
- F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108
- F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0:173:61//Hs.81234:AB007935
- F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//4.4e-146:763:93//Hs.
- 5 57738:U35246
  - F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9e-180:833:98//Hs.19542: AB018272
  - F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sapiens]//1.3e-42:510:70//Hs. 96759:AA469984
- 10 F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X78706
  - F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054
  - F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:AI187919
  - F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.89631:U48508 F-NT2RP3002603
- 15 F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:61//Hs.3845:AB014888
  - F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.121287:AF029900
  - F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.6e-13:441:63//Hs.155481: AJ006470
  - F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, complete cds//1.7e-05:615:58//Hs.
- 20 151518:U38847
  - F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:AA584308
  - F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo sapiens]//4.1e-38:493:70// Hs.41086:Al337400
  - F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:AI421991
- 25 F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans]//1.6e-61:294:100//Hs.128750:Al367584 F-NT2RP3002687
  - F-NT2RP3002688//EST//1.0:312:58//Hs.156800:Al352200
  - F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:Al393657
  - F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:AI279514
- 30 F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291
  - F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6) gene, partial cds//0.91:161:62// Hs.129736:AF040753
  - F-NT2RP3002785
  - F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713
- F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens]//1.4e-76:423:93//Hs.41068:AA844350 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds//2.2e-55:615:70//Hs.105940: AF004715
  - F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA524070
  - F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T33582
- 40 F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88//Hs.123090:AB001895
  - F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA626040
  - F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8e-181:853:98//Hs.6162:AB018314 F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:AI138765
- F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//1.4e-133:645:97//
  Hs.3826:U69560
  - F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.2e-13:594:57//Hs.74599: AB011160
  - F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.76:412:57//Hs.21198:AB018262 F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870
- 50 F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997 F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:Al287703
  - F-NT2RP3002985//Human TFIIB related factor hBRF (HBRF) mRNA, complete cds//0.071:550:58//Hs.32935: U28838
  - F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:AI218308
- 55 F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:M91083
  - F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C06446
  - F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749
  - F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609

- F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928
- F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079
- F-NT2RP3003078
- F-NT2RP3003101
- 5 F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//0.98: 88:68//Hs.99715:AA292700
  - F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:Al090740
  - F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1) mRNA, complete cds//0.013:438:57//Hs.101299:AF017061
- 10 F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975
  - F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA, complete cds//2.2e-20:430: 63//Hs.118397:AF053944
  - F-NT2RP3003150
  - F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.
- 15 37138:U35376
  - F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.045:410:59//Hs.6150:AB011093
  - F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:X78933
  - F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211
  - F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854
- 20 F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308
  - F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325
  - F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525
  - F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//6.0e-55:587:70//Hs.109606:
- 25 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//1.2e-129:617:98//Hs.155223: AF055460
  - F-NT2RP3003251//H.sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200
  - F-NT2Rp3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59// Hs.620:M69225
- 30 F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.98:261:59//Hs.30792: AF044924
  - F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:694:93//Hs.11702:L36983
  - F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953
  - F-NT2RP3003301//EST//1.0:58:74//Hs.158575:Al368947
- 35 F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1e-91:681:80//Hs.23094:M19503
  - F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947
  - F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:Al084058
  - F-NT2RP3003327//H.sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200
  - F-NT2RP3003330
- 40 F-NT2RP3003344

- F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//1.2e-42:644:66//Hs.2638:Z28339
- F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L78833
- F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//Hs.148090:D83542
- F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791
- 45 F-NT2RP3003385//ESTs, Highly similar to SKD3 [M.musculus]//7.0e-74:384:96//Hs.21263:H16363
  - F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850
  - F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//3.2e-22:430: 63//Hs.113272:U90653
  - F-NT2RP3003411//Human metallothionein-le gene (hMT-le)//0.99:116:62//Hs.74170:M10942
- 50 F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:Al422830
  - F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:243:61//Hs.62:M93425
  - F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.7e-182:853:98//Hs. 14934:AF004828
  - F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2e-175:826:98//Hs.26450: AB018268
  - F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98330
  - F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302
  - F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete cds//0.64:626:58//Hs.150828:

AF038169

F-NT2RP3003552

F-NT2RP3003555//ESTs//1.4e-12:81:98//Hs.144487:Al418322

F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365

5 F-NT2RP3003572//EST//0.27:105:69//Hs.162134:AA526311

F-NT2RP3003576//ESTs//1.2e-57:277:84//Hs.138852:AA284247

F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.123109:X56741

F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:564:61//Hs.104: D14012

10 F-NT2RP3003625

F-NT2RP3003656

F-NT2RP3003659

F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586

F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:N76184

15 F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds//0.013:190: 63//Hs.44585:U58334

F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69:246:62//Hs.118463:AF055000 F-NT2RP3003701//EST//0.93:79:69//Hs.145285:AI249848

F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478:61//Hs.48998:AB007865

20 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.4e-150:700:98//Hs.48513: AB018300

F-NT2RP3003746

F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230

F-NT2RP3003799

25 F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog//4.7e-41:432:73//Hs.1422: M19722

F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98: 242:57//Hs.114001:Z20656

F-NT2RP3003809//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds// 5.1e-07:624:59//Hs.96028:AF042832

F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//0.84:171:63//Hs. 102877:U41315

F-NT2RP3003825

F-NT2RP3003828//ESTs//2.1e-12:434:61//Hs.156864:Al346481

35 F-NT2RP3003831

30

F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242:98//Hs.25300: AF070611

F-NT2RP3003842//integrin, beta 8//1.0:345:60//Hs.832:M73780

F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335:68//Hs.26450:AB018268

40 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805:99//Hs.118738: AB018343

F-NT2RP3003876//ESTs, Highly similar to Rabin3 [R.norvegicus]//6.8e-39:243:90//Hs.124832:AA846576 F-NT2RP3003914//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//1.1e-107:499:99//Hs.105794:AA701659

45 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds//8.3e-49: 404:77//Hs.9006:AF057358

F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396

F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:AI359006

F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)//0.00070:433:58//Hs.

50 93909:AF042498

F-NT2RP3004013//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//2.8e-127:617:97//Hs. 142151:AA984061

F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283:62//Hs. 155302:U57317

55 F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234

F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774:67//Hs.26441:AB002317 F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:AI032875

F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression)//5.3e-90:520:90//Hs.

100007:X76091

F-NT2RP3004093

F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:69//Hs.81281:U79258

F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211:77//Hs.40100:AB002390

5 F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCOF7.1 [Xenopus laevis]//1.0e-126:590:99//Hs.129888:AI096509

F-NT2RP3004145

F-NT2RP3004148

F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578:98//Hs.157113:

10 AF032900

F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706

F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640

F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281: 62//Hs.101047:M31523

15 F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:AI221835

F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361

F-NT2RP3004242

F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240

F-NT2RP3004253//ESTs//1.2e-36:204:96//Hs.143588:Al149140

20 F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369:59//Hs.71346:Y00067 F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733:98//Hs. 158471:AF088982

F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:597:61//Hs.19261:AF007871 F-NT2RP3004332

25 F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285

F-NT2RP3004341//EST//0.0068:213:64//Hs.153208:X98426

F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA830999

F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-45:337:83//Hs.141429:AA631915

F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//
4.3e-125:608:98//Hs.128781:AA160707

F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1//2.3e-141:804:90//Hs.123122: X97249

F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-122:609:96//Hs.20132:AA203113

35 F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:60//Hs.153638:AF010403

F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.00023:357:59//Hs.99948:M97016

F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.0e-124:583:99//Hs.27349: AB007917

F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.48:399:58//Hs.22616:AB014564

40 F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219

F-NT2RP3004472

F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8e-152:715:98//Hs.5003:AB007925 F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]// 4.6e-118:547:99//Hs.124768:AA307735

F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:752:97//Hs.158311:AB012851 F-NT2RP3004498//ESTs, Moderately similar to ROSA26AS [M.musculus]//3.5e-89:425:99//Hs.126082:AI077718 F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256

F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0:370:59//Hs.158244:AB007948 F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.7647:M94046

50 F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110

F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:AI031571

F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7e-146:679:98//Hs.75970: AB014532

F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1e-171:793:98//Hs.74750: AB011126

F-NT2RP3004566//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//2.2e-66:362:94//Hs. 125870:Al364967

F-NT2RP3004569

- F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF50) mRNA, complete cds//3.3e-181:860:97// Hs.122752:AF026445
- F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0e-85:422:97//Hs.129928: AB007923
- 5 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs.72160:AJ006266
  - F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger protein, efp [H.sapiens]//6.4e-13:356:64// Hs.124138:Al266336
  - F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA909232
  - F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56//Hs.79706:U53204
- 10 F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436
  - F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//8.0e-177:827:98// Hs.118991:AA675919
  - F-NT2RP4000023//ESTs//1-4e-33:182:96//Hs.122722:AA455668
  - F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495
- 15 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556:85//Hs.129844:AF029761 F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.9e-13:441:62//Hs.155481: AJ006470
  - F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e-151:720:97//Hs.159597: AJ012449
- 20 F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743
  - F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:99//Hs.57929:AB011538 F-NT2RP4000111
  - F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548:98//Hs.64691: AB007952
- 25 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:63//Hs.75520:D26069 F-NT2RP4000150
  - F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3386:AF053356
  - F-NT2RP4000159
  - F-NT2RP4000167
- 30 F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946
  - F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825:98//Hs.13999: AB014600
  - F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA422006
  - F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731
- 35 F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425:71//Hs. 46468:U45984
  - F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.6e-158:771:97//Hs.155481: AJ006470
  - F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus]//1.9e-62: 384:89//Hs.115498:AA436298
  - F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728: AF091092
  - F-NT2RP4000263

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- F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580
- 45 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481
  - F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs. 143648:AB000732
  - F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112 F-NT2RP4000355
- 50 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:
  - F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-137:649:97//Hs.31323:AF044195
  - F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:Al382073
  - F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2// 0.098:291:59//Hs.994:M95678
    - F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965

- F-NT2RP4000398//Zinc finger protein 140 (clone pHZ-39)//4.9e-60:469:68//Hs.154205:U09368
- F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688
- F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315: AF027156
- 5 F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete cds//2.0e-34:431:73//Hs. 46468:U45984
  - F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087
  - F-NT2RP4000449//EST//0.84:113:65//Hs.145274:Al249468
  - F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853
- F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)//1.1e-05: 532:57//Hs.78683:Z72499
  - F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151:AB001535
  - F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//Hs.78862:D87742
  - F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.94:133:69//Hs.
- 15 159234:U89995
  - F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2//0.60:335:61//Hs.74605:X13293 F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594
  - F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904
  - F-NT2RP4440518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.0e-34:203:93//Hs.99423:
- 20 AJ010840
  - F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66//Hs.100837:AB002372 F-NT2RP4000524
  - F-NT2RP4000528
  - F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:Al348154
- 25 F-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//1.1e-27:162:93//Hs. 25597:H93026
  - F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351
  - F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053
  - F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.
- 30 4214:AF067730
  - F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513
  - F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396
  - F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367: 60//Hs.144626:AF100907
- F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//8.0e-167:676: 98//Hs.50748:AB004848
  - F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783
  - F-NT2RP4000724//ESTs, Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:78//Hs.111817:T80622
- F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178 F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440
  - F-NT2RP4000739//DESMOPLAKIN I AND II//0.99:192:63//Hs.74316:AL031058
  - F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162 F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123
- 45 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132: AB007939
  - F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:99//Hs.8173:AC005189
  - F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833
  - F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:W27603
- 50 F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs. 75875:U49278
  - F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367
  - F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:Al206803
  - F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843
- 55 F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901 F-NT2RP4000918
  - F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865

- F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503
- F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97// Hs.24812:AF069532
- F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:Al281371
- F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542
   F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888
   F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058
   F-NT2RP4000979
  - F-NT2RP4000984
- F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U90913 F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068
  - F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204 F-NT2RP4001004
  - F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718
- 15 F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs. 113287:AF009204
  - F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494 F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864: L40157
- 20 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157
  - F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP)//7.2e-13:441:63//Hs.155481: AJ006470
  - F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497
  - F-NT2RP4001079//Homo sapiens mRNA for putative Ca2+-transporting ATPase, partial//1.4e-131:634:98//Hs.
- 25 106778:AJ010953
  - F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//0.025:166:66//Hs. 146459:X66975
  - F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164 F-NT2RP4001095
- F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:448:98//Hs.105837:AA536054 F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//2.2e-26:171:92//Hs.14038:R06800
  - F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//Hs.109804:D64142
  - F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//5.8e-37:185:
- 35 100//Hs.126925:AA931237
  - F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.1433 82:AA476266
  - F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:Al358261
  - F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207
  - F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171
- 40 F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734
  - F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324
  - F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264
  - F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324
  - F-NT2RP4001207
- 45 F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:Al017636
  - F-NT2RP4001213//KRAB zinc finger protein {alternative products}//1.1e-45:187:74//Hs.22556:U37251
  - F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262
  - F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs. 122967:AF059569
- 50 F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs.106387:AF029778 F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:D87463 F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A1, 59kD, acidic component)//0.015:246:62// Hs.31121:U40571
  - F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578
- 55 F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs.110826:U80736
  - F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250
    - F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:Al375917

- F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110 F-NT2RP4001339 F-NT2RP4001343 F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39;686:64//Hs.112125:M12625 F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete 5 cds//2.0e-31:784:62//Hs.15432:U53445 F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356 F-NT2RP4001372 F-NT2RP4001373//Homo sapiens clone Dt1P1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101:Z50194 F-NT2RP4001375 10 F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190 F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:Al393918 F-NT2RP4001407//Homo sapiens mRNA for RGS5, complete cds//0.93:218:58//Hs.24950:AB008109 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957 F-NT2RP4001433//Zinc finger protein 10 (KOX 1)//1.1e-88:839:73//Hs.2479:X78933 F-NT2RP4001442 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153: AB018326 F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]//2.1e-90:460:96//Hs. 20 26676:AA033997 F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//Hs.75533:D10523 F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]//0.25:216:60//Hs. 63220:AA522707 F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395 F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:281:61//Hs.5923:X82260 25 F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:173:94//Hs.5570:Al377863 F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-35:329:76//Hs.154970:U03494 F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//0.0015:221:65//Hs.44481: F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs.30649:U50534 30 F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174 F-NT2RP4001567 F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN MET30-CBR5 INTERGENIC REGION [Saccharomyces cerevisiae]//1.1e-54:252:83//Hs.158208:AA167836 F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410 35 F-NT2RP4001574 F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98//Hs.108826:AL031228 F-NT2RP4001592 F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903 F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952 40 F-NT2RP4001634 F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN FKH1-STH1 INTERGENIC REGION [S.cerevisiae]//8.6e-57:287:97//Hs.117439:C18436 F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.5591:AB000409 F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MITOCHONDRIAL PRECUR-45 SOR [Saccharomyces cerevisiae]//1.0:311:59//Hs.57969:AA203629 F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//0.19:162: 67//Hs.30250:AF055376 F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:332:86//Hs.113283:AF018080 50 F-NT2RP4001696 F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927 F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs. 92614:M62302
  - F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198
    F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M27878
    F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656
    F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-34:400:68//Hs.154212: AC004522

- F-NT2RP4001803//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L36069
- F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131
- F-NT2RP4001823//Human faciogenital dysplasia (FGD1) mRNA, complete cds//3.1e-07:509:59//Hs.1572:
- 5 U11690
  - F-NT2RP4001828
  - F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:73//Hs.78398:D31888
  - F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749
- F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-57:813:65//Hs.6336: AB014572
  - F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.8e-12: 84:94//Hs.140232:AA705170
  - F-NT2RP4001889
  - F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-108:535:97//Hs.15144:AC005014
- 15 F-NT2RP4001896
  - F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848
  - F-NT2RP4001927
  - F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.8e-54:375:84//Hs.119294:
- 20 F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894
  - F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063
  - F-NT2RP4001953//ESTs//0.018:206:65//Hs.130105:AA904868
  - F-NT2RP4001966//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribos-
- omal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//1.7e-54: 788:65//Hs.23796:AL022718 F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete cds//0.0019:279:65//Hs.159439:AF092047
  - F-NT2RP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//0.58:463:55//Hs. 3826:U69560
- 30 F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:Al243139
  - F-NT2RP4002052
  - F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873
  - F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA, complete cds//0.97:227:60//
- 35 F-NT2RP4002075
  - F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.0e-38:243:90//Hs.139115: AA325104
  - F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654
  - F-NT2RP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152:70//Hs.25180:M96684
- F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0e-10:401:59//Hs.89616:M55284 F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204 F-NT2RP4002888
  - F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960
  - F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96//Hs.74456:U34995
- 45 F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071
  - F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.18:271:60//Hs.139745:U39067 F-NT2RP5003492
  - F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase, complete cds//6.1e-56:750:69// Hs.132884:AB006179
- 50 F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-14:348:62//Hs.154050: AC004131
  - F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.94:202:63//Hs.8152:AB014542 F-NT2RP5003522
  - F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:Al308943
- 55 F-NT2RP5003534
  - F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0e-69:373:94//Hs.108258: AB007934
  - F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:Al391729

- F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairina moschata]//4.4e-75:355:99//Hs.36727: AI051983
- F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304
- F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-171:815:98//Hs.81449:AF058922
- F-OVARC1000017//Homo sapiens mRNA for NTAK, complete cds//0.50:482:58//Hs.113264:AB005060
  - F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2e-37:238:89//Hs.69469:AF064603
  - F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549
  - F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor [H.sapiens]//6.7e-60:305:97//Hs.31696:
- 10 F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798
  - F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543
  - F-OVARC1000085

- F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442
- F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete . cds//0.00017:414:59//Hs.106387:AF029778
- 15 F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600
  - F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans]//2.9e-73:406:92//Hs.109463:Al205174 F-OVARC1000109
  - F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.3e-135:663:96//Hs.3688:AF069250
- 20 F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete cds//3.4e-43:532:72//Hs.118401: AB011134
  - F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:Al384010
  - F-OVARC1000139
  - F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293
- 25 F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414
  - F-OVARC1000151
  - F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305
  - F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)//0.10:504:59//Hs.154083:U70136
- 30 F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:Al249131
  - F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840
  - F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834
  - F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens] //2.7e-31:264:79//Hs.151895:AA196379
- 35 F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:466:68//Hs.8136:U81984
  - F-OVARC1000288//TESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.00084:170:65//Hs.107747:Al357868
  - F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306
  - F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287
  - F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECUR-
- 40 SOR [Felis catus]//0.51:193:66//Hs.6194:Al378579
  - F-OVARC1000321
  - F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds//0.0018:507:60// Hs.122359:AF051946
  - F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444
- 45 F-OVARC1000347
  - F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds//3.4e-06:353:62//Hs.121895:AF001450
  - F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:231:64//Hs.156016:D50930
  - F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162
- 50 F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682
  - F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:231:58//Hs.156016:D50930
  - F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]//1.7e-25:190:84//Hs.139513:AA259082
  - F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615
  - F-OVARC1000437//Filamin 1 (actin-binding protein-280)//0.93 :281:60//Hs.76279:X53416
- 55 F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:116:99//Hs.83987:U09284
  - F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:Al377423
  - F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.2e-140:566:99//Hs.12334: AB014583

- EP 1 074 617 A2 F-OVARC1000461//ESTs//1.0e-39:215:95//Hs.131532:Al024524 F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58//Hs.108112:AF070640 F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854 F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926 F-OVARC1000479 F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036 F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:AI023327 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115:539:99//Hs.111285:AF051850 F-OVARC1000526//ESTs//2.9e-08:368:611/Hs.42771:N26740 F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492 F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475 F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667 F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410 F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA, complete cds//0.87:135: 66//Hs.85302:U76421 F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358 F-OVARC1000576//ESTs//9.4e-22:124:98//Hs.24220:W22200 F-OVARC1000578//EST//4.7e-31:335:74//Hs.162881:AA652729 F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263:63//Hs.3080:U29725 F-OVARC1000605//EST//1.0:148:62//Hs.163346:AA883722 F-OVARC1000622//EST//4.3e-50:313:88//Hs.149580:AI281881 F-OVARC1000640//ESTs//2.6e-55:441:80//Hs.105319:AA470097 F-OVARC1000649//Human squamous cell carcinama of esophagus mRNA for GRB-7 SH2 domain protein, complete cds//1.6e-78:424:93//Hs.86859:D43772 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536:94//Hs.111862: AB011162 F-OVARC1000678//EST//1.3e-08:131:77//Hs.145970:Al277106 F-OVARC1000679//ESTs//0.66:223:61//Hs.134782:H74279 F-OVARC1000681//EST//0.017:315:61//Hs.147799:AI221639 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.8e-153:549:99//Hs. 125315:AF027156 F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs.4764:AB018306 F-OVARC 1000700 F-OVARC1000703//ESTs//0.41:100:68//Hs.160699:AI284320 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds// 1.2e-110:451:91//Hs.13476:AF038661 F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318:91//Hs.7049: AI141736 F-OVARC1000746//ESTs//3.2e-123:570:99//Hs.127295:AA918411 F-OVARC1000769//ESTs//0.072:177:67//Hs.142573:AA601196 F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-2 [H.sapiens]//1.2e-38:194:99// Hs.157059:W28130 F-OVARC1000781//ESTs//4.0e-14:113:89//Hs.41972:AA626793 F-OVARC1000787//EST//0.92:91:64//Hs.163258:AA828835 F-OVARC1000800//ESTs//1.6e-44:193:81//Hs.163971:N27584 F-OVARC1000802//ESTs//4.6e-43:395:80//Hs.115401:AA400032 F-OVARC1000834//ESTs//1.9e-91:431:99//Hs.154450:AA069390
- 45
  - - F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432:100//Hs.155995: AB014543
- F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//Hs.18910:AF045584 50 F-OVARC1000862//ESTs, Highly similar to gene Fif protein [M.musculus]//6.1e-31:183:93//Hs.108620:AA418155 F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.54:133:69//Hs. 159234:U89995
  - F-OVARC1000883//ESTs//0.44:154:63//Hs.98183:AA417143
- F-OVARC1000885//EST//0.91:152:63//Hs.160765 :AI313323 55
  - F-OVARC1000886//ESTs//4.6e-08:375:61//Hs.131653:AI025777
  - F-OVARC 1000890

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F-OVARC1000891

- F-OVARC1000897//ESTs//1.1e-07:145:69//Hs.119878:AA706818
- F-OVARC1000912//EST//3.6e-08:376:61//Hs.158782:Al376601
- F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3e-85:419:97//Hs.9028:AF039691 F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA424456
- 5 F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//4.3e-64:623:72//Hs.114440: M11119
  - F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078
  - F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.sapiens]//2.4e-29:157:97//Hs. 136243:AA307843
- 10 F-OVARC 1000948
  - F-OVARC1000959//EST//0.65:293:55//Hs.134725:Al088986
  - F-OVARC1000960//Ley I-L//1.4e-41:425:72//Hs.37062:AC005952
  - F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288
  - F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:AI283069
- 15 F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2557:Y00661
  - F-OVARC1000996//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//6.8e-10:312:65//Hs. 155302:U57317
  - F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete cds//0.0056:209:62//Hs.10458: AF088219
- 20 F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114
  - F-OVARC1001004
  - F-OVARC1001010
  - F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus]//3.8e-47:234:99//Hs.110327:AA205866
  - F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.0076:
- 25 624:57//Hs.75063:AL023584
  - F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus]//3.9e-97:578:89//Hs.111974:Al050735
  - F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//8.6e-152:733:97//Hs.9899:AF099149
  - F-OVARC 1001040//ESTs//2.2e-38:204:96//Hs.128927:AI168074
  - F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017385
- 30 F-OVARC1001051
  - F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//1.1e-46:381:81//Hs. 154968:U02020
  - F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:Al312873
  - F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans]//1.4e-21:183:84//Hs.46680:AA809451
- 35 F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//6.6e-132:620:98//Hs. 3426:AF082657
  - F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA709013
  - F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001937
  - F-OVARC1001085//H.sapiens mRNA for sortilin//0.99:142:67//Hs.104247:X98248
- 40 F-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.3e-75:289:95//Hs.21753:AJ005897
  - F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds//1.2e-73:351:86//Hs.12912:AF015913
  - F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//2.1e-151:710:98//Hs.26584: AF051782
- 45 F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA813102
  - F-OVARC1001118
  - F-OVARC1001129
  - F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.75451:AF055008
  - F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA621725
- 50 F-OVARC1001162
  - F-OVARC1001167
  - F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:AI078279
  - F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA813287
  - F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA226159
- F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1 PRECURSOR [Homo sapiens]//1.8e-11:192:69//Hs.130020:AA887581
  - F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:58//Hs.91103:AC005551
  - F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//1.5e-13:199:71//Hs.109966:

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F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.4e-52:324:90//Hs.114673:W72675

F-OVARC1001200//ESTs//3.9e-16:104:94//Hs.125520:AA883889

5 F-OVARC1001232//Cyclin A//0.95:124:67//Hs.85137:X51688

F-OVARC1001240//EST//0.017:351:60//Hs.120655:AA745676

F-OVARC1001243//ESTs//0.78:291:59//Hs.132458:AI424825

F-OVARC1001244//RING3 PROTEIN//2.8e-19:118:95//Hs.75243:D42040

F-OVARC1001261//EST//1.9e-42:225:96//Hs.158854:Al377837

10 F-OVARC1001268//ESTs//0.66:239:61//Hs.132525:AA576821

F-OVARC1001270//ESTs//0.99:204:60//Hs.144647:AA625224

F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8e-144:644:96//Hs.155995: AB014543

F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]//0.11:355:60//Hs.108812:AA044835

15 F-OVARC1001296//ESTs//1.1e-46:237:98//Hs.33746:N78172

F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.20:188:64//Hs. 152455:AF044209

F-OVARC1001329//ESTs//1.4e-97:486:97//Hs.125886:AA884264

F-OVARC1001330

F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)//0.021:232:62//Hs.79410:U62531

F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]//2.5e-76:363:99//Hs.105837:AA536054

F-OVARC1001342//EST//0.98:97:65//Hs.148210:AA897493

F-OVARC1001344//EST//5.3e-10:241:64//Hs.138777:N67251

F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete cds//0.64:198:61//Hs.105940: AF004715

F-OVARC1001360//ESTs//4.9e-87:429:97//Hs.130145:Al264633

F-OVARC1001369//ESTs//6.3e-07:371:62//Hs.131653:AI025777

F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4e-69:533:74//Hs.109299:

30 AB014554

F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//2.5e-49:365:73//Hs. 129735:AF010144

F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL//4.1e-149:683:99// Hs.151428:AJ224819

F-OVARC1001391//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.097:235: 65//Hs.25674:AF072242

F-OVARC1001399//ESTs//1.1e-35:264:83//Hs.59379:W28225

F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//1.3e-150:707:98//Hs.21586:AB006651

F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-49:586:69//Hs.74597:U52426

40 F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T83651

F-OVARC1001436

F-OVARC1001442

F-OVARC1001453

F-OVARC1001476//ESTs, Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631-KRE11 INTERGEN-

45 IC REGION [S.cerevisiae]//1.9e-125:581:99//Hs.110950:AI041823

F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584568

F-OVARC1001489//EST//4.9e-72:341:100//Hs.148191:AA897343

F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//2.6e-86:479:92//Hs.6534: AF016507

50 F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)//1.1e-97:538:92//Hs.75813:L33243 F-OVARC1001525

F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:U53786

F-OVARC1001547//EST//0.0046:237:62//Hs.54638:N90595

F-OVARC1001555

F-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA//6.8e-57:275:98//Hs.155160:

F-OVARC1001600//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.0035: 271:60//Hs.108465:Al144299

- EP 1 074 617 A2 F-OVARC1001610//ESTs, Weakly similar to F22E10.5 [C.elegans]//1.4e-43:216:99//Hs.120002:Al038398 F-OVARC1001611 F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500 F-OVARC1001668//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.3e-37:217:94//Hs.14409:AB011144 F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e-49:393:81//Hs.95582: AB006867 F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229 F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.428:U03858 F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807 F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863 F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80//Hs.155652:X06825 F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI148588 F-OVARC1001762 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds// 1.4e-150:706:98//Hs.155377:U97670 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.8e-117:580:96//Hs.15869: F-OVARC 1001768//ESTs//0.035:179:64//Hs.87279:AI218697 F-OVARC1001791 F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830 F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:Al005102 F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.77:362:58//Hs.116753: AR018287 F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs. 69949:M94172 F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825 F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453 F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567 F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537 F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973 F-OVARC1001861 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300: F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709 F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127 F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs. 158095:AB007953 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds// 2.6e-57:300:96//Hs.6216:AF061749 F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:Al263834 F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261 F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263 F-OVARC1001928 F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204 [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794 F-OVARC1001949//KRAB zinc finger protein {alternative products}//1.8e-17:294:67//Hs.22556:U37251 F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228
- 45
  - F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III
- 50 F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639 F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-23: 213:78//Hs.105292:AA504776
  - F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417
  - F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6e-160:739:98//Hs.108258: AB007934
- 55 F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:Al375865
  - F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063
  - F-OVARC1002107

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- F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7e-101:498:96//Hs.75258: AF054174
- F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913
- F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399:62//Hs.112725:AF056022
- 5 F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795
  - F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097
  - F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:329:58//Hs.107747:Al357868
  - F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.00010:300:64//Hs.118929: X79568
- F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:178:64//Hs.108447:AJ000517 F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230
  - F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:Al378928
  - F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//1.2e-52:550:72//Hs. 42400:AF022789
- 15 F-PLACE1000014
  - F-PLACE1000031
  - F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088
  - F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494
  - F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:AI076755
- 20 F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499
  - F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-47:266: 93//Hs.30026:Al356771
  - F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-15:203:70//Hs.157422:R85366
- 25 F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30:324:60//Hs.76460:U49082 F-PLACE1000094
  - F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//6.2e-82:476:92// Hs.111081:Al380378
  - F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//7.7e-27:205:85//Hs.9670:
- 30 AA632135

- F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//2.5e-151:737:97//Hs. 151017:AF058291
- F-PLACE1000185
- F-PLACE1000213
- 35 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:Al167255
  - F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226
  - F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022
  - F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:Al278202
  - F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294
- 40 F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047
  - F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675
  - F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991: M37197
  - F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0: 262:58//Hs.102732:U88153
  - F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024
  - F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516
  - F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR [Homo sapiens]//8.7e-63:346: 93//Hs.19501:AA742260
- F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174
  F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:
  U33053
  - F-PLACE1000424
  - F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590
- F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included) //2.7e-52:421:80//Hs.69747:M35531
  - F-PLACE1000453//Human mRNA for MTG8a protein, complete cds//0.026:240:60//Hs.31551:D43638
  - F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878

- EP 1 074 617 A2 F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60//Hs.153014:AB002353 F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573 F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds//0.0046:223:65//Hs. 75578:M85289 F-PLACE1000562 F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538 F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:525:72//Hs.21838:AF038179 F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD//2.3e-85:503:88//Hs.62661:M55542 F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e-165:798:97//Hs.159597: AJ012449 F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751 F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.98:215:60//Hs.8152:AB014542 F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986 F-PLACE1000636 F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.0e-154:747: 96//Hs.5819:AF102265 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//7.5e-158:775:97//Hs.29595:AJ005896 F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//1.0e-57:675: 69//Hs.128763:AF009353 F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949 F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:70//Hs.47313:D87447 F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288 F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//0.72:331:57//Hs.37110:U10694 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858 F-PLACE1000769 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//1.1e-139:663:98//Hs.31921: AB014548 F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:362:59//Hs.44782:Z82215 F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079 F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189 F-PLACE1000841//EST//0.47:143:61//Hs.144096:Al032180 F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:63//Hs.110826:U80736 F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428 F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455 F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201 F-PLACE1000948 F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//7.9e-10:294:66//Hs. 80261:L43821 F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cDNA yk28h2.5 [C.elegans]//9.3e-45:309:88// F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:62//Hs.8597:L11672 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds//2.6e-141:694:96//Hs.158497: F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913 F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//0.050:338:61//Hs.1974:M92432

  - F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80//Hs.6940:Z48633
  - F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876
- 50 F-PI ACE 1001024

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- F-PLACE1001036//EST//1.0:133:65//Hs.161424:Al424741
- F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:284:59//Hs.79706:U53204
- F-PLACE1001062
- F-PLACE1001076//EST//0.84:223:59//Hs.161147:Al417859
- 55 F-PLACE1001088
  - F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//1.0e-96:489:96//Hs.95448:AF065485
  - F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817
  - F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//8.2e-66:676:

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71//Hs.150406:AF022158
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F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//1.5e-16:122:91//Hs.1257:M30704

F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135

- 5 F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-28:421:66//Hs.8763:W30741 F-PLACE1001238
  - F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494
  - F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929
  - F-PLACE1001272//COATOMER BETA'SUBUNIT//0.012:50:96//Hs.75724:X70476
- 10 F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:N51283
  - F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.2e-08:586: 58//Hs.124161:AF065164
  - F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.91:221:61//Hs. 16533:D87930
- 15 F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6e-08:370:60//Hs.42672:AF016052
  - F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385
  - F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591
  - F-PLACE1001351
  - F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds//2.8e-26:155:95//Hs.61638:AB018342
- 20 F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//3.4e-44:393:79//Hs.152005: AF009615
  - F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748
  - F-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//2.6e-09: 117:84//Hs.21301:AF093419
- F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 [H.sapiens]//0.00083:187:64//Hs.5399:N30646
  - F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, complete
  - CDS//0.0038:496:57//Hs.97681:AJ223333
  - F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mRNA//7.0e-45:456:75//Hs.
- 30 154069:U06452
  - F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//6.5e-71:365:96//Hs.110404: AF091087
  - F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232
  - F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987
- 35 F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510
  - F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:Al379455
  - F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716
  - F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529
  - F-PLACE1001503
- 40 F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914
  - F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753
  - F-PLACE1001545
  - F-PLACE1001551
  - F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835
- 45 F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266:U06233
  - F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406:AF069987
  - F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:Al342230
  - F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005
  - F-PLACE1001611//Human faciogenital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572:U11690
- 50 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.4e-76:702:75//Hs.159277: AB018341
  - F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198
  - F-PLACE1001640
  - F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927
- F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//2.8e-148:726:96//Hs.3688:AF069250
  - F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//1.1e-95:481:92//Hs.24309:Al125696

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F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete cds//6.0e-30:347:76//Hs.
101555:U93869
F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:73//Hs.12413:D83776
F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:Al391686
F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0084:484:60//Hs.129892:AB011094
F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.1480:M60052
F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159
F-PLACE1001745
F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361
F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//2.8e-160:773:97//Hs.4812:
F-PLACE1001756//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.7e-35:269:83//Hs.5247:AF029750
F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283
F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, complete cds//3.4e-52:548:72//Hs.
150981:U47050
F-PLACE1001781
F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115
F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138
F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//
3.6e-110:546:96//Hs.40820:AF058953
F-PLACE1001821
F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494
F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214
F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906
F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343257
F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220
F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//4.0e-153:685:95//Hs.
F-PLACE1001928//H.sapiens HUMM9 mRNA//0.063:196:66//Hs.2750:X74837
F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58//Hs.106387:AF029778
F-PLACE1001989
F-PLACE1002004
F-PLACE1002046
F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465:58//Hs.153322:D42108
F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555
F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707
F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2e-39:635:64//Hs.38176:AB011178
F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA, complete cds//4.3e-83:388:99//
Hs.5171:AF069765
F-PLACE1002115//EST//0.18:215:62//Hs.135747:Al002637
F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.2e-13:384:61//Hs.737:M62831
F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSOR [Homo sapiens]//0.89:60:
75//Hs.144290:T61747
F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631
F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:79//Hs.40100:AB002390
F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366891
F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627
F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674
F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.90798:U79289
F-PLACE1002213//ESTs//0.041;146:67//Hs.119162:AA399989
F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:AI024442
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F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291

F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710

F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675 F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279

F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067

F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935

2148

F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-75:434:83//Hs.23094:M19503

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F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//2.6e-23:458:66//Hs.
         40993-AF000148
        F-PLACE1002438//EST//0.81:48:77//Hs.158575:Al368947
         F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//7.1e-07:270:
         66//Hs.150406:AF022158
         F-PLACE1002465
         F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369:63//Hs.129361:AJ007581
         F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523
         F-PLACE1002493
         F-PLACE1002499
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         F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708:59//Hs.
         111967:U76010
         F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482
         F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583:95//Hs.88756:
15
         AB018256
         F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//3.1e-115:566:96//Hs.99348:
         AC004774
         F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198:86//Hs.51124:AF019369
         F-PLACE1002571//Homo sapiens mRNA for TP55, complete cds//0.99:274:59//Hs.138202:AF027866
         F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627
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         F-PLACE1002583//EST//0.0028:348:61//Hs.160396:Al393725
         F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279:74//Hs.109606:
         D44497
         F-PLACE1002598//EST//0.011:209:62//Hs.131470:AI024187
         F-PLACE1002604//EST//0.47:220:61//Hs.145434:Al198915
25
         F-PLACE1002625
         F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693:62//Hs.80562:X04412
         F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706
         F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:
         804:97//Hs.124903:AF068180
30
         F-PLACE1002714//Human involucrin mRNA//3.6e-08:509:60//Hs.157091:M13903
         F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230:58//Hs.159196:
         1192971
         F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080
         F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728
35
         F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:AI049827
         F-PLACE1002782//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0031:298:62//Hs.26285:
         F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:Al368926
         F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567:70//Hs.77546:D79994
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         F-PLACE1002815
         F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687:73//Hs.9028:AF039691
         F-PLACE1002834//ESTs//2.6e-41:393:74//Hs.120206:AI089163
         F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:Al334167
         F-PLACE1002851//EST//0.0034:102:72//Hs.129630:AI000405
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         F-PLACE1002853//ESTs//1.1e-20:136:90//Hs.125895:AA889024
         F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627
         F-PLACE1002908//ESTs//3.8e-48:325:88//Hs.54702:Al040029
         F-PLACE1002941//ESTs//5.0e-18:128:88//Hs.17376:AA855056
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         F-PLACE1002962
         F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus]//0.031:372:59//Hs.8021:Al041815
         F-PLACE1002991
         F-PLACE1002993
         F-PLACE1002996//ESTs, Weakly similar to T20D3.3 [C.elegans]//1.3e-12:104:86//Hs.124808:T86959
         F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510//0.99:192:64//Hs.92660:
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F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0e-131:632:97//Hs.129872:

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F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7e-14:555:58//Hs.154740:
        AB014567
        F-PLACE1003045
        F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491
        F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//Hs.102137:U31875
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        F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419
        F-PLACE1003136
        F-PLACE1003145
        F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590
        F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:W01997
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        F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797
         F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransferase mRNA, complete cds//0.98:
         221:60//Hs.139756:U59209
         F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532
         F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:Al208770
15
         F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208
         F-PLACE1003249//Insulin-like growth factor 1 (somatomedia C)//0.99:175:62//Hs.85112:X57025
         F-PLACE1003256
         F-PLACE1003258//H.sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.29285:X99802
         F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106
20
         F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.3e-51:700:67//Hs.
         37138:U35376
         F-PLACE1003334
         F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:AI023308
         F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568
25
         F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//
         2.6e-144:773:92//Hs.6564:U92715
         F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]//8.9e-35:332:
         78//Hs.163820:H71277
         F.-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:57//Hs.143897:AF075575
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         F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858
         F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:Al343009
         F-PLACE1003375//EST//0.75:119:68//Hs.160270:Al149069
         F-PLACE1003383
         F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]//8.9e-113:590:
35
         94//Hs.125175:Al142546
         F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178
         F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.40:206:62//Hs.30223:X90846
         F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912
         F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874
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         F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635
         F-PLACE1003516//Human kpni repeat mma (cdna clone pcd-kpni-8), 3' end//3.4e-85:357:86//Hs.103948:K00627
         F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145
         F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6940:Z48633
         F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248
45
         F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans]//3.6e-110:543:97//Hs.120416:AA057428
         F-PLACE1003553
         F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780
         F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:499:58//Hs.65993:AF000367
         F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932
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         F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194
         F-PLACE1003592//ESTs, Moderately similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//1.4e-50:287:
         93//Hs.154799:AA130620
          F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965
          F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.89650:L38961
55
          F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97//Hs.56851:D83200
          F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00065:236:64//Hs.22116:
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AF064104

- F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896 F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3e-122:737:87//Hs.23094:M19503 F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105 F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762 F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.021:445:58//Hs.158275:Al365413 5 F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56//Hs.76730:AB002299 F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1.4e-133:669:95//Hs.98658: AF053305 F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101 F-PLACE1003723//Homo sapiens mRNA for T lymophocyte specific adaptor protein//8.5e-09:393:60//Hs.103527: 10 AJ000553 F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//1.8e-53:260:99//Hs.102928: A1346344 F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648 F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983 15 F-PLACE1003768//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.7e-40:608:68//Hs.139107:K00629 F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944 F-PLACE1003783 F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0:457:57//Hs.62318:AB018308 F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:314:60//Hs.1050:M85169 20 F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201:68//Hs.40806:AA018786 F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165 F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124 F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:Al370359 F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:Al091257 25 F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770 F-PLACE1003886 F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:702:67//Hs.153322:D42108 F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050 F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944 30 F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142 F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F03069 F-PLACE1003923//interferon, alpha 16//0.48:278:60//Hs.56303:M28585 F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537 35 F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:Al123536 F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds//2.0e-47:522: 71//Hs.3136:U42412 F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812 F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940 40 F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516 F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration oncogene spi1//0.85:164:64//Hs. 153045:X52056 F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta polypeptide 1//3.1e-41:422:74//Hs.3620: 45 X04526 F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [C.elegans]//8.2e-82:418:96//Hs.156161:Al333779 F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552 F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64//Hs.76986:D83785 F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666 F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201 50 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds// 1.3e-145:695:98//Hs.24640:AF069493 F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722
  - F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273
    F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689
    F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R.norvegicus]//1.1e-98:479:97//Hs. 31718:N29128
    - F-PLACE1004270//Homo sapiens CAGF9 mRNA, partial cds//0.00010:369:63//Hs.110826:U80736

- F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573:56//Hs.154139: AB007914
- F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds//2.0e-157:756: 97//Hs.127007:AF084830
- 5 F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:Al271884
  - F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576
  - F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M34677
  - F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797:94//Hs.11171:Y11588 F-PLACE1004336
- F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//1.9e-140: 688:97//Hs.16232:AF100153
  - F-PLACE1004376//ESTs, Weakly similar to F27D4.4 [C.elegans]//3.9e-109:521:98//Hs.14079:AA306552
  - F-PLACE1004384//Human HsLIM15 mRNA for HsLimI5, complete cds//2.0e-49:466:76//Hs.37181:D64108 F-PLACE1004388
- 15 F-PLACE1004405//EST//0.010:191:64//Hs.147600:Al217871
  - F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579
  - F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190
  - F-PLACE1004437//Human NAD\*-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.9e-131:536:99//Hs.155410:U49283
- 20 F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:Al348867
  - F-PLACE1004460
  - F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363
  - F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085
  - F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416
- 25 F-PLACE1004491//EST//2.5e-58;285;99//Hs.97603;AA398163
  - F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680
  - F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//2.5e-147:699:97// Hs.122752:AF026445
  - F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24150
- 30 F-PLACE1004518
  - F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314
  - F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387: AA058854
  - F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371
- 35 F-PLACE1004629//Centromere protein B (80kD)//0.0015:242:64//Hs.85004:X05299
  - F-PLACE1004645
  - F-PLACE1004646//Retinal pigment epithelium-specific protein (65kD)//1.4e-12:386:63//Hs.2133:U18991
  - F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590
  - F-PLACE1004664
- 40 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene// 1.5e-66:357:95//Hs.77705:U07563
  - F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs. 80019:AF035606
  - F-PLACE1004681//EST//0.00092:303:61//Hs.149560:Al281589
- 45 F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561
  - F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.48483:AF007131
  - F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:96:71//Hs.125740:AA884845
  - F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:Al306542
  - F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891
- 50 F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA700148
  - F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680
  - F-PLACE1004743
  - F-PLACE1004751//ESTs, Highly similar to CMP-N-ACETYLNEURAMINATE-BETA-1,4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:260:90//Hs.6863:W52470
- 55 F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//1.7e-172:828:97//Hs.104715:AF084367
  - F-PLACE1004777//Human myosin IXb mRNA, complete cds//1.0e-29:556:63//Hs.159629:U42391
  - F-PLACE1004793
  - F-PLACE1004804

- F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:Al310340
- F-PLACE1004814//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//2.4e-78:415:95//Hs.80965:AA493284
- F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:69//Hs.22111:AB002362
- 5 F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047
  - F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943
  - F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338:57//Hs.8546:U97669 F-PLACE1004838
  - F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//0.89:200:66//Hs.21537:X80910
- 10 F-PLACE1004868
  - F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772
  - F-PLACE1004900
  - F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:Al424382
  - F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA904929
- 75 F-PLACE1004918//Human tumor susceptiblity protein (TSG101) mRNA, complete cds//4.1e-24:402:64//Hs. 118910:U82130
  - F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//9.7e-86:519:88//Hs.17839: AF099936
  - F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592
- 20 F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851
  - F-PLACE1004969
  - F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds//0.031: 235:60//Hs.27610:U34605
  - F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331:83//Hs.153468:
- 25 AB011147

- F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:Al218520
- F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831
- F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459
- F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:H15159
- 30 F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:Al308943
  - F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594
  - F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761:98//Hs.14687:
  - F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.0e-11:757:56//Hs. 122967:AF059569
  - F-PLACE1005077//EST//0.79:283:591/Hs.89276:AA283899
  - F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740
  - F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401:80//Hs.153468: AB011147
- F-PLACE1005101//Homo sapiens (clone zapl28) mRNA, 3' end of cds//8.2e-20:194:80//Hs.75437:L40401 F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds// 8.9e-18:538:62//Hs.104640:AF000561
  - F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405:57//Hs.73166:U76366
  - F-PLACE1005111//ESTs//0.66:191.63//Hs.106446:N93227
- 45 F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//Hs.2557:Y00661
  - F-PLACE1005146//ESTs, Weakly similar to hypothetical protein II [H.sapiens]//4.8e-12:360:63//Hs.142177: H11741
  - F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:72//Hs.154326:D42087
  - F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259:60//Hs.128316:
- 50 AB014541
  - F-PLACE1005181//ESTs, Weakly similar to No definition line found [C.elegans]//4.4e-126:583:99//Hs.25347:
  - F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:N70417
  - F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009
- F-PLACE1005232//ESTs, Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]//0.56:192:60// Hs.47334:W72370
  - F-PLACE1005243
  - F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941

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F-PLACE1005266//Kalimann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M97252
        F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1e-150:706:98//Hs.118087:
        AB011182
        F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947
        F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:66//Hs.101642:
5
        X60673
        F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//0.83:239:62//Hs.80684:X62534
         F-PLACE1005313
        F-PLACE1005327//ESTs, Weakly similar to No definition line found [C.elegans]//6.0e-81:459:91//Hs.146177:
10
         R51650
         F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:88//Hs.134031:AC004794
         F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.96:510:56//Hs.159183:AB018297
         F-PLACE1005373
         F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:Al141348
         F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751
15
         F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951
         F-PLACE1005467//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.74095:L20433
         F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66925
         F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frames//3.5e-126:744:87//Hs.23094:M19503
         F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N39323
20
         F-PLACE1005481//EST//0.27:153-:64//Hs.120066:AA707973
         F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029
         F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105
         F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747
         F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572
25
         F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:Al339335
         F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:Al359385
         F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144
         F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR
         [Saccharomyces cerevisiae]//4.5e-51:258:97//Hs.7736:W81261
30
         F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:Al160278
         F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472:U48436
         F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594
         F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851
         F-PLACE1005611//ESTs, Weakly similar to B0035.14 [C.elegans]//3.5e-32:197:92//Hs.8241:AA283057
35
         F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234
         F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867
         F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991
         F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765:
40
         F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618
         F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.086:223:59//Hs.27349:
         AB007917
         F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457
         F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437
45
         F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:Al004944
         F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59//
         Hs.75111:D87258
         F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:377:62//Hs.162:X16302
         F-PLACE1005763//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN
50
         [Rattus norvegicus]//5.7e-49:252:88//Hs.24309:Al125696
         F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493
         F-PLACE1005802
         F-PLACE1005803
         F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.5e-128:636:96//Hs.125315:
55
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F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//8.4e-156:739:98//Hs.11183:

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EP 1 074 617 A2
F-PLACE1005828//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.1e-42:
327:81//Hs.138404:R70986
F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436:58//Hs.75770:L41870
F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:Al379497
F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905
F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242
F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487
F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:Al031552
F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300
F-PLACE1005898
F-PLACE1005921
F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504
F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:AI288274
F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342:57//Hs.89839:
M18391
F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142
F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:X69978
F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357
F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468
F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:66//Hs.107747:Al357868
F-PLACE1005966//Human zinc fmger/leucine zipper protein (AF10) mRNA, complete cds//1.0:215:63//Hs.7885:
U13948
F-PLACE1005968
F-PLACE1005990
F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:312:77//Hs.42674:U61981
F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256
F-PLACE 1006011
F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743
F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.021:202:64//Hs.158319:
AB018332
F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97//Hs.98782:X99906
F-PLACE1006076//EST//0.29:92:64//Hs.161536:N80395
F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//4.1e-147:679:99//Hs.4976:
AF039023
F-PLACE1006129
F-PLACE1006139
F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:79//Hs.153014:AB002353
F-PLACE1006157//ESTs, Weakly similar to ETX1 {alternatively spliced} [H.sapiens]//2.9e-12:119:84//Hs.23153:
R92857
F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868
F-PLACE10061641/ESTs//0.099:223:60//Hs.8108:AA902721
F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:92//Hs.152894:AC005239
F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:Al074005
F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:99//Hs.30464:AF091433
F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:N49608
F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//3.5e-59:369:88//Hs.
135623:AA134719
F-PLACE1006205
F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]
//0.0089;166:63//Hs.127179;Al279486
F-PLACE1006225
F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668
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F-PLACE1006262

AB014548

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F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185 F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:AI085802

F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3e-168:791:98//Hs.31921:

#### F-PLACE1006318

- F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:AI246503
- F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:Al361492
- F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249
- 5 F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481
  - F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.153529:AF070581
  - F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07:403:61//Hs.105940: AF004715
  - F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693
- 10 F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539:97//Hs.22396:AF062085
  - F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:74//Hs.21560:AB002296
  - F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525:98//Hs. 131846:AF069735
  - F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531:65//Hs.101414:
- 15 AB011129
  - F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds// 1.0:248:60//Hs.88219:AF060866
  - F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381 F-PLACE1006470
- F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds// 5.0e-46:520:71//Hs.131953:AF059194
  - F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511
  - F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493
  - F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE I ENHANCER-BINDING PROTEIN 2//0.98:505:
- 25 56//Hs.75063:AL023584

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- F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706542
- F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA699358
- F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:Al356219
- F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383:58//Hs.32963:D31784
- F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464:57//Hs.1540:L36529 F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372:65//Hs.17630:
  - AB018280 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds// 2.2e-168:781:99//Hs.155377:U97670
- 35 F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99088
  - F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.79110:M60858
  - F-PLACE1006629//Homo sapiens (clone s22i71) mRNA fragment//0.097:229:63//Hs.26956:L40396
  - F-PLACE1006640//ESTs//0.00019:380:59//Hs.13672:AI131473
  - F-PLACE1006673//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.6e-12:113:83//Hs.3385:N25917
  - F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284:60//Hs.153638:AF010403
  - F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05:382:63//Hs.43627: U35612
  - F-PLACE1006754//Biliary glycoprotein//8.9e-27:305:72//Hs.50964:X16354
- 45 F-PLACE1006760//ESTs//0.10:207:62//Hs.152589:AA954152
  - F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251:64//Hs.89591:M97252
  - F-PLACE1006782//ESTs//1.2e-90:423:100//Hs.132826:Al075783
  - F-PLACE1006792//ESTs//1.5e-10:439:58//Hs.138501:AI051228
  - F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10:84:95//Hs. 123642:M83941
  - F-PLACE1006800//ESTs//0.00068:360:61//Hs.157876:Al422017
    - F-PLACE1006805//ESTs//4.6e-103:491:98//Hs.140465:AA769892
    - F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.47:403:56//Hs.15832:AB014518
  - F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-103:619:87//Hs.23094:M19503
- 55 F-PLACE1006829//ESTs//1.5e-22:141:94//Hs.142988:AA142876
  - F-PLACE1006860//EST//0.0062:206:65//Hs.158793:Al376773
  - F-PLACE1006867//ESTs//0.068:218:62//Hs.91166:AA551273
  - F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.0:268:58//Hs.5333:AB018254

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F-PLACE1006883//ESTs//1.6e-75:398:94//Hs.119544:T95601
F-PLACE1006901//ESTs//1.9e-13:87:96//Hs.134737:AI089187
F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443
F-PLACE1006917
F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423913
F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211
F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565
F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.127:L12723
F-PLACE1006961//ESTs, Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]//3.2e-07:67:98//Hs.
21806:AA630312
F-PLACE1006962//H.sapiens ir1B mRNA//2.3e-16:202:71//Hs.135202:X63417
F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.14:
191:67//Hs.8813:AF032922
F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753
F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//
3.1e-05:594:58//Hs.32951:AF034102
F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971
F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//1.0e-117:775:84//Hs.23094:M19503
F-PLACE1007053//Homo sapiens mRNA for ARNO3 protein//0.35:63:82//Hs.129811:AJ223957
F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:361:60//Hs.75813:L33243
F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987
F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glyco-
gen storage disease type III)//0.18:268:63//Hs.904:U84010
F-PLACE1007111//EST//0.0066:260:60//Hs.147903:Al223385
F-PLACE1007112
F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:Al160121
F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-II//0.13:302:60//Hs.78869:M81601
F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965
F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.00090:412:59//Hs.8546:U97669
F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64//Hs.79706:U53204
F-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//2.0e-58:405:87//
 Hs.80598:D50495
 F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141
F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467
F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//Hs.121556:Y15909
 F-PLACE1007274
F-PLACE1007276//ATPase, Cu++ transporting, alpha polypeptide (Menkes syndrome)//0.94:167:64//Hs.606:
 L06133
 F-PLACE1007282
F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:Al091436
F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412
 F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydroxylase (CYP7b1) mRNA, complete cds//0.88:298:58//
 Hs.144877:AF029403
 F-PLACE1007342
 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.7e-121:
 567:98//Hs.76596:AF096870
 F-PLACE1007367//H.sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77//Hs.19949:X98173
 F-PLACE1007375
 F-PLACE1007386//ESTs//0.00066:61:91//Hs.149318:Al248642
 F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:Al041287
 F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//3.8e-18:128:92//
 Hs.14387:AF093771
 F-PLACE1007416
 F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:AI024436
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F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93//Hs.6445:L40391

F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:AI090359

F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714 F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103

- F-PLACE1007484//ESTs//7.1e-18:127:91//Hs.100251:AA535975 F-PI ACE1007488 F-PLACE1007507//ESTs//1,2e-99:274:98//Hs.123462:AA903385 F-PLACE1007511//Keratin 19//4.2e-31:586:64//Hs.23761:Y00503 F-PLACE1007524//ESTs//6.8e-71:356:97//Hs.163067:AA897296 5 F-PLACE1007525//ESTs//0.073:242:59//Hs.128711:AA856979 F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.93:468:57//Hs.113283:AF018080 F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:Al076755 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.0e-70:733:71//Hs.65238: 10 AB014561 F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI001863 F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA584257 F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:AI089163 F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2e-12:778:56//Hs.33010:AB014533 15 F-PLACE1007621 F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA781867 F-PLACE1007645 F-PLACE1007649 F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA476266 F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:AI027055 20 F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:Al348503 F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63//Hs.1103:X02812 F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.75789:D87953 F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-149:709:97//Hs.4812: 25 AF061243 F-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//4.5e-36:233:89//Hs.108797: AA476815 F-PLACE1007729//ESTs, Moderately similar to RETRO VIRUS-RELATED PROTEASE [H.sapiens]//0.00033:270: 64//Hs.104129:AA923278 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.6e-156:728:98//Hs.153121: 30 AB014585 F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:68//Hs.159347:M62424 F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030 F-PLACE1007746//ESTs//6.7e-55:330:89//Hs.153392:Al089469 F-PLACE1007791//EST//0.39:261:62//Hs.145991:AI277656 35 F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA640504 F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA533107 F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841 F-PLACE1007843//EST//0.020:307:59//Hs.145535:Al261635 F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//6.3e-38:396:77//Hs.23094:M19503 40 F-PLACE1007852 F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.3e-190:894:98//Hs.28020: F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:Al038387 F-PLACE1007877 F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943
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  - F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755:97//Hs. 92381:AB007956
  - F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:N24002
- F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA056538 50
  - F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813:98//Hs. 5671:AF084530
  - F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155: 730:98//Hs.78106:AF079529
- F-PLACE1007969//ESTs, Weakly similar to hnRNA-binding protein M4 [H.sapiens]//5.1e-45:264:92//Hs.42222: 55
  - F-PLACE1007990//ESTs//1.2e-104:493:99//Hs.118445:Al097043
  - F-PLACE1008000//Homo sapiens veli 1 mRNA, complete cds//5.7e-63:578:74//Hs.150380:AF087693

- F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031
- F-PLACE1008044
- F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382
- F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:151:71//Hs.159437:
- 5 U44060
  - F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds//1.0:461:58//Hs.155494: LI60975
  - F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds//0.034:497:58//Hs. 100431:AF044197
- 10 F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769
  - F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874
  - F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:Al218683
  - F-PLACE1008177//ESTs, Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]//5.1e-20:124:95//Hs.146238:Al263135
- 15 F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427
  - F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524
  - F-PLACE1008201
  - F-PLACE1008209
  - F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001856
- F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//Hs.77318:L13385
  - F-PLACE1008273
  - F-PLACE1008275//EST//0.77:74:71//Hs.145907:Al275113
  - F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs. 159897:AB007970
- F-PLACE1008309//Homo sapiens serine phosphatase FCP1a (FCP1) mRNA, complete cds//0.16:263:63//Hs. 4076:AF081287
  - F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071
  - F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414: AB011129
- F-PLACE1008331//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA496362
  F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579
  F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:
  - F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911
- 35 F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:Al289171
  - F-PLACE1008398
  - F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461: 62//Hs.25674:AF072242
  - F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326
- 40 F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943
  - F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene coding for Aminopeptidase P (EC 3.4.11.9, XAA-Pro/X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel gene. Contains ESTs, STSs, GSSs and a gaaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653 F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499
- F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [human, epidermoid carcinoma cell line A431, mRNA, 3 genes, 1718 nt]//0.019:530:58//Hs.72248:S72487
  F-PLACE1008437
  - F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335
  - F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901
- 50 F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084:210:63//Hs.27590:AB002381 F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complete cds//6.8e-07:469:60//Hs.1177:
  - F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//1.0:304: 60//Hs.24040:AF006823
- 55 F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:Al274697
  - F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887:D38081
  - F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//1.1e-45:507:71//Hs.8003:AC004997
  - F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete cds//1.0:95:71//Hs.117546:U31767

- F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:Al283069
- F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.9e-175:812:98//Hs.23255: AB018334
- F-PLACE1008621//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//1.2e-15:350:66//Hs.151087: AA649326
- F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:N26794

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- F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560
- F-PLACE1008627//ESTs//3.0e-62:302:99//Hs.120766:H82458
- F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211
- 10 F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394
  - F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D38535
  - F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622:99//Hs. 147967:AF044333
  - F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728
- F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA encoding mitochondrial protein, complete cds//8.3e-25:137:97//Hs.90443: AF038406
  - F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs.119534:AJ224741
  - F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080
- F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus]//4.3e-17:285:69//Hs.35460:H65503 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:503:97//Hs.6458: AF060543
  - F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127:68//Hs.111380:AA258772 F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542
- F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104: 376:98//Hs.7179:AF011905
  - F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318:61//Hs.75668:M81883
  - F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1 / thailand)]//0.73:354:59//Hs.26322:AA156858
- 30 F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:Al052728
  - F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:Al221563
  - F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701:68//Hs.23094:M19503 F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323
  - F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753:98//Hs.62318: AB018308
    - F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:W84771
    - F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:Al394026
    - F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937
    - F-PLACE1008947//Human TBP-associated factor (hTAFII130) mRNA, partial cds//2.4e-13:625:58//Hs.24644:
  - F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:AI024950
    - F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:96//Hs.34780:AJ003112
    - F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762
    - F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689
- F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93:100//Hs.119689: \$70585
  - F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:Al239698
  - F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:Al090525
  - F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800
- 50 F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:AI093091
  - F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:Al337031
  - F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X68011
  - F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:Al040890
  - F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788
- F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds// 1.1e-139:671:97//Hs.99742:AF035586
  - F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718:59//Hs.35804:D25215
  - F-PLACE1009150//Human HsLIM15 mRNA for HsLiml5, complete cds//1.7e-50:440:78//Hs.37181:D64108

- F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-46:440:69//Hs. 158095:AB007953
- F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.28:245:61//Hs.92614: M62302
- 5 F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250
  - F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770
  - F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:Al282821
  - F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100
- F-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans]//3.6e-117:588:95//Hs.54943: 278396
  - F-PLACE1009190//EST//0.046:95:70//Hs.131646:AI025689
    - F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131
    - F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77//Hs.146403:M29540
    - F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575
- F-PLACE1009298//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]// 1.9e-21:121:98//Hs.124768:AA307735
  - F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338
  - F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds//9.7e-08:411: 59//Hs.23731:U83192
- 20 F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-91:594:86//Hs.23094:M19503
  - F-PLACE1009335//EST//0.037:169:63//Hs.148875:AI240767
  - F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473
  - F-PLACE1009368
  - F-PLACE1009375
- 25 F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317:81//Hs.43681:AL022394
  - F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs.9450:M27878
  - F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61//Hs.101174:AF047863
  - F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:210:86//Hs.3404:AF035262
  - F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599:68//Hs.155291:D13630
- 30 F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350:58//Hs.82128:AJ012159
  - F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:93//Hs.76987:AF012872
  - F-PLACE1009459//H.sapiens garp gene mRNA, complete CDS//1.0:241:60//Hs.151641:Z24680
  - F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2// 0.00039:347:60//Hs.994:M95678
- F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67Al//4.1e-91:464:96//Hs.155049: AC004531
  - F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:Al308839
  - F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608:63//Hs.16165:AB002405
  - F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526:78//Hs.8517:U70728
- 40 F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417
  - F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:Al416956
  - F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866
  - F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs.147918:U38291
  - F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806
- 45 F-PLACE1009596//ESTs, Weakly similar to LIS-1 protein [H.sapiens]//4.1e-16:281:66//Hs.13889:Al341394
  - F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313:79//Hs.113283:AF018080
  - F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:Al074011 F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:Al094085
  - F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773
  - F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087
    - F-PLACE1009639

- F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816:98//Hs.21862: AB011159
- F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494
- F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701:98//Hs.109590:AF062534 F-PLACE1009708//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926 F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650

F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789

F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024 F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989

F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-130:600:95//Hs.16411:AL030996

F-PLACE1009845

10 F-PLACE1009861

F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021

F-PLACE1009886

F-PLACE1009888//EST//0.044:255:58//Hs.160695;AI282889

F-PLACE1009908

15 F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717

F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379

F-PLACE1009925

F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153

F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:Al306446

F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345 F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:Al139114

F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:Al201540

F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545: AB014529

25 F-PLACE1010023

F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878

F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//5.2e-63:312:98//Hs. 142151:AA984061

F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183: AF065482

F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424

F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925

F-PLACE1010089//ESTs, Highly similar to PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus

35 musculus]//1.8e-38:212:95//Hs.98067:AA236822

F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//1.8e-08:100:89//Hs.11469: U69567

F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683: AF020761

40 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs. 122967:AF059569

F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682

F-PLACE1010134//H.sapiens hbrm mRNA//1.2e-14:380:64//Hs.77590:X72889

F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740

45 F-PLACE1010152

F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792

F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582

F-PLACE1010202//ESTs, Weakly similar to No definition line found [C.elegans]//2.3e-72:391:94//Hs.35225: H69637

50 F-PLACE1010231

F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349: AB007917

F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590

F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:Al201540

55 F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813

F-PLACE1010310//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74095:L20433

F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248

F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:Al367875

- F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659
- F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117
- F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855
- F-PLACE1010364//EST//0.11:292:58//Hs.135771:Al005648
- 5 F-PLACE10I0383//EST//6.1e-08:107:76//Hs.136441:AA564986
  - F-PLACE1010401
  - F-PLACE1010481//Human BLu protein (BLu) mRNA, complete cds//0.94:254:61//Hs.125257:U70824
  - F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//7.2e-152:702:99//Hs.13313: AF039081
- 10 F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:Al038500
  - F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:Al302100
  - F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.0:175: 64//Hs.159273:AF054177
  - F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472
- 15 F-PLACE1010562//EST//1.0:164:66//Hs.147868:Al222979
  - F-PLACE1010579//EST//0.39:279:58//Hs.158960:Al380148
  - F-PLACE1010580//ESTs, Moderately similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229:N44661
  - F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds//9.9e-148:707:97//Hs.19851:AF045186
  - F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394
  - F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858
  - F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61//Hs.106387:AF029778
  - F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H.sapiens]//0.012:258:62//Hs.144375:AA484200
- 25 F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461
  - F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225
  - F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5e-66:363:95//Hs.10801:AB011102
  - F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076
  - F-PLACE1010662

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- F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs. 37138:U35376
  - F-PLACE1010714//EST//0.018:253:59//Hs.148028:Al270027
  - F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393: 96//Hs.50758:AF092564
- 35 F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial//0.97:314:59//Hs.14574: AJ131244
  - F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391
  - F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//5.1e-80:407:96//Hs.80965:AA493284
- F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus] //6.0e-45:251:94//Hs.11379:AA594140
  - F-PLACE1010786
  - F-PLACE1010800
  - F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157
- 45 F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085
  - F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1 [H.sapiens]//2.9e-28:245:79//Hs. 132736:AA583494
  - F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048
  - F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//5.8e-67:336:97//Hs. 130135:AA905493
  - F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244
  - F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:98//Hs.118087: AB011182
  - F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671
- F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:167:65//Hs.1050:M85169 F-PLACE1010900
  - F-PLACE1010916//EST//0.55:151:66//Hs.145800:Al269981
  - F-PLACE1010917

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EP 1 074 617 A2
F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:H26537
F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653:98//Hs.74750:
F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//2.9e-91:437:98//Hs.66392:
AF064244
F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:W30985
F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA555154
F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:444:59//Hs.585:X04506
F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632
F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:Al379721
F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931
F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032
F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds//0.28:179:67//Hs.1177:
U10886
F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//6.2e-
11:207:68//Hs.994:M95678
F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1//6.1e-35:310:78//Hs.2407:Z49194
F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds//0.74:228:61//
Hs.153640:U56998
F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320
F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663
F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037
F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:AI214317
F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:Al370857
F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949
F-PLACE1011160
F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443
F-PLACEL011185//EST//1.4e-34:261:83//Hs.140250:AA708114
F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds//6.9e-
124:576:99//Hs.159140:AF038664
F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]//9.7e-101:469:99//Hs.8241:AA283057
F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cDNA CEESL70F [C.elegans]//2.6e-62:221:
88//Hs.101821:W27452
F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA015751
F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds//1.4e-147:675:99//Hs.23168:
F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21//5.9e-71:350:98//Hs.15144:AC005014
F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA495803
F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds//3.4e-09:191:65//Hs.140950:
F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915
F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160
F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310
F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696:
99//Hs.5819:AF102265
F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.5e-20:120:81//Hs.
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159897:AB007970 F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D38535

F-PLACE1011375//ESTs, Moderately similar to potassium channel protein Raw3 [R.norvegicus]//6.7e-68:325:99// Hs.107245:AA627053

F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA904868

F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N95552

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AB018255

F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.5e-158:743:98//Hs.10801: AB011102

55 F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frames//1.9e-53:557:72//Hs.23094:M19503 F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:Al025204 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.5e-152:703:99//Hs.111138:

- F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183: F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264 F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI285997 5 F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319 F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA883476 F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84//Hs.153563:AF011333 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67: 268:86//Hs.86371:AF054180 F-PLACE1011586//Homo sapiens hLRpl05 mRNA for LDL receptor related protein 105, complete cds//0.98:153: 10 65//Hs.143641:AB009462 F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778 F-PLACE1011641 F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631 15 F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661 F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086 F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745 F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640 F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234 F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366 20 F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350 F-PLACE1011725 F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853 F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891 F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:Al208240 25 F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:Al393693 F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660 F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664 F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152 30 F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913 F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:478:56//Hs.107747:Al357868 F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817 F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838: 35 AF059617 F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763 F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514 F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591 F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514 40 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0e-148:690:98//Hs.88756: AB018256 F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.5e-54:290:81//Hs. 92381:AB007956 F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:Al205503 45 F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330 F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627 F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831 F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627 F-PLACE2000017
- 50 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, partial cds// 5.7e-85:844:72//Hs.7928:AF082557
- - F-PLACE2000030
  - F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.85:234:66//Hs.11342:U91512
  - F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.058:348:62//Hs.94653:AB011179
- 55 F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59//Hs.79706:U53204
  - F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128
  - F-PLACE2000050//ESTs//3.0e-36;270;83//Hs.155512;AA663966
  - F-PLACE2000061

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20:418:64//Hs.130181:X85019

05:100:73//Hs.104239:AA488082

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F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:662:86//Hs.23759:M98457
F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135:631:98//Hs.9443:
AF027219
F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333
F-PLACE2000100
F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:Al219219
F-PLACE2000111//H.sapiens mRNA for I-acylglycerol-3-phosphate O-acyltransferase//0.76:215:65//Hs.6587:
U56417
F-PLACE2000115
F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:79//Hs.153014:AB002353
F-PLACE2000132
F-PLACE2000136//ESTS, Moderately similar to hypothetical protein [H.sapiens]//1.2e-08:245:64//Hs.140343:
AA718911
F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U54645
F-PLACE2000164
F-PLACE2000170
F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:Al219179
F-PLACE2000176
F-PLACE2000187
F-PLACE2000216
F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933
F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:63//Hs.21560:AB002296
F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367:98//Hs.22926:AB018338
F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366:73//Hs.119387:
AB007958
F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62//Hs.144672:AJ000522
F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560
F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869
F-PLACE2000317
F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; beta polypeptide//6.1e-24:295:76//Hs.30:
F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593:61//Hs.103983:U66088
F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326:61//Hs.85004:X05299
F-PLACE2000347//ESTs, Moderately similar to F18547_1 [H.sapiens]//3.7e-16:139:82//Hs.28209:AI073817
F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645
F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045
F-PLACE2000371//EST//0.65:107:65//Hs.157677:Al358861
F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032
F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638
F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.
 158095:AB007953
 F-PLACE2000398
 F-PLACE2000399
 F-PLACE2000404
 F-PLACE2000411
F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463:74//Hs.113283:AF018080
 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966
 F-PLACE2000427
F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719
F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257
F-PLACE2000438//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2)//1.9e-
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F-PLACE2000458//H.sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107:X87241

F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381

F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324:81//Hs.113283:AF018080 F-PLACE2000455//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.0e-

F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:520:81//Hs.113283:AF018080

- F-PLACE3000004/Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262,
- F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384
- F-PLACE3000020//Prostaglandin 12 (prostacyclin) receptor (IP)//0.00081:500:61//Hs.393:D38128

F-PLACE3000029

- 5 F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:Al082248
  - F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842
  - F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//1.0:186:62//Hs. 122752:AF026445
  - F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:83//Hs.23711:AB018295
- 10 F-PLACE3000121
  - F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081
  - F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603
  - F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243
  - F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016
- 15 F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:Al365871
  - F-PLACE3000148
  - F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336: AB014572
  - F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:Al336023
- 20 F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253: LI79666
  - F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468: AB011147
  - F-PLACE3000160
- 25 F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219
  - F-PLACE3000194
  - F-PLACE3000197
  - F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546
  - F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975
- 30 F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61// Hs.77522:X62744
  - F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216
  - F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377
  - F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//9.2e-
- 35 56:200:85//Hs.133089:AF064019
  - F-PLACE3000226
  - F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:Al201568
  - F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene
- 40 and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046
  - F-PLACE3000244
  - F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858
  - F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650
- 45 F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944
  - F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770
  - F-PLACE3000310
  - F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:Al269586
  - F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219
- 50 F-PLACE3000331

- F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987: AB014545
- F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741
- F-PLACE3000350//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE SULU [Caenorhabditis elegans]//2.9e-59:474:77//Hs.125850:AA885355
- F-PLACE3000352//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194
  - F-PLACE3000353//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78: 234:63//Hs.7498:U41514

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EP 1 074 617 A2
F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441
F-PLACE3000363
F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928
F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641
F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432
F-PLACE3000399//Clathrin, light polypeptide (Lcb)//5.2e-70:391:81//Hs.73919:X81637
F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785
F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270
F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI219715
F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541
F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:
116:78//Hs.77579:AF013263
F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens]//1.6e-51:260:98//Hs.122512:
H61502
F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:
AB018344
F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161
F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:
183:93//Hs.108326:AB006202
F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874
F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888
F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190
F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:
AB018352
F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1.1e-06:244:63//Hs.154050:
AC004131
F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533
F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.
40993:AF000148
F-PLACE4000063
F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713
F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819
F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058
F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:
AB007931
F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751
F-PLACE4000129
F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627
F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856
F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367
F-PLACE4000192
 F-PLACE4000211
 F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594
 F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329
 F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:Al304317
 F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding
 mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250
 F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609
 F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886
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- F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200 50 F-PLACE4000261
  - F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202: 100//Hs.118849:AA215645
  - F-PLACE4000270
- 55 F-PLACE4000300

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- F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.155952:U88966
- F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365
- F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798

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F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:Al147292
F-PLACE4000367
F-PLACE4000369
F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256
F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:Al379823
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F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046

F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-47:605:71//Hs.153026: AB014540

F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//4.7e-33:159:81//Hs.154257:Al275982

F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.3e-45:263:92//Hs.2397:Z70200 10 F-PLACE4000445

F-PLACE4000450

F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874

F-PLACE4000487//Sialophorin (gpL115, leukosialin, CD43)//3.0e-14:189:71//Hs.80738:X52075

F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951 15

F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:Al126289

F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731

F-PLACE4000522//ESTs, Highly similar to NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 1 PRECUR-SOR [Homo sapiens]//0.047:119:65//Hs.129053:AA767022

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F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.0035:510:59//Hs.39163: AF000986

F-PLACE4000581

F-PLACE4000590//ESTs, Highly similar to POL POLYPROTEIN [Friend murine leukemia virus (isolate 57)]//3.4e-13:275:68//Hs.113980:Al034080

F-PLACE4000593//ESTS, Weakly similar to F25D7.1 [C.elegans]//5.2e-28:239:79//Hs.109084:AI004675 F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074

F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//3.5e-47:562:69//Hs.129685: AB002446

F-PLACE4000650 30

F-PLACE4000654

F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:AI028132

F-SKNMC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.85004:X05299

F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//2.5e-36:197:96//Hs.118634:U66688

F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds//2.5e-148:706:98//Hs.109299: AB014554

F-SKNMC1000050//Calpain, large polypeptide L2//4.1e-53:330:90//Hs.76288:M23254

F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877

F-THYRO1000017//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313 40

F-THYRO1000026//H.sapiens OBF-1 mRNA for octamer binding factor 1//2.9e-35:299:81//Hs.2407:Z49194 F-THYRO1000034

F-THYRO1000035//ESTs//4.1e-37:317:79//Hs.141254:Al334099

F-THYRO1000040//ESTs//0.30:331:59//Hs.87176:AI148326

F-THYRO1000070//Human mRNA for KIAA0347 gene, complete cds//0.069:278:63//Hs.101996:AB002345 45 F-THYRO1000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:722:77//Hs.6654:AB014557

F-THYRO1000085

F-THYRO1000092//ESTs//3.1e-100:469:99//Hs.132207:AI148065

F-THYRO1000107

F-THYRO1000111//Human Line-1 repeat mRNA with 2 open reading frames//6.8e-106:690:86//Hs.23094:M19503 50 F-THYRO1000121

F-THYRO1000124//Human mRNA for alanine aminotransferase//0.0026:420:58//Hs.103502:U70732

F-THYRO1000129//Homo sapiens TED protein (TED).mRNA, complete cds//2.8e-155:732:98//Hs.87619:

F-THYRO1000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203 55

F-THYRO1000156//EST//0.32:102:68//Hs.139634:AA478416

F-THYRO1000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:85//Hs.155464:AF088219

F-THYRO1000173//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//1.1e-05:261:61//Hs.

#### 152936:D63475

F-THYRO1000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7e-41:270:87//Hs.101238:Y11312

F-THYRO1000187//EST//0.11:227:62//Hs.101773:H23270

F-THYRO1000190//ESTs//0.82:194:63//Hs.128818:AA976883

F-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//2.4e-175:805:99//Hs.43445: AJ005698

F-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.0e-88:616:84//Hs.79672: AB014552

F-THYRO1000206//EST//0.96:291:61//Hs.104962:AA443848

10 F-THYRO1000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.11506:U79297

F-THYRO1000241//EST//0.48:102:69//Hs.160764:Al313322

F-THYRO1000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.9450:M27878

F-THYRO1000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.61:211:64//Hs.60103:AB014590 F-THYRO1000270

15 F-THYRO1000279//ESTs//0.0020:104:72//Hs.121476:AI215500

F-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:848:98//Hs.25846:AB016068 F-THYRO1000320//ESTs, Weakly similar to Similar to glutamate decarboxylase [C.elegans]//7.6e-92:431:99//Hs. 122719:AA777803

F-THYRO1000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.80731:M63175

20 F-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2e-164:763:98//Hs.12002: AB018333

F-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//6.9e-34:177:84//Hs.7833: U29091

F-THYRO1000368//ESTs//0.0011:55:96//Hs.34994:AA252919

25 F-THYRO1000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.081:240:62//Hs.118401: AB011134

F-THYRO1000387//EST//3.6e-14:197:71//Hs.139399:AA416855

F-THYRO1000394//ESTs, Weakly similar to No definition line found [C.elegans]//5.8e-39:245:91//Hs.119095: T79413

30 F-THYRO1000395//EST//5.8e-69:333:99//Hs.156524:AA724572

F-THYRO1000401//ESTs//1.8e-24:132:98//Hs.54852:W26238

F-THYRO1000438//EST//1.9e-05:217:63//Hs.115930:AA579773

F-THYRO1000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.096:306:60//Hs.155024:U00115

F-THYRO1000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X52520

F-THYRO1000484//EST, Weakly similar to putative p150 [H.sapiens]//8.9e-22:248:76//Hs.162011:AA513663 F-THYRO1000488

F-THYRO1000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200

F-THYRO1000502//ESTs//1.0:350:57//Hs.119749:AA689298

F-THYRO1000505//Interleukin 13//0.95:245:60//Hs.845:U31120

F-THYRO1000558//EST//1.3e-24:351:64//Hs.142326:AA351877

F-THYRO1000569//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.28:229:61// Hs.100058:AB006713

F-THYRO1000570//EST//0.80:171:61//Hs.112790:AA609949

F-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds//2.4e-168:808:97//Hs. 151411:AF075587

F-THYRO1000596//EST//9.5e-94:461:96//Hs.135397:Al056322

F-THYRO1000602//EST//4.9e-06:80:80//Hs.162135:AA526331

F-THYRO1000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2685:Z50053

F-THYRO1000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081

50 F-THYRO1000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941

F-THYRO1000641//ESTs//0.00017:375:58//Hs.32703:AA054125

F-THYRO1000658//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.8e-09:127:77//Hs. 116007:S79267

F-THYRO1000662

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45

55 F-THYRO1000666//ESTs//1.9e-28:149:99//Hs.105187:Al394157

F-THYRO1000676//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//5.7e-49:281:77//Hs. 116007:S79267

F-THYRO1000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46:368:57//Hs.26557:AA480380

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F-THYRO1000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452
        F-THYRO1000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324
        F-THYRO1000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59//Hs.79706:U53204
         F-THYRO1000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085
         F-THYRO1000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74//Hs.7977:AB007871
5
         F-THYRO1000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1.0:209:62//Hs.19492:
         F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:57//Hs.158132:D63481
         F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:
10
         452:58//Hs.11538:AF006084
         F-THYRO1000787
         F-THYRO1000793
        F-THYRO1000796
         F-THYRO1000805//Homo sapiens mRNA from chromosome 5q21-22, clone:sF2//9.4e-36:561:68//Hs.129685:
15
         F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:75//Hs.154326:D42087
         F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339
         F-THYRO1000843
         F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788
         F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170
20
         F-THYRO1000865//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-33:
         190:75//Hs.133526:N21103
         F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531
         F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-43:318:79//Hs.
25
         92381:AB007956
         F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.0e-179:
         839:98//Hs.78106:AF079529
         F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79217:M77836
         F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs.112432:AC005263
         F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65//Hs.83558:D86963
30
         F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear
         gene encoding mitochondrial protein, complete cds//2.7e-15:123:90//Hs.106469:AF042169
         F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907
         F-THYRO1000983
35
         F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646
         F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:Al224307
         F-THYRO1001003
         F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124:AF019369
         F-THYRO1001033//H.sapiens mRNA for cylicin II//0.0061:287:60//Hs.3232:Z46788
         F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.51048:X68830
40
         F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:72//Hs.153014:AB002353
         F-THYRO1001100//Human DNA-binding protein mRNA, 3'end//2.1e-74:741:74//Hs.159249:Z99130
         F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447:62//Hs.124024:AF053700
         F-THYRO1001121//ESTs//0.92:257:61//Hs.118246:N95416
         F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:H70425
45
         F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074
         F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788
         F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385
         F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163
50
         F-THYRO1001204
         F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.155464:AF088219
         F-THYRO1001262//ESTs//7.9e-44:279:87//Hs.138856:H47461
         F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.6467:AJ002309
         F-THYRO1001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:
55
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F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836 F-THYRO1001313//ESTs//1.0:244:61//Hs.127488:AA528182

AF027156

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F-THYRO1001320//ESTs//0.062:126:67//Hs.133296:Al311872
        F-THYRO1001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560:68//Hs.153563:AF011333
        F-THYRO1001322//ESTs//0.12:238:61//Hs.29169:N66545
        F-THYRO1001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207
        F-THYRO1001363//ESTs//1.0e-16:178:78//Hs.163954:N57939
        F-THYRO1001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187:79//Hs.12385:AB007877
        F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4e-157:740:97//Hs.138488:
        AB014607
        F-THYRO1001401//EST//4.6e-14:171:76//Hs.157587:Al356993
        F-THYRO1001403//ESTs//2.2e-50:464:79//Hs.118046:N49946
10
        F-THYRO1001405//ESTs//1.7e-44:226:98//Hs.156667:Al347694
         F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62//Hs.477:U05659
         F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788
         F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//4.6e-33:153:81//
         Hs.102877:U41315
15
         F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099
         F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71//Hs.44782:Z82215
         F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:78//Hs.51048:X68830
         F-THYRO1001487//EST//1.0:88:71//Hs.160760:Al311943
         F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904
20
         F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663
         F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211
         F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:N24046
         F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335
         F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546:95//Hs.25306:AF070572
25
         F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27655
         F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs.75551:L12535
         F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849
         F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071
         F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:W07046
30
         F-THYRO1001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2e-13:108:86//Hs.141045:AA191659
         F-THYRO1001656//Solute carrier family 2 (facilitated glucose transporter), member 4//0.099:540:55//Hs.95958:
         M91463
         F-THYRO1001661//ESTs//0.12:53:92//Hs.151586:W45568
         F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//8.0e-166:780:98//
35
         Hs.118633:AJ225089
         F-THYRO1001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF010238
         F-THYRO1001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:57//Hs.122908:AF070552
         F-THYRO1001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691
         F-THYRO1001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//2.5e-51:296:92//
40
         Hs.3826:U69560
         F-THYRO100173 8//EST//6.9e-30:180:94//Hs.58641:W81229
         F-THYRO1001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813
         F-THYRO1001746//EST//0.96:119:63//Hs.144107:AI053590
         F-THYRO1001772//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-21:
45
         182:81//Hs.118053:N75725
         F-THYRO1001793//ESTs//1.9e-93:439:99//Hs.150116:Al299324
         F-THYRO1001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//Hs.11711:AB002295
         F-THYRO1001828
         F-THYRO1001854//EST//0.038:128:67//Hs.160649:AI241823
50
         F-THYRO1001895//Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor//9.6e-13:288:65//Hs.
         51061:M24283
         F-THYRO1001907//EST//1.9e-12:126:80//Hs.139296:AA350198
         F-VESEN1000122
         F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885
55
         F-Y79AA1000033
         F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:230:66//Hs.431:L13689
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F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629:64//Hs.75305:

#### U78521

F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680

F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053

F-Y79AA1000181//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//

5 0.0022:684:58//Hs.83190:U29344

F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860

F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs. 9242:AF081192

F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079

10 F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:Al278623

F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134

F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:64//Hs.23311:AB002365

F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D50919

F-Y79AA1000328

15 F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313: AF071309

F-Y79AA1000346

F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853

F-Y79AA1000355

20 F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908

F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897

F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs.155464:AF088219

F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018

F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:

25 AF082516

F-Y79AA1000480

F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871

F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521

F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:AF053356

F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991: AF068706

F-Y79AA1000574//Human mRNA for GC box bindig protein, complete cds//0.95:258:62//Hs.150557:D31716

F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811: AF091080

F-Y79AA10006277/Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580: AF060503

F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513

F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850: 98//Hs.83023:AF093670

40 F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969

F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:Al198377

F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067

F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468

F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:

45 AF098799

F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231

F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:244:60//Hs.12307:AF056085

F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.87:466:59//Hs.122967: AF059569

50 F-Y79AA1000805

F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568

F-Y79AA1000827//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]// 0.0048:630:57//Hs.83190:U29344

F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956

55 F-Y79AA1000850//ESTs, Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368:99//Hs.86660:AA398644

F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA, 3' end//0.14:499:58//Hs.37288: D16815

F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:Al341699

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F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//6.9e-69:
        310:94//Hs.76822:Al359536
        F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150:64//Hs.1116:L04270
        F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.73809:M23892
         F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//Hs.79706:U53204
5
         F-Y79AA1001023
         F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:100//Hs.78489:U63329
         F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:772:60//Hs.82208:L46590
         F-Y79AA1001061//ESTs//6.3e-41:303:84//Hs.55855:AA621381
         F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:Al357511
10
         F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047
         F-Y79AA1001078
         F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247:66//Hs.
         55967:AF022654
         F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381
15
         F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155:63//Hs.5444:AB018293
         F-Y79AA1001177//Human hSIAH2 mRNA, complete cds//6.5e-09:299:65//Hs.20191:U76248
         F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646
         F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965
         F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054
20
         F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U48436
         F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85279:U34879
         F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and
         IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//4.0e-135:441:97//Hs.23170:AJ005892
         F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:AI393240
25
         F-Y79AA1001299//Human Ini1 mRNA, complete cds//2.2e-116:323:93//Hs.155626:U04847
         F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395
         F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:AI017555
         F-Y79AA1001384
         F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.66731:U81599
30
         F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]//1.5e-90:424:96//Hs.154221:H23167
         F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:Al088489
         F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61//Hs.83484:X70683
         F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465
          F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Homo sapiens]//0.95:
35
          256:63//Hs.29974:AI360447
          F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744
          F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659
          F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851
          F-Y79AA1001581//Cyclin-dependept kinase inhibitor 1C (p57, Kip2)//2.5e-05:272:64//Hs.106070:U22398
40
          F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783
          F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA393109
          F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:AI363426
          F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.00078:520:57//Hs.12334:
          AB014583
45
          F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:421:94//Hs.107039:W27244
          F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X04385
          F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243:61//Hs.3620:
          X04526
          F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302
 50
          F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877
          F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:
          609:58//Hs.77297:L76191
          F-Y79AA1001711//ESTs//5.2e-29:224:83//Hs.100461:Al018620
          F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183:66//Hs.113082:AB007903
 55
          F-Y79AA1001805//ESTs//1.1e-62:315:98//Hs.16141:W56079
          F-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//2.9e-62:313:
```

98//Hs.15709:W81213

F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533 F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:142:90//Hs.103349:Al141124 F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215:67//Hs.104115:X52332 F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62//Hs.106387:AF029778 F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:Al343173 5 F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430:58//Hs. F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:Al424382 F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611 10 F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943 F-Y79AAl002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-53:348:88//Hs.18122:Al338045 F-Y79AA1002093 F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865 F-Y79AA1002115 F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395 15 F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:165:90//Hs.6473:AA853955 F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5e-05:393:62//Hs.77864:AB014538 F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515 F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldotenax]//2.3e-113:568: 20 96//Hs.111637:AA305890 F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338:73//Hs.26662:U55984 F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477 F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:63//Hs.1560:D42045 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1e-176:821:98//Hs.100729: 25 AB014592 F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748:98//Hs.96731: F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489 30 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:622:97//Hs.30898: AB014534 F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999 F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete 35 cds//0.028:587:58//Hs.2363:L36069 F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377 F-Y79AA1002399 F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569 F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142 40 F-Y79AA1002431 F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263:69//Hs.55452:AC003973 F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:61//Hs.162:X16302 45 Homology Search Result Data 5. [0310] The result of the homology search of the Human Unigene using the clone sequence of 3'-end. [0311] Data include 50 the name of clone, title of the top hit data, the P-value: the length of the compared sequence: identity (%), and the Accession No. of the top hit data, as in the order separated by //. 55

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[0312] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0313] Data are not shown for the clones in which the P-value was higher than 1.

- R-HEMBA1000005//ESTs, Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F54F2.9 IN CHROMOSOME III [Caenorhabditis elegans]//5.6e-93:501:93//Hs.13015:AA628434
- R-HEMBA1000030//Human POU domain protein (Brn-3b) mRNA, complete cds//0.83:314:61//Hs.266:U06233 R-HEMBA1000042//Archain//1:4e-45:282:89//Hs.33642:X81198
- 5 R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528:72//Hs.154326:D42087
  - R-HEMBA1000050//EST//0.043:155:63//Hs.149031:Al243340
  - R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329
  - R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA410788
  - R-HEMBA1000129//ESTs, Weakly similar to contains similarity to helicases [C.elegans]//4.4e-90:502:90//Hs.
- 10 55918:AA151667

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- R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-100:514:94//Hs.27197: AB018340
- R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-45:435:77//Hs.153026: AB014540
- R-nnnnnnnnnn//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//7.7e-92:428: 100//Hs.126925:AA931237
  - R-HEMBA1000158
  - R-nnnnnnnnn//ESTs, Weakly similar to F13B12.1 [C.elegans]//1.3e-05:58:91//Hs.5570:Al377863
  - R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545
- 20 R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366
  - R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927
  - R-HEMBA1000201//Human Ini1 mRNA, complete cds//3.0e-25:137:99//Hs.155626:U04847
  - R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311
  - R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532
- 25 R-nnnnnnnnn//EST//2.2e-100:498:96//Hs.161570:W80404
  - R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70//Hs.127649:AB007874
  - R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.3e-23:276:75//Hs.5737: AB007944
  - R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019
- 30 R-HEMBA1000251//ESTs//0.96;411:56//Hs.120277;Al243808
  - R-HEMBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424
  - R-nnnnnnnnnn//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.9e-14:208:73//Hs.93332: AA811920
  - R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485
- 35 R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962
  - R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409
  - R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0:122:67//Hs.129748:AB011099 R-nnnnnnnnn//ESTs//7.4e-76:386:97//Hs.22276:AA191323
  - R-nnnnnnnnnn/Human Ca2\*-dependent activator protein for secretion mRNA, complete cds//8.8e-30:160:98// Hs.151301:U36448
  - R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus]//1.1e-103:489:99//Hs.108881:AI018024 R-nnnnnnnn//ESTs//9.3e-99:472:98//Hs.163512:AA903238
  - R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:Al302560
  - R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//
    - R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:AI422243
    - R-HEMBA1000357//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//9.4e-89:432:87//Hs.139107: knn629
    - R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857
- 50 R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938
  - R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388:77//Hs.3610:D86960
  - R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83// Hs.73614:U83460
  - R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878
- 55 R-HEMBA1000392//ESTs//3.9e-105:531:96//Hs.130661:Al340248
  - R-HEMBA1000396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens]//1.1e-44:447:75//Hs.42849:N31920
  - R-HEMBA1000411//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//6.1e-92:373:99//Hs.48675: AI005282

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R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:Al270700
         R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140
         R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:87//Hs.158122:AJ001189
         R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143
5
         R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014
         R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349
         R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316
         R-HEMBA1000460
         R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370
10
         R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs.155464:AF088219
         R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster
         ring canel protein. [H.sapiens]//1.1e-31:181:94//Hs.61454:AA312449
         R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528
         R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087
         R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571
15
         R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318
         R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531
         R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885
         R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414
         R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280
20
         R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD//4.0e-55:203:92//Hs.155510:
         U15782
         R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sapiens]//1.3e-117:550:99//Hs.
         99722:AI422277
25
         R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809
         R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//Hs.91916:AF035317
         R-nnnnnnnnnn//ESTs//2.3e-66:342:97//Hs.71916:AA219699
         R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:Al281881
         R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//1.8e-108:550:96//Hs.26799:
30
         W74481
         R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196
         R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:H07128
         R-nnnnnnnnnnn
         R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788
         R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944
35
         R-HEMBA1000591//Homo sapiens mRNA for EIB-55kDa-associated protein//3.9e-113:591:94//Hs.155218:
         AJ007509
         R-HEMBA1000592//TYROSINE-PROTEIN KINASE
         ITK/TSK//0.024:309:61//Hs.89519:L10717
40
         R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041
         R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, complete cds//1.5e-19:129:93//Hs.
         158334:U86136
         R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424
         R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438
45
         R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:422:97//Hs.26252:
         AA643235
         R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:
         AB014590
         R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390
50
         R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929
         R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136
         R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:Al123922
        R-HEMBA1000682//ESTs, Weakly similar to putative pi 50 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403
         R-HEMBA1000686//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:
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R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563: AF057280

R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672

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AI141736

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R-HEMBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213
R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-COA hydratases/isomerases [C.elegans]//7.2e-113:
572:95//Hs.28644:AI018612
R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:449:75//Hs.74478:
1133931
R-HEMBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777
R-HEMBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110
R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286:82//Hs.155464:AF088219
R-HEMBA1000752//EST//0.041:39:94//Hs.127772:AA961131
R-HEMBA1000769//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.6e-32:309:75//Hs.
10458:AF088219
R-HEMBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612
R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen,
antigen detected by monoclonal and antibody IA4))//1.3e-48:284:90//Hs.103458:X53795
R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291:87//Hs.154326:D42087
R-HEMBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939
R-HEMBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027
R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds//2.2e-
44:228:98//Hs.18192:AF048977
R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410:77//Hs.154103:AF061258
R-HEMBA1000851
R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)//3.7e-33:284:80//Hs.159608:
U46689
R-HEMBA1000867//EST//2.0e-17:211:74//Hs.145670:Al265794
R-HEMBA1000869//ESTs//3.1e-16:237:71//Hs.116518:AA653202
R-HEMBA1000870//ESTs//1.6e-43:222:98//Hs.69564:AA203608
R-HEMBA1000872//ESTs//1.9e-93:453:98//Hs.152622:AA594951
R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329:79//Hs.155464:AF088219
R-HEMBA1000908//ESTs//1.6e-51:291:92//Hs.12247:Al203154
R-HEMBA1000910//EST//0.98:139:64//Hs.132687:AI033672
R-HEMBA1000918//EST//9.6e-30:152:84//Hs.162136:AA526508
R-HEMBA1000919
R-HEMBA1000934//ESTs//4.1e-38:254:89//Hs.87784:AA460597
R-HEMBA1000942//ESTs//3.5e-20:172:69//Hs.160065:AI018619
R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78//Hs.33187:
R-HEMBA1000946//ESTs//1.6e-68:352:96//Hs.21331:H93074
R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347:81//Hs.5247:AF029750
R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362:84//Hs.
159187:AB007977
R-HEMBA1000971//ESTs//2.8e-41:246:91//Hs.104287:Al363498
R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341:81//Hs.44766:AJ007590
R-HEMBA1000974//ESTs//1.4e-32:166:100//Hs.149274:Al018170
R-HEMBA1000975//Oxytocin receptor//2.7e-46:563:73//Hs.2820:X64878
R-HEMBA1000985//ESTs//4.4e-05:125:69//Hs.147434:Al214464
R-HEMBA1000986//ESTs//7.8e-44:266:84//Hs.163784:N54902
R-HEMBA1000991//EST//1.4e-42:162:86//Hs.149580:Al281881
R-HEMBA1001007
R-HEMBA1001008//ESTs//2.3e-82:463:92//Hs.10339:AA058764
R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280:
```

50 100//Hs.128738:AA970836

R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587:95//Hs.158287: AB007937

R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140:95//Hs.58393:X05360

R-HEMBA1001020//ESTs//0.52:86:72//Hs.69683:AA115292 55 R-HEMBA1001022//ESTs//3.4e-18:102:100//Hs.63243:Al123912 R-HEMBA1001024//ESTs//1.9e-07:262:61//Hs.124399:AA832336 R-HEMBA1001026//ESTs//0.0017:142:67//Hs.144109:Al345543

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R-nnnnnnnnnnn//Ankyrin G//0.23:244:60//Hs.75893:U13616
         R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186:79//Hs.132942:
         AB014521
         R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:Al357886
         R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813
5
         R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X14420
         R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//2.7e-21:417:64//Hs.
         127338:AB007961
         R-HEMBA1001080
         R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA410788
10
         R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674
         R-HEMBA1001094
         R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245
         R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-46:396:80//Hs.155464:AF088219
         R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974
15
         R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320
         R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879:M15530
         R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341
         R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265
         R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323:83//Hs.155464:AF088219
20
         R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-
         39:309:82//Hs.96337:AA225358
         R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:238:60//Hs.127338:
         AB007961
         R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896
25
         R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothetical protein 5 [H.sapiens]//0.27:305:
         62//Hs.100238:U69194
         R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:333:81//Hs.113283:AF018080
         R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316
         R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160:87//Hs.103102:W55932
30
         R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728
         R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:Al061435
         R-nnnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:239:87//Hs.103919:AA159181
         R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:Al352674
         R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534
35
         R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:Al298324
         R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs.155464:AF088219
         R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68//Hs.20912:AB012162
         R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:Al333214
         R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019
40
         R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977
         R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:Al282950
         R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC
         REGION [S.cerevisiae]//1.3e-77:458:92//Hs.9398:N41838
         R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259
45
         R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:249:78//Hs.113283:AF018080
         R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816
         R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837
         R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334
         R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550
50
         R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458
         R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:Al246482
         R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439
         R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204
55
         R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081
         R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714
         R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364
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R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:Al380343

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R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199
         R-HEMBA1001415
        R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:183:82//Hs.42674:U61981
         R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704
         R-HEMBA1001435//ESTs//5.6e-23:292:70//Hs.116315:AA629263
         R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:Al419982
         R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546
         R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077
         R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-47:304:88//Hs.23094:M19503
         R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:Al417220
10
         R-HEMBA1001463
         R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:66//Hs.36232:D80008
         R-HEMBA1001478
         R-HEMBA1001497
         R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426
15
         R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-79:528:84//Hs.23094:M19503
         R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269
         R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA-702493
         R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:N64723
         R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270
20
         R-HEMBA1001557//ESTs//4.2e-83:413:97//Hs.47546:AA181348
         R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304:88//Hs.155464:AF088219
         R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259:62//Hs.2229:X82324
         R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456:77//Hs.159275:AF030880
         R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030
25
         R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652
         R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63//Hs.146395:AB002329
         R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431:88//Hs.26625:W25874
         R-HEMBA1001608//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.3e-73:533:82//Hs.103948:
30
         R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana]
         //4.5e-93:537:90//Hs.20218:AA628530
         R-nnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:362:60//Hs.132206:AF039694
         R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158
35
         R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623
         R-nnnnnnnnnnn//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442:95//Hs.63888:AA203398
         R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554
         R-HEMBA1001658
         R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427:61//Hs.106511:
40
         R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:
         92//Hs.107254:AC005943
         R-HEMBA1001675
         R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds//4.2e-103:534:
45
         94//Hs 7381:AF038962
         R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424
         R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916
         R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.3e-98:483:96//Hs.31720:
50
         AB014598
         R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960
         R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095
         R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus nor-
         vegicus]//1.8e-46:236:98//Hs.132948:AA194452
         R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166:88//Hs.155464:AF088219
55
         R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN
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SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//7.1e-88:431:96//Hs.29203:Al344105

R-HEMBA1001731//EST//0.25:100:68//Hs.149171:Al245712

R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:77//Hs.153014:AB002353 R-HEMBA1001744 R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:Al358623 R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162 R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145 5 R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306 R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721 R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053 R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243 R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823 10 R-nnnnnnnnnnn//Zinc finger protein 148 (pHZ-52)//0.78:232:57//Hs.112180:AF039019 R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//9.0e-114:548:98//Hs. 118164:AB007969 R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:Al369334 R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF068179 15 R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07290 R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707 R-nnnnnnnnnnn//ESTs//2.2e-101:480:99//Hs.159940:AA971578 R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:147:97//Hs.23476:AA401210 R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250 20 R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513 R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446 R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//1.1e-109:553:96//Hs.78946: AB014517 R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853 25 R-HEMBA1001866//Myelin oligodendrocyte glycoprotein {alternative products}//1.9e-37:357:76//Hs.53217: Z48051 R-nnnnnnnnnn//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//2.3e-32:193:94//Hs. 9489:R84329 R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.66710:X96969 30 R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128 R-HEMBA1001910 R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.5e-73: 347:100//Hs.30991:AA994438 R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//5.1e-57:320:91//Hs. 35 R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:Al273706 R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:Al027125 R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//5.5e-107: 534:96//Hs.154934:AF000145 40 R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-99:482:98//Hs.96849:AA879470 R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:82//Hs.40100:AB002390 R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668 R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:Al192452 45 R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866 R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421 R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048 R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/ 50 Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//1.8e-106:517:97//Hs.11050:AL031178 R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932 R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717 R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:88//Hs.153014:AB002353 55

R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930

R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta)//1.6e-91:448:97//Hs.5687:AJ005801

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R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//Hs.1189:D38550
        R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:Al131538
        R-HEMBA1002039//H.sapiens mRNA for phosphoinositide 3-kinase//0.68:256:64//Hs.101238:Y11312
        R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-51:254:85//Hs.15731:
        AB011135
        R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA572764
        R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:Al200996
        R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354
        R-HEMBA1002102//Thiopurine S-methyltransferase//1.4e-46:403:79//Hs.51124:AF019369
        R-HEMBA1002113//Prostaglandin 12 (prostacyclin) synthase //1.4e-76:280:90//Hs.61333:D83402
10
        R-HEMBA1002119//Homo sapiens OR7E12P pseudogene, complete sequence//1.4e-87:362:94//Hs.103443:
        AF065854
         R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:94:100//Hs.107747:Al357868
         R-HEMBA1002139//H.sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X83957
         R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734
15
         R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199
         R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642
         R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337
         R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//1.4e-36:400:75//Hs.75474:
         AF023674
20
         R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915
         R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043
         R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081
         R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457
         R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete
25
         cds//6.0e-42:419:73//Hs.159523:AF001622
         R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:
         R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357
         R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503
30
         R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:Al202342
         R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:Al393315
         R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151
         R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:
35
         AB014606
         R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//
         Hs.25664:AF089814
         R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202
         R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426
40
         R-HEMBA1002257
         R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGEN-
         IC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:W72675
         R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314
         R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595
         R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:Al280818
45
         R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679
         R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-130:642:96//Hs.6162:
         AB018314
         R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822
         R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094
50
         R-nnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.9e-123:
         661:93//Hs.119023:AF092563
         R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435
         R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237
         R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:91//Hs.25527:AC005954
55
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R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens)//5.6e-87:429:96//Hs.13209:Al417849

R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:80//Hs.74554:D38522

R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238AA476267

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R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069
        R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085
        R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395
        R-nnnnnnnnnn//ESTs, Weakly similar to F08G12.1 [C.elegans]//5.4e-95:488:95//Hs.108115:AA582193
        R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80//Hs.43681:AL022394
5
        R-HEMBA-1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:88//Hs.155464:AF088219
        R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:Al188995
        R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133
         R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449
         R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990
10
         R-nnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//2.3e-113:456:92//Hs.6764:
         AJ011972
         R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715
         R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1e-106:564:93//Hs.129928:
15
         AB007923
         R-HEMBA1002542//ESTs//1.0e-101:539:93//Hs.93872:AA524700
         R-HEMBA1002547//EST//8.7e-27:151:96//Hs.132145:AI041804
         R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:Al281881
         R-HEMBA1002555//ESTs//1.1e-77:461:91//Hs.38750:N30012
         R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264:89//Hs.32567:AF073519
20
         R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:78//Hs.155464:AF088219
         R-nnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//1.4e-120:587:97//Hs.151411:
         AF075587
         R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904
         R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838
25
         R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055
         R-HEMBA1002621
         R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.2e-77:380:97//Hs.91338:
         AB018351
         R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881
30
         R-HEMBA1002629//ESTs//0.00014:50:100//Hs.119132:AA398715
         R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041
         R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970
         R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, com-
         plete cds//1.5e-53:406:81//Hs.108966:U48696
35
         R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296:84//Hs.6232:
         AB018307
         R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945
         R-HEMBA1002678//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-
          104:560:92//Hs.161748:T64896
40
         R-nnnnnnnnnn//EST//0.15:136:69//Hs.129570:AA995396
         R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247:62//Hs.142023:M88282
         R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477
         R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.0e-46:302:86//Hs.15519:
45
         AB018315
         R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884
         R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287:81//Hs.132942:
         AB014521
          R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168
          R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163
50
          R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526
          R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:Al375792
          R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090
          R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0e-106:545:95//Hs.74750:
          AB011126
55
          R-HEMBA1002770//EST//0.34:294:59//Hs.43091:N22127
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R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342:58//Hs.48824:D87717

R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491

R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75//Hs.153563:AF011333

R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:Al279709 R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320

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R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//1.4e-116:559:97//Hs.28307:
         AF071185
         R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//Hs.79706:U53204
         R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:AI092013
         R-HEMBA1002833//ESTs, Highly similar to ribosome-binding protein p34 [R.norvegicus]//4.3e-25:137:98//Hs.
         5337:AA243757
         R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514
10
         R-HEMBA1002863//ESTs//1.1e-67:359:94//Hs.124699:W27830
         R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:AI220827
         R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670
         R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//1.2e-107:541:95//
15
         Hs.33787:AF037261
         R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71//Hs.95140:D80011
         R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820
         R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:88//Hs.154326:D42087
         R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481
         R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:Al254165
20
         R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679
         R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732
         R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:Al190892
         R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085
         R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124:AF019369
25
         R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:Al000405
         R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3e-30:162:99//Hs.5734:AB014579
         R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs.155464:AF088219
         R-nnnnnnnnnn//ESTs//3.2e-18:102:100//Hs.146255:AA197064
         R-HEMBA1002999//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//7.9e-113:560:
30
         96//Hs.125749:Al377682
         R-HEMBA1003021//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.3e-42:290:85//Hs. 113283:AF018080
         R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480
         R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:Al038577
         R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827
35
         R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:Al240366
         R-HEMBA1003041//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN
         CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5.6e-34:280:79//Hs.114905:AA088442
         R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//1.3e-
40
         119:578:97//Hs.44097:AF054182
         R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627
         R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF010238
         R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903
         R-HEMBA1003077//ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:434:99//Hs.14146:W92235
         R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402
45
         R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:AI075249
         R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:AF088219
         R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223
         R-HEMBA1003096//ESTs. Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100:531:94//
50
         Hs.104800:AA709155
         R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624
         R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:AI150058
         R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13:109:88//Hs.
         118717:U86751
         R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:Al370845
55
         R-HEMBA1003136//ESTs, Weakly similar to MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE [Saccharo-
         myces cerevisiae]//9.2e-114:577:95//Hs.27059:Al088615
         R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219
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R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670

R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933 R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389 R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000 R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804 5 R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026: AB014540 R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943 R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265 R-HEMBA1003220//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR 10 [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817 R-HEMBA10032227/ESTs, Weakly similar to weak similarity to HSP90 [C.elegans]//1.1e-42:310:85//Hs.23294: W27666 R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305 R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834 15 R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs. 152663:AF068864 R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929 R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219 R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392 20 R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785 R-HEMBA1003281 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836: AB011109 R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266 25 R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353 R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504 R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs. 124224:AB001872 R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869 30 R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119 R-HEMBA1003328//H.sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176: R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357 35 R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:Al148540 R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651 R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588 R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247 R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-40 11:261:65//Hs.87578:AI125363 R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847 R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127 R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204 R-nnnnnnnnnnn//ESTs//1.7e-24:188:85//Hs.70266:Z78309 45 R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563 R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013 R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058696 R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:Al225121 R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516 50 R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080 R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688 R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760 R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058 R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817 55 R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673 R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sapiens]//2.8e-93:495:93//Hs. 91619:AA552351

R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734 R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522 R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:Al342058 R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H.sapiens]//4.0e-63:343:93//Hs. 5 58598:AA625440 R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099 R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892 R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065 R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:Al244212 R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087 10 R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:Al371042 R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374 R-HEMBA1003615 R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167 R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387 15 R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888 R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021 R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//9.3e-24: 189:84//Hs.142208:AA209438 R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830 20 R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010 R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783 R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs. 67619:AB007957 R-HEMBA1003662//Human TBX2 (TXB2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049 25 R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635 R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H.sapiens]//4.1e-87:434:97//Hs. R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083 R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-101:528:95//Hs. 30 22934:AA581379 R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916 R-HEMBA1003692//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//2.0e-43:360:80//Hs.110194: R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:Al279064 35 R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs. 1139:X77777 R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080 R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA, complete cds//1.2e-33:377:74//Hs.24040:AF006823 40 R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847 R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839 R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592 R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:96//Hs.11282:Al147040 45 R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247 R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089 R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214 R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//2.1e-101:558:93//Hs.18171:AA524327 R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600 50 R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236 R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:100//Hs.107747:Al357868 R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295 R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344 R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:Al264163 55 R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs.155464:AF088219 R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 [Paramecium

tetraurelia)//6.5e-71:357:96//Hs.107573:AA524333

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R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161
        R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033
        R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547
        R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS [Homo sa-
        piens]//2.1e-59:295:98//Hs.161661:AA166911
5
        R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:79//Hs.61408:AF070621
        R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930
        R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294:86//Hs.13572:AF068179
        R-HEMBA1003902//ESTs//1.8e-43:300:85//Hs.146811:AA410788
        R-HEMBA1003908//ESTs//3.5e-91:477:94//Hs.6638:AA536187
10
         R-HEMBA1003926//ESTs//7.9e-44:294:87//Hs.164036:AA845659
         R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5e-48:276:81//Hs.72660:AB011157
         R-HEMBA1003939
         R-HEMBA1003942//ESTs//1.6e-81:428:94//Hs.50418:AA524669
         R-HEMBA1003950//ESTs//8.1e-54:283:95//Hs.145528:Al261545
15
         R-HEMBA1003953//ESTs//3.8e-30:194:89//Hs.99681:AA504591
         R-HEMBA1003958//ESTs//4.0e-45:394:77//Hs.141602:N63562
         R-HEMBA1003959//ESTs//5.2e-28:197:86//Hs.9951:W56253
         R-HEMBA1003976//ESTs//2.0e-29:232:84//Hs.133947:AI074525
         R-HEMBA1003978//ESTs//3.2e-115:549:98//Hs.76798:AI050882
20
         R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-91:
         448:97//Hs.117834:AA766771
         R-HEMBA1003987//ESTs//8.1e-36:193:88//Hs.151844:N92756
         R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360:81//Hs.150275:D87682
         R-HEMBA1004000//EST//5.5e-62:308:97//Hs.50438:N74105
25
         R-HEMBA1004011//ESTs//8.6e-85:431:96//Hs.36185:R99899
         R-HEMBA1004012//ESTs//1.3e-40:309:83//Hs.140329:AA714011
         R-HEMBA1004015//ESTs//5.1e-97:453:99//Hs.111446:Al333774
         R-HEMBA1004024//ESTs//5.2e-19:159:79//Hs.138856:H47461
         R-HEMBA1004038//ESTs//1.3e-41:346:79//Hs.146173:AA906191
30
         R-HEMBA1004042//ESTs//0.0012:201:69//Hs.24248:AA528253
         R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H.sapiens]//1.5e-22:365:70//Hs.99692:AA811804
         R-HEMBA1004048//ESTs//9.5e-104:497:98//Hs.77735:Al125469
         R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176:96//Hs.8997:M11717
         R-HEMBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754
35
         R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.2e-78:577:82//Hs.113283:AF018080
         R-HEMBA1004074//EST//1.0:152:61//Hs.149093:Al243988
         R-HEMBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652
         R-HEMBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251
         R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:69//Hs.90998:D50918
40
         R-HEMBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562
         R-HEMBA1004133
         R-HEMBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736
         R-HEMBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320
         R-HEMBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs.155464:AF088219
45
         R-HEMBA1004150//GRANCALCIN//0.99:357:59//Hs.79381:M81637
         R-HEMBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:84//Hs.154326:D42087
         R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:96//Hs.59988:AF067855
         R-HEMBA1004199
         R-HEMBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701
50
         R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.7e-107:552:94//Hs.
         10092:Al189282
         R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275:98//Hs.15832:
          R-HEMBA1004207//Leptin receptor//1.1e-117:573:97//Hs.54515:U50748
55
          R-HEMBA1004225//EST//9.7e-34:186:95//Hs.137567:R20617
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R-HEMBA1004227I/ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.0e-

16:117:91//Hs.92033:AA255832

EP 1 074 617 A2 R-HEMBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:83//Hs.153014:AB002353 R-HEMBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389 R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:72//Hs.154103:AF061258 R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus norvegicus]//2.1e-61:221:86//Hs.7089:W37284 R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962 R-HEMBA1004267//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//1.4e-89:465:95//Hs.113660:D20018 R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931 R-nnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553:96//Hs.93677: AF091081 R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus]//4.4e-92:559:89//Hs.28298:AA203228 R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538: 97//Hs.101766:AF022795 R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferring//1.7e-34:223:75//Hs.81884: U13061 R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.6e-93:496:94//Hs.14337:AA534961 R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426 R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679 R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415:64//Hs.51199:X16281 R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904 R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714 R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561 R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:Al310231 R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336 R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686: R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353 R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458: X77494 R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869 R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057 R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264 R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084 R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219 R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717 R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365: AA648933 R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs. 12940:AI123518 R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503 R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829 R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033 R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172 R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306

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R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034

R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941 50

R-HEMBA1004507

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R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTER-GENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271

R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:

281:89//Hs.58414:AA196947 55

R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972

R-HEMBA1004554

R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924

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R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]//1.0:305:60//Hs.30272:AA134913
        R-HEMBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA582243
        R-HEMBA1004586//ESTs//2.6e-73:384:96//Hs.9582:R39769
        R-nnnnnnnnnnn//ESTs//6.0e-22:190:82//Hs.42530:N41661
        R-HEMBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA780767
5
        R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//4.6e-52:327:85//Hs.
        159897:AB007970
        R-HEMBA1004629//ESTs//2.3e-19:215:76//Hs.111995:Al375915
        R-HEMBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA810785
        R-HEMBA1004632//ESTs//1.0:128:66//Hs.159182:AA831152
10
        R-HEMBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III
        [Caenorhabditis elegans]//4.8e-111:532:98//Hs.12263:AA282393
        R-HEMBA1004638//ESTs//1.2e-66:341:95//Hs.122687:Al278454
         R-HEMBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA625442
         R-HEMBA1004669//ESTs//0.00039:116:74//Hs.138725:N76348
15
         R-HEMBA1004670//ESTs//1.7e-16:116:89//Hs.56825:AI057560
         R-HEMBA1004672//EST//6.7-e-76:315:97//Hs.20821:R19368
         R-HEMBA1004693//ESTs//6.4e-68:327:99//Hs.159066:AI093252
         R-HEMBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA043562
         R-HEMBA1004705//EST//0.0034:271:58//Hs.112503:AA599042
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         R-HEMBA1004709//EST//1.3e-55:392:85//Hs.149580:Al281881
         R-HEMBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449:76//Hs.155464:AF088219
         R-HEMBA1004725//EST//1.8e-71:424:88//Hs.155712:Al309235
         R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequencer//2.1e-44:467:73//Hs.91916:AF035317
         R-HEMBA1004733//EST//0.99:84:65//Hs.161372:Al423151
25
         R-HEMBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73275
         R-HEMBA1004736//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//9.5e-39:296:
         82//Hs.51187:U82828
         R-HEMBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59651
         R-HEMBA1004751//ESTs//8.0e-23:155:88//Hs.149464:Al279428
30
         R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:281:89//Hs.89887:D38081
         R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475:84//Hs.8102:L06498
         R-HEMBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N68679
         R-HEMBA1004758//EST//2.0e-43:367:80//Hs.133006:AI049504
         R-HEMBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87380
35
         R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//
         1.4e-47:379:81//Hs.141273:H66705
         R-HEMBA1004770//ESTs//0.0014:246:61//Hs.124857:AA687092
         R-HEMBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA699633
         R-HEMBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W74476
40
         R-HEMBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA848167
         R-nnnnnnnnnnn
         R-HEMBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W87732
         R-HEMBA1004806
         R-HEMBA1004807//ESTs//6.2e-77:362:100//Hs.140945:N47676
45
         R-HEMBA1004816//EST//4.3e-18:246:72//Hs.150552:AI053784
         R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//5.0e-14:141:85//Hs.80510:
         M74002
         R-HEMBA1004847
         R-HEMBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA577120
50
         R-HEMBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95267
         R-HEMBA1004864
         R-HEMBA1004865//EST//6.7e-18:191:75//Hs.129944:AA429362
         R-HEMBA1004880//EST//4.4e-70:346:98//Hs.145094:AA452409
         R-HEMBA1004889//ESTs//4.8e-117:496:97//Hs.15641:W63676
55
         R-HEMBA1004900//ESTs//1.2e-15:283:68//Hs.157606:Al357470
         R-HEMBA1004909//ESTs//7.3e-44:366:79//Hs.140329:AA714011
         R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-50:313:89//Hs.40100:AB002390
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R-HEMBA1004923//ESTs//0.013:162:64//Hs.143655:AI128388 R-HEMBA1004929//EST//2.3e-48:250:97//Hs.131589:AI025053

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R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:
         80//Hs.1361:M55053
         R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:530:98//Hs.18029:Al422883
5
         R-HEMBA1004934//ESTs//1.3e-103:522:96//Hs.40415:AA037215
         R-HEMBA1004944//ESTs//6.0e-21:97:84//Hs.141973:N21434
         R-HEMBA1004954//ESTs//7.9e-112:596:93//Hs.6226:W61007
         R-HEMBA1004956//ESTs//3.1e-58:280:100//Hs.120750:AA741074
         R-HEMBA1004960//ESTs//6.9e-89:476:93//Hs.163738:AA601040
10
         R-HEMBA1004972//ESTs//3.0e-72:381:95//Hs.55014:AA934035
         R-HEMBA1004973//ESTs//2.7e-91:441:98//Hs.28144:AI292065
         R-HEMBA1004977//ESTs//2.0e-95:446:99//Hs.29690:Al168404
         R-HEMBA1004978//Homo sapiens natual killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187:67//Hs.
         129734:AJ001683
15
         R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:91//Hs.146395:AB002329
         R-HEMBA1004983//ESTs//0.16:482:57//Hs.131929:Al021894
         R-HEMBA1004995
         R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482:78//Hs.141601:N63520
         R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551:96//Hs.103180:Al365212
20
         R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542:94//Hs.31921:
         R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//
         8.4e-95:491:94//Hs.16085:Al261382
         R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:85//Hs.22271:D26067
25
         R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens]//2.6e-48:443:78//Hs.139019:N99348
         R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Canis familiaris]//1.2e-87:542:87//
         Hs.16258:AI376436
         R-HEMBA1005050//ESTs//6.3e-46:311:86//Hs.159510:AA297145
         R-HEMBA1005062//ESTs//1.1e-14:216:68//Hs.129935:AA994451
30
         R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303:73//Hs.79385:U90905
         R-HEMBA1005075//EST//0.65:214:62//Hs.133991:AI075789
         R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U17077
         R-HEMBA1005083//ESTs//2.8e-74:356:98//Hs.132272:Al393958
         R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//1.7e-111:545:96//Hs.11170:
35
         AF080561
         R-HEMBA1005113//ESTs//1.1e-101:512:95//Hs.7972:AI052739
         R-HEMBA1005123//Ley I-L//3.6e-58:519:77//Hs.37062:AC005952
         R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85//Hs.19949:X98173
         R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//4.7e-36:394:75//Hs.
40
         67619:AB007957
         R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-32:362:77//Hs.132206:
         AF039694
         R-HEMBA1005159//EST//7.4e-47:252:94//Hs.134930:Al093397
45
          R-HEMBA1005185//ESTs//5.2e-48:305:89//Hs.14920:AA910914
          R-HEMBA1005201//ESTs//4.7e-58:293:97//Hs.23752:C05766
         R-HEMBA1005202//ESTs//1.0:169:59//Hs.153423:Al198239
          R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) mRNA, complete cds//0.84:191:
          61//Hs.26931:AF061836
          R-HEMBA1005223//ESTs//0.75:90:70//Hs.127446:AA167284
50
          R-HEMBA1005232//EST//0.056:162:67//Hs.65649:F13687
          R-HEMBA1005241//ESTs//3.6e-113:564:96//Hs.12770:W84331
          R-HEMBA1005244//ESTs//6.4e-22:118:100//Hs.21396:AA114834
          R-HEMBA1005251//ESTs//8.5e-36:213:92//Hs.161554:AA393896
          R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//6.1e-49:277:93//Hs.72660:AB011157
55
          R-HEMBA1005274//ESTs//3.7e-65:322:98//Hs.105166:AA668862
          R-HEMBA1005275//ESTs//2.1e-29:298:73//Hs.33393:R83391
          R-HEMBA1005293//ESTs//3.5e-93:448:98//Hs.12066:AI208611
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R-HEMBA1005296//ESTs//4.3e-33:168:100//Hs.13916:AI025750
         R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:82//Hs.155464:AF088219
         R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:83//Hs.32567:AF073519
         R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI095046
         R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59169
5
         R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA126472
         R-HEMBA1005331//Intercellular adhesion molecule 2//7.6e-39:256:87//Hs.83733:X15606
         R-HEMBA1005353//ESTs//1.7e-81:406:96//Hs.155374:Al341467
         R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//4.7e-46:294:81//Hs.
         129735:AF010144
10
         R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptide//1.0:210:62//Hs.4:X03350
         R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:Al091653
         R-HEMBA1005374//ESTs//1.5e-107:502:99//Hs.118208:AA947305
         R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311:80//Hs.54486:X54150
         R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//4.0e-88:489:
15
         92//Hs.43864:AA131568
         R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863278
         R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA676725
         R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI052059
         R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R98757
20
         R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//1.8e-118:
         453:99//Hs.4854:AF041248
         R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:264:61//Hs.136309:AB007960
         R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:305:87//Hs.6445:L40391
         R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA745961
25
         R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA024494
         R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-45:320:85//Hs.153014:AB002353
         R-HEMBA1005472//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//8.4e-73:464:87//Hs.103948:
         K00627
         R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA100445
30
         R-HEMBA1005497
         R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA410788
         R-HEMBA1005506//75 kda infertility-related sperm protein [human, testis, mRNA Partial, 2427 nt]//0.11:295:60//
         Hs.62608:S58544
         R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90870
35
         R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//2.6e-82:387:99//Hs.67466:
         AI219740
         R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA203322
         R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:AA601045
         R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.5e-44:179:84//Hs.42674:U61981
40
         R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA410788
         R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//8.6e-115:578:95//Hs.
         17035:AI080471
         R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W72350
          R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90926
45
         R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//Hs.2180:M57627
         R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.3e-77:439:91//Hs.22897:R43193
         R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:
          182:76//Hs.133526:N21103
          R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA489709
50
          R-HEMBA1005576//EST//0.91:52:73//Hs.149518:Al280497
          R-HEMBA1005577
          R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:561:64//Hs.57929:AB011538
          R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:C06392
          R-HEMBA1005583//ESTs//8.3e-79:413:95//Hs.62348:AA419539
55
          R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403:83//Hs.75680:M15990
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R-HEMBA1005593//ESTs//3.3e-30:139:80//Hs.142273:W37905 R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:Al274820

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R-HEMBA1005606//EST//1.0e-12:313:64//Hs.162402:AA573125
        R-HEMBA1005609//ESTs//0.49:278:58//Hs.76235:W56390
        R-HEMBA1005616//EST//1.3e-98:470:99//Hs.122230:AA781422
        R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//2.8e-95:539:92//Hs.
        19400:AA662845
5
         R-HEMBA1005627//Human mRNa for adipogenesis inhibitory factor//5.5e-38:317:78//Hs.1721:X58377
         R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-11:279:65//Hs.15245:AF041081
         R-HEMBA1005632//EST//1.5e-10:181:70//Hs.120259:AA731522
         R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.4e-25:234:80//Hs.
10
         10458:AF088219
         R-HEMBA1005666//ESTs//2.3e-103:534:95//Hs.14512:AA205973
         R-HEMBA1005670//ESTs//2.6e-39:166:81//Hs.139414:AI279477
         R-HEMBA1005679//Esterase D/formylqlutathione hydrolase//1.3e-50:322:88//Hs.82193:M13450
         R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-43:343:81//Hs.154103:AF061258
         R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete cds//0.0050:235:64//Hs.159437:
15
         U44060
         R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//
         1.7e-47:376:84//Hs.26988:U66406
        R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA772055
        R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:Al159943
20
         R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP)//1.2e-45:398:79//Hs.155481:
         AJ006470
         R-HEMBA1005737//ESTs//2.5e-57;416;83//Hs.23245;AA053815
         R-nnnnnnnnnn//EST//0.098:125:68//Hs.136945:AA765672
         R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:N47096
25
         R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:
         R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA173974
         R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195:84//Hs.
         10458:AF088219
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         R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:Al038601
         R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA514960
         R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:AI039201
         R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:AI080618
         R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA098911
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         R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA757917
         R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970
         R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:Al022252
         R-HEMBA1005894
         R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:Al215686
         R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:AI076363
         R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA970632
         R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.5e-45:446:75//Hs.59403:
         R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079;AA370867
45
         R-HEMBA1005962//ESTs//1.8e-87;409:100//Hs.161292;AI199418
         R-HEMBA1005963
         R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.
         26285:AF082516
         R-HEMBA1005991//Human antisecretory factor-1 mRNA, complete cds//2.0e-45:551:70//Hs.148495:AF050199
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         R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:Al080618
         R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:Al379875
         R-HEMBA1006005//EST//1.0:105:63//Hs.145273:Al249436
         R-nnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444:67//Hs.26450:AB018268
         R-HEMBA1006035//ESTs//4.5e-94:465:97//Hs.44625:N49951
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R-HEMBA1006036//ESTs//6.1e-90:420:100//Hs.126771:AA916508 R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490

R-nonnnnnnnnn

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R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612
R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517
R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313
R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//
Hs.73614:U83460
R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297
R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:Al279293
R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:Al198931
R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635
R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:
AB007958
R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542
R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212
R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U31930
R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627
R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906
R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125
R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557
R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]//3.3e-114:581:95//
Hs.23617:AA928683
R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522
R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:
R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881
R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive [M.musculus]//1.2e-97:529:93//Hs.
 10552:AA524401
R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]//2.7e-88:484:
 92//Hs.104129:AA923278
R-nnnnnnnnnn//H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770
R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 [S.
cerevisiae]//1.6e-66:377:91//Hs.108674:W25821
 R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:AI084735
 R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019
 R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:Al202037
 R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:
 R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculus]//5.6e-76:417:94//Hs.111754:
 R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219
 R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184
 R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204
 R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN IN SHP1-SEC17 INTERGENIC
 REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.42343:Al417075
 R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382
 R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008
 R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787
 R-HEMBA10063771/EST//0.0097:145:621/Hs.133027:AI049830
 R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:
 AB011166
 R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651
 R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-87:5 82:84//Hs.23094:M19503
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R-HEMBA1006424//ESTs, Weakly similar to pot. ORF II [H.sapiens]//6.3e-13:263:66//Hs.43127:AA258004 R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964 R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380 R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033

R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:Al218923 R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778

R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878

- R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:487:58//Hs.32963:D31784 R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895
- R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-17:342:63//Hs.111730:AA604403 R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441
- 5 R-HEMBA1006474
  - R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40:365:78//Hs. 46468:U45984
  - R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.132243:Y07701
  - R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223
- 10 R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350
  - R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720
  - R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387
  - R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117
  - R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:135:72//Hs.2161:M62505
- 15 R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117:570:96//Hs.153858: AB014566
  - R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300
  - R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:AI057628
  - R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934
- 20 R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331
  - R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48:287:91//Hs.79507:AB011154 R-HEMBA10065597/ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]//1.8e-109:547:96//Hs.21122:AA191594
  - R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:Al283064
- 25 R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876
  - R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725
  - R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876
  - R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29:276:76//Hs.144563: AF057280
- 30 R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390
  - R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155464:AF088219 R-HEMBA1006612
  - R-nnnnnnnnn//ESTs//1.2e-25:225:80//Hs.138852:AA284247
  - R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630
- 35 R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:90//Hs.22271:D26067
  - R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.7e-91:426:100//Hs.139469:Al299889
  - R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//3.4e-37:186: 100//Hs.109818:AA411185
- 40 R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777
  - R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196: U40282
  - R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427
  - R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:Al282511
- 45 R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:Al263102
  - R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594
  - R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:Al041842
  - R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:Al269435
  - $R-HEMBA1006695//Homo\ sapiens\ apoptotic\ protease\ activating\ factor\ 1\ (Apaf-1)\ mRNA,\ complete\ cds//1.9e-32:$
- 50 261:79//Hs.77579:AF013263 R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:Al032695
  - R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H.sapiens]//1.1e-92:483:94//Hs. 6525:Al205313
  - R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062
- 55 R-HEMBA1006717
  - R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002
  - R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627
  - R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:Al334099

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R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646
        R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763
        R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:Al281881
        R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562
        R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:Al092936
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        R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705
        R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:Al334978
        R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333
        R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305
        R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272
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        R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556
        R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087
        R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665
        R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:
15
         R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453
         R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739
         R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117
         R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:213:84//Hs.9096:AA029400
         R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308
20
         R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712
         R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382
         R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:
         AJ010841
         R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321
25
         R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457
         R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827
         R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325
         R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679
         R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440
30
         R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293
         R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-112:558:96//Hs.107905:Al248363
         R-HEMBA1007045
         R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788
         R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839
 35
         R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140
         R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:Al208272
         R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:Al096866
         R-HEMBA1007078//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//7.2e-
          40:163:83//Hs.152369:AA504818
 40
          R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:Al348087
          R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025
          R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597
          R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121493:D25272
          R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438
 45
          R-HEMBA1007147
          R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818
          R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674
          R-nnnnnnnnnnn//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085
          R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:Al302954
 50
          R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051
          R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:D86987
          R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990
          R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4e-98:471:97//Hs.27197:
          AB018340
 55
          R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864
          R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934
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R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394

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R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062
R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:Al221207
R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543
R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804
R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990
R-HEMBA1007301
R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:Al337917
R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//5.5e-15:311:64//Hs.142764:
R-HEMBA1007322//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:
K00629
R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.
154069:U06452
R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848
R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684
R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333
R-HEMBB1000005//ESTs, Weakly similar to putative p150 [H.sapiens]//3.3e-44:341:71//Hs.111730:AA604403
R-HEMBB1000008//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-
40:292:83//Hs.129708:AF064090
R-HEMBB1000018//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969
R-HEMBB1000024//ESTs//7.5e-21:234:76//Hs.157049:Al345418
R-HEMBB1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332
R-HEMBB1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449
R-HEMBB1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME
III [Caenorhabditis elegans]//6.0e-92:477:95//Hs.4877:AA418465
R-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//
Hs.20815:AF084928
R-HEMBB1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702
R-HEMBB1000044//EST//7.6e-70:367:95//Hs.140860:R42954
R-HEMBB1000048//EST//1.5e-45:262:91//Hs.157627:Al357802
R-HEMBB1000050//ESTs//0.039:91:74//Hs.163189:AA236903
R-HEMBB1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107
R-HEMBB1000055//ESTs, Moderately similar to UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX SUB-
UNIT VI REQUIRING PROTEIN [H.sapiens]//1.1e-72:350:99//Hs.116490:AA659584
R-HEMBB1000059//ESTs//1.7e-10:200:70//Hs.163954:N57939
R-HEMBB1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:80//Hs.4953:D63997
R-HEMBB1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:70//Hs.153014:AB002353
R-HEMBB1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193
R-HEMBB1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5e-18:298:69//Hs.153026:
R-HEMBB1000113//EST//8.2e-94:437:100//Hs.136893:AA805239
R-HEMBB1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521
R-HEMBB1000136//ESTs//0.043:262:59//Hs.61304:AA025692
R-HEMBB1000141//ESTs//5.0e-38:254:79//Hs.141658:N77915
R-HEMBB1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951
R-HEMBB1000173//EST//9.6e-44:258:76//Hs.161917:AA483223
R-HEMBB1000175//ESTs//4.8e-98:475:97//Hs.149740:Al199558
R-HEMBB1000198//ESTs//1.0:123:62//Hs.116602:AA665965
R-HEMBB1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:86//Hs.153014:AB002353
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R-HEMBB1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:86//Hs.153014:AB0023 8-HEMBB1000217//ESTs//2.2e-105:496:99//Hs.65973:Al339364

R-HEMBB1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.1e-48:292:79//Hs.133089:AF064019

R-HEMBB10002267/ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//5.1e-73:449:89//Hs.16803:AA843214

55 R-HEMBB1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106

R-HEMBB1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs.155464:AF088219

R-HEMBB1000250//EST//8.8e-12:284:64//Hs.145960:AI276783

R-HEMBB1000258//EST//4.5e-14:315:66//Hs.162551:AA584782

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R-HEMBB1000264
         R-HEMBB1000266//ESTs, Weakly similar to similar to the beta transducin family [C.elegans]//2.7e-102:556:93//
         Hs.16079:AA083522
         R-HEMBB1000272//ESTs//4.3e-91:480:94//Hs.107467:H11385
         R-HEMBB1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9e-24:198:72//Hs.101414:
5
         AB011129
         R-HEMBB1000284//ESTs//4.8e-64:389:91//Hs.118043:N50458
         R-HEMBB1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:87//Hs.153014:AB002353
         R-HEMBB1000312//ESTs//6.0e-23:272:73//Hs.121354:AA758601
10
         R-HEMBB1000317//ESTs//7.5e-90:424:99//Hs.150042:AI298034
         R-HEMBB1000318//Small inducible cytokine A5 (RANTES)//3.3e-41:318:80//Hs.155464:AF088219
         R-HEMBB1000335//ESTs//3.7e-15:324:65//Hs.85077:AA968576
         R-HEMBB1000336//ESTs//6.4e-76:402:95//Hs.17207:H92480
         R-HEMBB-1000337//ESTs//2.1e-80:391:97//Hs.118990:Al378084
         R-HEMBB1000338//Small inducible cytokine A5 (RANTES)//4.0e-39:274:85//Hs.155464:AF088219
15
         R-HEMBB1000339//EST//5.8e-41:336:79//Hs.151873:AA205736
         R-HEMBB1000341//ESTs//3.8e-19:310:68//Hs.37573:H59651
         R-HEMBB1000343//EST//1.1e-77:396:95//Hs.162664:AA605020
         R-HEMBB1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:65//Hs.36232:D80008
         R-HEMBB1000369//ESTs//1.6e-21:234:73//Hs.111583:AA463590
20
         R-HEMBB1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.3e-56:335:77//Hs.
         92381:AB007956
         R-HEMBB1000376//H.sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.66710:X96969
         R-HEMBB1000391//ESTs//6.6e-50:316:88//Hs.142259:AA828840
25
         R-HEMBB1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8e-109:531:97//Hs.16184:AJ001642
         R-HEMBB1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:X98173
         R-HEMBB1000404//ESTs//0.088:298:59//Hs.61607:AA032026
         R-HEMBB1000420//EST//2.2e-78:376:98//Hs.160787:Al336591
         R-HEMBB1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087
         R-HEMBB1000438//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//0.30:214:63//
30
         Hs.142209:AA873303
         R-HEMBB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990
         R-HEMBB1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221
         R-HEMBB1000455//EST//4.8e-14:421:65//Hs.68832:AA088438
35
         R-HEMBB1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396
         R-HEMBB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390
         R-HEMBB1000487//EST//0.78:87:68//Hs.134601:AI081506
         R-HEMBB1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs.155464:AF088219
         R-HEMBB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080
         R-HEMBB1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125
40
         R-HEMBB1000510//EST//1.4e-45:139:97//Hs.152260:AA489703
         R-HEMBB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087
         R-HEMBB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080
         R-HEMBB1000530//ESTs//2.7e-73:425:90//Hs.141254:Al334099
45
         R-HEMBB1000550//EST//2.9e-11:113:79//Hs.161503:N68662
         R-HEMBB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:
         AF052288
         R-HEMBB1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986
         R-HEMBB1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258
50
         R-HEMBB1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709
         R-HEMBB1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618
         R-HEMBB1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247
         R-HEMBB1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895
         R-HEMBB1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704
55
         R-HEMBB1000592//ESTs//1.8e-97:455:99//Hs.94229:W65391
         R-HEMBB1000598//Human anti secretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199
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R-HEMBB1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125 R-HEMBB1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249

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R-HEMBB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152
        R-HEMBB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531
        R-HEMBB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522
        R-HEMBB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582
        R-HEMBB1000643//ESTs//0.0049:191:62//Hs.55445:W31963
5
         R-HEMBB1000649//ESTs, Moderately similar to hTAFII68 [H.sapiens]//4.0e-76:399:95//Hs.124106:AA948100
         R-HEMBB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939
         R-HEMBB1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988
         R-HEMBB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705
         R-HEMBB1000673//EST//0.58:46:82//Hs.142286:AA338293
10
         R-HEMBB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454
         R-nnnnnnnnnnn//Homo sapiens neuroan1 mRNA, complete cds//6.5e-52:287:93//Hs.158300:AF040723
         R-HEMBB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs.155464:AF088219
         R-HEMBB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412
         R-HEMBB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-50:245:99//Hs.111730:AA604403
15
         R-HEMBB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//Hs.10351:AB002306
         R-HEMBB1000726//EST//5.3e-49:303:88//Hs.149580:Al281881
         R-HEMBB100073 8//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121493:D25272
         R-HEMBB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925
         R-HEMBB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522
20
         R-HEMBB1000770//EST//1.0e-75:359:99//Hs.136564:AA642445
         R-HEMBB1000781//ESTs//5.3e-66:317:99//Hs.28827:AI125541
         R-HEMBB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771
         R-HEMBB1000790//PLATELET GLYCOPROTEIN V PRECURSORY//1.3e-37:193:75//Hs.73734:Z23091
         R-HEMBB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718
25
         R-HEMBB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961
         R-HEMBB1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs.155464:AF088219
         R-HEMBB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI052447
         R-HEMBB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124
         R-HEMBB1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs.155464:AF088219
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         R-HEMBB1000827//EST//2.8e-40:295:84//Hs.149580:AI281881
         R-HEMBB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176
         R-HEMBB1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545
         R-HEMBB1000840//ATPase, Na<sup>+</sup>/K<sup>+</sup> transporting, beta 2 polypeptide//1.3e-43:163:84//Hs.78854:AF007876
         R-HEMBB1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.5e-41:367:78//Hs.129740:
35
         R-HEMBB1000852//EST//1.2e-09:188:70//Hs.127869:AA968599
         R-HEMBB1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.0e-41:483:73//Hs.2379:U23942
         R-HEMBB1000876//EST//0.0022:211:63//Hs.125552:AA884141
         R-HEMBB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247
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         R-HEMBB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI004740
         R-HEMBB1000888//EST//8.2e-07:196:64//Hs.118276:W15258
         R-HEMBB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.1e-46:327:83//Hs.51048:X68830
         R-HEMBB1000893//EST//4.7e-34:242:85//Hs.149580:AI281881
         R-HEMBB1000908//EST//0.95:27:100//Hs.142568:AA285066
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         R-HEMBB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983
         R-HEMBB1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:367:73//Hs.149323:AB002325
         R-HEMBB1000915//ESTs//0.00018:188:61//Hs.44847:AI222742
          R-HEMBB1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84//Hs.127649:AB007874
          R-HEMBB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA365784
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          R-HEMBB1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:350:91//Hs.49163:AA532881
          R-HEMBB1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1e-84:546:86//Hs.23094:MI9503
          R-HEMBB1000973//ESTs//6.8e-95:445:99//Hs.105859:Al419354
          R-HEMBB1000975//ESTs//1.2e-39:197:100//Hs.26176:Al032007
          R-HEMBB1000981//EST//7.7e-58:284:98//Hs.60179:AA007242
55
          R-HEMBB1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369
          R-HEMBB1000991//EST//0.99:58:72//Hs.100246:T23625
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R-HEMBB1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482:70//Hs.154103:AF061258

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R-HEMBB1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112
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R-HEMBB1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//2.3e-25:339:71//Hs.129992: H58762

R-HEMBB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI191214

5 R-HEMBB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814

R-HEMBB1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:305:76//Hs.113283:AF018080

R-HEMBB1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562

R-HEMBB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385

R-HEMBB1001047//EST//6.2e-33:232:74//Hs.160146:AI049975

10 R-HEMBB1001051//ESTs//3.7e-79:385:98//Hs.95290:AA046107

R-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.1e-87:497:91//Hs.15832: AR014518

R-HEMBB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125:81//Hs.5737: AB007944

15 R-HEMBB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785

R-HEMBB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381

R-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:512:97//Hs.12953:AF034803

R-HEMBB1001096//Human HsLIM15 mRNA for HsLiml5, complete cds//1.2e-20:233:70//Hs.37181:D64108

R-HEMBB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:82//Hs.153014;AB002353

20 R-HEMBB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296:87//Hs.113283:AF018080

R-HEMBB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426

R-HEMBB1001117//ESTs//1.1e-80:471:90//Hs.61935:T75092

R-HEMBB1001119//ESTs//4.0e-38:213:84//Hs.109140:Al289942

R-HEMBB1001126

25 R-HEMBB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24: 285:73//Hs.554:M25077

R-HEMBB1001137//ESTs//4.6e-10:66:100//Hs.74924:Al332962

R-HEMBB1001142//EST//6.4e-48:315:85//Hs.149580:Al281881

R-HEMBB1001151

30 R-HEMBB1001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.3e-65:331:96//Hs.154179:AA579197

R-HEMBB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878

R-nnnnnnnnn//ESTs//3.5e-41:233:93//Hs.129218:AA991162

R-HEMBB1001177

35 R-HEMBB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349

R-HEMBB1001199

R-HEMBB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183

R-HEMBB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549

R-HEMBB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573

R-HEMBB1001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//3.1e-44:298:87//Hs.103458:X53795

R-HEMBB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817

R-HEMBB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]//3.8e-80:400:96// Hs.71873:AA148213

45 R-HEMBB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560

R-HEMBB1001249//ESTs//3.8e-34:360:70//Hs.150727:Al292236

R-HEMBB1001253//EST//0.0011:84:77//Hs.124579:AA853987

R-HEMBB1001254//ESTs//4.5e-95:444:99//Hs.161059:Al431268

R-HEMBB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.

50 159897;AB007970

R-HEMBB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087

R-HEMBB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412

R-HEMBB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//2.6e-104:515:97//Hs.16606:W81021

55 R-HEMBB1001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840

R-HEMBB1001294//ESTs//1.9e-100:476:99//Hs.109017:Al057112

R-HEMBB1001302

R-HEMBB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154

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R-HEMBB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627
        R-HEMBB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627
        R-HEMBB1001317//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:
         M29873
         R-HEMBB1001326//ESTs//0.85:174:62//Hs.133487:Al393754
        R-HEMBB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222
         R-HEMBB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365
         R-HEMBB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639
        R-HEMBB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470
        R-HEMBB1001346
10
        R-HEMBB1001348//ESTs//1.1e-43:295:85//Hs.163604:R94354
         R-HEMBB1001356//EST//6.0e-11:89:88//Hs.152366:AA486721
         R-HEMBB1001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-
         12:129:79//Hs.9792:AA027055
         R-HEMBB1001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087
15
         R-HEMBB1001367//ESTs//1.2e-19:165:82//Hs.146314:R99617
         R-HEMBB1001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155464:AF088219
         R-HEMBB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205
         R-HEMBB1001384//ESTs//6.6e-110:547:96//Hs.6671:Al341699
         R-HEMBB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970
20
         R-HEMBB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350
         R-HEMBB1001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//0.88:365:58//Hs.389:X76342
         R-HEMBB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644
         R-HEMBB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59651
         R-HEMBB1001429//EST//3.8e-59:543:76//Hs.158803:Al376846
25
         R-HEMBB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317
         R-HEMBB1001443//ESTs//4.8e-54:270:98//Hs.21898:Al088201
         R-HEMBB1001449//ESTs//3.2e-43:170:84//Hs.150727:Al292236
         R-HEMBB1001454//ESTs//9.1e-46:304:86//Hs.139190:N55515
         R-HEMBB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67293
30
         R-HEMBB1001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78//Hs.41742:AB007881
         R-HEMBB1001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:61//Hs.13275:Al341468
         R-HEMBB1001482//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//0.80:53:83//Hs.26799:W74481
         R-HEMBB1001500//EST//1.4e-13:310:67//Hs.162663:AA604515
         R-HEMBB1001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630:
35
         R-HEMBB1001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME
         III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915
         R-HEMBB1001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159
         R-HEMBB1001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459
40
         R-HEMBB1001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353
         R-HEMBB1001537//Homo sapiens KIAA0409 mRNA, pardal cds//3.2e-47:318:80//Hs.5158:AB007869
         R-HEMBB1001555//ESTs//2.6e-13:182:71//Hs.112671:Al377274
         R-HEMBB1001562//ESTs//1.7e-43:316:83//Hs.151365:AA643962
         R-HEMBB1001564//EST//1.3e-35:141:81//Hs.162197:AA53521
45
         R-HEMBB1001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329
         R-HEMBB1001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944
         R-HEMBB1001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219
         R-HEMBB1001588//EST//8.3e-27:363:69//Hs.141603:N66015
         R-HEMBB1001603//ESTs//1.2e-101:482:99//Hs.12403:Al090184
50
         R-HEMBB1001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044
         R-HEMBB1001619//EST//1.7e-38:476:70//Hs.139093:AA166888
         R-HEMBB1001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:D25272
         R-HEMBB1001635//ESTs//9.5e-34:304:82//Hs.140444:Al002082
          R-HEMBB1001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633
55
         R-HEMBB1001641//EST//2.4e-06:67:86//Hs.162398:AA572813
          R-HEMBB1001653//ESTs//4.8e-80:381:99//Hs.140502:AA806438
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R-HEMBB1001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577

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R-HEMBB1001668//ESTs//0.73:212:62//Hs.8928:N32572
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R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.9e-117:573:97//Hs.24439: AB014546

R-HEMBB1001684//ESTs, Moderately similar to Tbcl [M.musculus]//5.4e-106:523:97//Hs.26939:AA804534

5 R-HEMBB1001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.9e-43:292:86//Hs.96337:AA225358

R-HEMBB1001695//ESTs//3.7e-101:539:94//Hs.78289:R60867

R-HEMBB1001704//EST//0.96:248:57//Hs.163025:AA703038

R-HEMBB1001706//ESTs//1.3e-39:308:81//Hs.141318:N71080

R-HEMBB1001707//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.9e-32:277:73//Hs.142764: AA205569

R-HEMBB1001717//ESTs//1.6e-34:225:87//Hs.57883:AA218645

R-HEMBB1001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]// 8.6e-11:158:71//Hs.141263:H64113

15 R-HEMBB1001736//ESTs//0.0035:223:60//Hs.21354:AA203403

R-HEMBB1001747//EST//9.9e-55:293:81//Hs.112866:AA620488

R-HEMBB1001749//ESTs//2.5e-13:95:91//Hs.139888:N25287

R-HEMBB1001753//ESTs//2.6e-07:141:70//Hs.144604:AI052059

R-HEMBB1001756//EST//2.6e-06:165:64//Hs.121195:AA757211

20 R-HEMBB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264:74//Hs.70008: L00352

R-HEMBB1001762//ESTs//2.1e-81:447:93//Hs.152766:AA211369

R-HEMBB1001785//ESTs//0.040:390:58//Hs.116651:AA993406

R-HEMBB1001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253

25 R-HEMBB1001802//Desmin//9.9e-95:497:93//Hs.119104:M63391

R-HEMBB1001812//ESTs//1.2e-12:91:78//Hs.138852:AA284247

R-HEMBB1001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143:76//Hs.23094:M19503 R-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//5.5e-106:498:98//Hs.159396:AF056209

30 R-HEMBB1001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//9.6e-39:288:73//Hs. 67619:AB007957

R-HEMBB1001839

55

R-HEMBB1001850//EST//0.020:119:68//Hs.32767:H38125

R-HEMBB1001863//ESTs//4.5e-17:226:72//Hs.157253:Al357539

35 R-HEMBB1001867//ESTs//2.3e-16:254:68//Hs.123664:AA806106

R-HEMBB1001868//EST//9.8e-30:155:100//Hs.160572:AA888397

R-HEMBB1001869//ESTs//2.8e-42:376:78//Hs.141973:N21434

R-HEMBB1001872//EST//0.85:156:64//Hs.119501:AA487980 R-HEMBB1001874//EST//0.64:107:70//Hs.147482:AI215572

40 R-HEMBB1001875//EST//0.079:199:59//Hs.121810:AA775240

R-HEMBB1001880//Thromboxane A2 receptor//9.0e-47:297:88//Hs.89887:D38081

R-HEMBB1001899//ESTs//6.3e-68:323:100//Hs.121538:AA609310

R-HEMBB1001905//ESTs//4.4e-19:227:73//Hs.146173:AA906191

R-HEMBB1001906//ESTs//1.6e-90:463:95//Hs.28266:H46725

45 R-HEMBB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915

R-HEMBB1001910//EST//6.0e-37:308:78//Hs.162197:AA535216

R-HEMBB1001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750

R-HEMBB1001915//ESTs//3.1e-73:395:93//Hs.17054:AI139897

R-HEMBB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390

50 R-HEMBB1001922//H.sapiens mRNA for novel member of serine-arginine domain protein, SRrp129//7.4e-38:531: 70//Hs.153086;Y11251

R-HEMBB1001925/Human mRNA for KIAA0327 protein, complete cds//9.5e-19:199:77//Hs.149323:AB002325

R-HEMBB1001930//EST//1.9e-18:136:78//Hs.132635:Al032875

R-HEMBB1001944//EST//0.034:228:57//Hs.93664:N23366

R-HEMBB1001945//ESTs//1.8e-83:439:95//Hs.7341:N57875

R-HEMBB1001947//ESTs//5.6e-109:533:97//Hs.48855:AA134589

R-HEMBB1001950//ESTs//1.5e-107:583:93//Hs.8033:N94998

R-HEMBB1001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788

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R-HEMBB1001953//Human mRNA for KIAA0080 gene, partial cds//6,2e-50:284:83//Hs.74554:D38522
         R-HEMBB1001957//EST//4.8e-50:382:81//Hs.149580:Al281881
         R-HEMBB1001962//ESTs//1.5e-20:143:88//Hs.11924:W26972
         R-HEMBB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296:88//Hs.153468:
5
         AB011147
         R-HEMBB1001973//ESTs//1.4e-48:303:88//Hs.132722:AA618531
         R-HEMBB1001983//ESTs//2.6e-72:374:95//Hs.141022:H06475
         R-HEMBB1001988//ESTs//2.0e-31:204:88//Hs.142531:N91572
         R-HEMBB1001990//ESTs//9.4e-115:574:96//Hs.44426:AA173223
10
         R-HEMBB1001996
         R-HEMBB1001997//ESTs//7.6e-78:380:98//Hs.32682:H37798
         R-HEMBB1002002//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-18:222:71//Hs.103948:
         R-HEMBB1002005//EST//2.2e-41:339:80//Hs.160833:Al345334
         R-HEMBB1002009//EST//2.9e-44:245:94//Hs.28788:R66896
15
         R-HEMBB1002015//EST//0.0027:198:63//Hs.160868:AI359052
         R-HEMBB1002042//ESTs//1.1e-75:529:84//Hs.106919:AA523900
         R-HEMBB1002043//ESTs//7.9e-40:292:83//Hs.70279:AA757426
         R-HEMBB1002044//ESTs//2.1e-92:460:94//Hs.115897:AA156638
20
         R-HEMBB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:301:85//Hs.113283:AF018080
         R-HEMBB1002049//ESTs//3.8e-77:409:94//Hs.122624:R82638
         R-HEMBB1002050//ESTs//8.7e-45:330:82//Hs.44702:AI148840
         R-HEMBB1002068//ESTs//8.3e-70:333:99//Hs.134807:AI090671
         R-HEMBB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486:81//Hs.
25
         129735:AF010144
         R-HEMBB1002092//ESTs//6.5e-46:331:83//Hs.22910:W18193
         R-HEMBB1002094//EST//3.6e-45:280:88//Hs.149580:AI281881
         R-HEMBB1002115
         R-HEMBB1002139//ESTs//4.2e-45:318:85//Hs.107657:AA126814
30
         R-HEMBB1002142//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//
         1.4e-45:281:88//Hs.125231:AF068006
         R-HEMBB1002152//EST//4.3e-39:250:89//Hs.156552:AA833553
         R-HEMBB1002189//H.sapiens mRNA for translin associated protein X//1.4e-47:328:85//Hs.96247:X95073
         R-HEMBB1002190//ESTs//8.3e-05:122:70//Hs.41974:AF039185
35
         R-HEMBB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs.301:U18934
         R-HEMBB1002217//EST//6.6e-50:303:89//Hs.149580:AI281881
         R-HEMBB1002218//ESTs//2.3e-19:150:86//Hs.136031:W95841
         R-HEMBB1002232//ESTs//8.9e-47:445:77//Hs.163971:N27584
         R-HEMBB1002247//EST//6.6e-09:236:65//Hs.130578:AI004631
40
         R-HEMBB1002249//ESTs//5.2e-16:325:64//Hs.156253:Al334807
         R-HEMBB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590:88//Hs.23094:M19503
         R-HEMBB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:83//Hs.84123:AB002363
         R-HEMBB1002266//ESTs//4.4e-98:472:98//Hs.65366:AI189112
         R-HEMBB1002280//EST//2.9e-41:247:90//Hs.161917:AA483223
45
         R-HEMBB1002300//ESTs//8.4e-19:229:75//Hs.138463:N72305
         R-HEMBB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138:67//Hs.155174:AB007892
         R-HEMBB1002327//EST//0.042:249:61//Hs.121097:AA714637
         R-HEMBB1002329//ESTs//1.7e-94:453:99//Hs.7114:R24312
         R-HEMBB1002340//ESTs//5.8e-15:163:77//Hs.26378:H10228
50
         R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//0.85:46:84//Hs.42644:AJ010841
         R-HEMBB1002358//ESTs//2.0e-52:319:81//Hs.140255;AA708322
         R-HEMBB1002359//ESTs//2.7e-106:517:97//Hs.13634:AI051613
         R-HEMBB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:65//Hs.74554:D38522
         R-HEMBB1002371//Catalase//3.3e-22:235:77//Hs.76359:X04085
55
         R-HEMBB1002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120:78//Hs.142296:AF072467
         R-HEMBB1002383//ESTs//3.5e-108:520:98//Hs.45140:D80055
         R-HEMBB1002387
         R-HEMBB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-23:
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168:77//Hs.133526:N21103
         R-HEMBB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.2e-57:304:90//Hs.144563:
         R-HEMBB1002442//ESTs//2.7e-48:289:87//Hs.155243:N70293
5
        R-HEMBB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:87//Hs.153014:AB002353
        R-HEMBB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:71//Hs.154326:D42087
        R-HEMBB1002458//EST//1.8e-72:343:100//Hs.162006:AA508089
        R-HEMBB1002477//ESTs//1.6e-38:215:93//Hs.18240:AA460083
        R-HEMBB1002489//ESTs//1.2e-101:534:94//Hs.7981:H15176
10
         R-HEMBB1002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969
         R-HEMBB1002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017
        R-HEMBB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98//Hs.141515:T41142
         R-HEMBB1002509//ESTs//2.7e-97:459:99//Hs.127638:AI014615
         R-HEMBB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265:95//Hs.48827:AA873278
15
         R-HEMBB1002520//EST//7.2e-40:198:84//Hs.140493:AA804538
         R-HEMBB1002522//Human putative transmembrane receptor IL-1Rrp mRNA, complete cds//0.50:142:69//Hs.
         159301:U43672
         R-HEMBB1002531//EST//0.024:147:61//Hs.148305:AA909605
         R-HEMBB1002534//EST//3.1e-22:168:84//Hs.146794:AI149478
20
         R-HEMBB1002545//ESTs//9.2e-90:421:99//Hs.118317:AI033259
         R-HEMBB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C.elegans]//5.1e-22:210:81//Hs.11896:
         T68813
         R-HEMBB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSORY//1.9e-45:344:82//Hs.51048:X68830
         R-HEMBB1002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189
25
         R-HEMBB1002582//ESTs//0.00036:91:76//Hs.140039:AA047045
         R-HEMBB1002590//ESTs//1.0e-37:210:84//Hs.36658:N91138
         R-HEMBB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:87//Hs.154326:D42087
         R-HEMBB1002600//EST//2.5e-17:147:84//Hs.121918:AA777424
         R-HEMBB1002601//ESTs//7.8e-68:358:95//Hs.101489:R66923
30
         R-HEMBB1002603//EST//1.1e-47:281:90//Hs.149580:AI281881
         R-HEMBB1002607//ESTs//5.4e-75:379:97//Hs.29438:H42896
         R-HEMBB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.2e-07:
         140:70//Hs.155456:AA707265
         R-HEMBB1002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//8.5e-47:278:83//Hs.
35
         159187:AB007977
         R-HEMBB1002614//ESTs//3.4e-81:383:99//Hs.13012:Al094150
         R-HEMBB1002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.
         137574-AF055917
         R-HEMBB1002623//ESTs//1.6e-45:288:87//Hs.138852:AA284247
        R-HEMBB1002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:AF088219
40
         R-HEMBB1002664//EST//8.9e-49:315:87//Hs.149580:AI281881
        R-HEMBB1002677//ESTs//0.65:159:62//Hs.163517:Al419775
         R-HEMBB1002683//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//8.6e-54:543:75//Hs.2638:
         Z28339
        R-HEMBB1002684//ESTs//3.0e-18:148:87//Hs.158270:AA776646
45
        R-HEMBB1002686//ESTs//6.1e-80:419:96//Hs.103002:W02753
        R-HEMBB1002692//ESTs//3.3e-58:451:82//Hs.141254:Al334099
         R-HEMBB1002697//ESTs//6.2e-86:423:98//Hs.129812:AA769487
         R-HEMBB1002699//EST//5.6e-46:322:84//Hs.140231:AI054398
50
         R-HEMBB1002702//ESTs//5.6e-36:412:72//Hs.154993:AA142842
        R-HEMBB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:M73547
        R-HEMBB1002712//ESTs//9.0e-96:451:99//Hs.136806:AA805682
        R-MAMMA1000009//ESTs//3.0e-78:392:96//Hs.163947:AA678701
        R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247:87//Hs.155464:AF088219
        R-MAMMA1000020//Zinc finger protein 2 (A1-5)//4.9e-49:384:80//Hs.155533:X60152
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        R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154:71//Hs.32511:AB007901
        R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277:84//Hs.93121:
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AB018304

- R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA287165
- R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA996350
- R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545:83//Hs.69747:M35531
- 5 R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065
  - R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:313:83//Hs.46918:AF052099
  - R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241
  - R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-22:287:71//Hs.136063:U51713
  - R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:86//Hs.70008: L00352
  - R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.1e-08: 96:80//Hs.115088:AA230172
- 15 R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577
  - R-MAMMA1000133
  - R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017
  - R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288:78//Hs. 159897:AB007970
- 20 R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:Al281881
  - R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59: 562:75//Hs.77579:AF013263
  - R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787
  - R-MAMMA1000171//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.5e-39:173:83//Hs.53531:
- 25 AJ224162

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- R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEINS [Gallus gallus]//2.4e-07:63: 90//Hs.90367:Al357069
- R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611
- R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054
- 30 R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:Al281881
  - R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [M.musculus]//1.4e-41:272:90//Hs.68398: AA421103
  - R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70425
  - R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946
- 35 R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322:86//Hs.15519: AB018315
  - R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090
  - R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041
- 40 R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF010238
  - R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814
  - R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//2.7e-57:304:78//Hs. 159187:AB007977
  - R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124:AF019369
- 45 R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694
  - R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//3.1e-58:295:83//Hs. 92381:AB007956
  - R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066
  - R-MAMMA1000287
- 50 R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.155174:AB007892
  - R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:76//Hs.22271:D26067
  - R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:Al335251
  - R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434
  - R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491
- 55 R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]//8.6e-54:278:97//Hs.139170:
  - R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881
  - R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204:61//Hs.154919:AB014525

R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159

R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces cerevisiae]//0.42:172:61//Hs. 11463:AA535912

R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:82//Hs.154326:D42087

5 R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659

R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523

R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065

R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106: 92//Hs.32170:AB015132

10 R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AB01060

R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus] //9.1e-47:316:81//Hs.138698:N38973

R-MAMMA1000410//Archain//1.8e-40:443:74//Hs.33642:X81198

R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304:72//Hs.119387:

15 AB007958

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R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:Al334099

R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58: 282:82//Hs.97203:U83171

R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081

20 R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067

R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:81//Hs.40100:AB002390

R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs. 154069:U06452

R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461

25 R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68: 302:85//Hs.97203:U83171

R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179

R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447

R-MAMMA1000458

30 R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176

R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361

R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959

R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886

R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759

35 R-MAMMA1000500//Small inducible cytokine A5 (RANTES)//4.7e-43:283:86//Hs.155464:AF088219

R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390

R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390

R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267

R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:Al292236

R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131

R-MAMMA1000567//EST//0.33:49:79//Hs.147754:Al220561

R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211

R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77//Hs.6200:AB007872

R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548

45 R-MAMMA1000594//Small inducible cytokine A5 (RANTES)//3.0e-45:225:80//Hs.155464:AF088219

R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042

R-MAMMA1000605//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs. 116007:S79267

R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN

50 SIS1-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:Al344105

R-MAMMA1000616//EST//0.071:169:60//Hs.144096:Al032180

R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361

R-MAMMA1000623

R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:Al361002

55 R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203

R-MAMMA1000664//Homo sapiens mRNA for putative lipoic acid synthetase, partial//3.2e-43:400:76//Hs.53531: AJ224162

R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:Al281881

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R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3'REGION [Klebsiella pneumoniae]//8.4e-98:464:98//Hs.31431:Al022065 R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476 R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212 R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343 R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644 R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333 R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//1.2e-29:158:79//Hs.142764: AA205569 R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515 R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329 R-MAMMA1000723//Homo sapiens mRNA for alpha(I,2)fucosyltransferase, complete cds//5.6e-52:350:82//Hs. 46328:D87942 R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267 R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893 R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-35:371:74//Hs.141429:AA631915 R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:253:98//Hs.31575:AF100141 R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//2.3e-116:557:98//Hs.71472:AA632288 R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:Al224205 R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-90:568:86//Hs.23094:M19503 R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627 R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131 R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256 R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465:76//Hs.153014:AB002353 R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204 R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439 R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150 R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163 R-MAMMA1000802//Clathrin, light polypeptide (Lcb)//1.5e-45:358:76//Hs.73919:X81637 R-MAMMA1000831//ESTs//1.3e-1,04:510:97//Hs.17494:AA572675 R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:AI281881 R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902 R-MAMMA1000842//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//9.4e-35 44:363:79//Hs.96337:AA225358 R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097 R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955 R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R76251 R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-47:281:91//Hs.40100:AB002390 40 R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212 R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:Al419311 R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922 R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:324:80//Hs.46918:AF052099 R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399 45 R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:Al032875 R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243 R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128 R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cds//3.2e-40:542:68//Hs.154872: 50 R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107

R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:Al310215

R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-53:307:91//Hs.146395:AB002329

R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017093

R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA701634 55

R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA399989

R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//7.7e-38:269:74//Hs.108966:U48696

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R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335
        R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:Al133727
        R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281
        R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428
        R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//9.3e-79:567:
5
         80//Hs.1361:M55053
         R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178
         R-MAMMA1000957//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen,
         antigen detected by monoclonal and antibody IA4))//7.5e-49:340:85//Hs.103458:X53795
         R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.0e-48:216:85//Hs.153468:
10
         AB011147
         R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI281881
         R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204
         R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cds//8.0e-39:338:79//Hs.93121:
15
         R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI281881
         R-MAMMA1000998//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//3.9e-50:
         445:77//Hs.77579:AF013263
         R-MAMMA1001003//Sialophorin (gpL115, leukosialin, CD43)//4.1e-51:282:82//Hs.80738:X52075
         R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-82:405:97//Hs.25863:AA630313
20
         R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:309:86//Hs.153563:AF011333
         R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814
         R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536
         R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H47461
         R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-50:298:91//Hs.40100:AB002390
25
         R-nnnnnnnnnn//ESTs//3.6e-86:445:95//Hs.122625:R68650
         R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881
         R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1.7e-13:273:65//Hs.98738:
         AI015487
30
         R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532
         R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748
         R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:68//Hs.153014:AB002353
         R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944
         R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-84:556:85//Hs.23094:M19503
         R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222
35
         R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926
         R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//
         6.4e-34:262:82//Hs.129727:AF035587
         R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete cds//4.2e-27:232:76//Hs.
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         61840:U28686
         R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576
         R-MAMMA1001126//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.
         116007:S79267
         R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-59:460:81//Hs.5247:AF029750
         R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029
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         R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399
         R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF068179
         R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131
         R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-58:409:84//Hs.5247:AF029750
         R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-91:430:99//Hs.129982:AI420970
50
         R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251
         R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959
         R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519
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R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79//Hs.73919:X81637

R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348

R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148

musculus]//2.6e-80:358:96//Hs.163827:AA074202

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R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.

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EP 1 074 617 A2
R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293
R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202
R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315
R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701
R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619
R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:Al191307
R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:
R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149
R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:
AB014561
R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001
R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus mus-
culus]//1.1e-108:546:95//Hs.18999:N30643
R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:
AB011144
R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371
R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876
R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.2e-27:348:70//Hs.15731:
R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426
R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.0e-43:300:85//Hs.
46468:U45984
R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, complete cds//8.8e-12:188:70//Hs.
55771:AF004709
R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471
R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426
R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs.32567:AF073519
R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127
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R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127 R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478 R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322 R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216 R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881

R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831

R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275
R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs. 19122:AF038957

R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:Al335267

R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:Al222168

R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618

R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67//Hs.155174:AB007892 R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542

R-MAMMA1001465

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R-MAMMA1001476//Homo sapiens yolk sac permease-like molecule 3 (YSPL3) mRNA, complete cds//0.79:182:

66//Hs.136529:AF058317 R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78//Hs.43681:AL022394

R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065

R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:69//Hs.74554:D38522 R-MAMMA1001510

50 R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242

R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.66710:X96969

R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//Hs.108966:U48696

R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140

55 R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapiens]//1.9e-111:549:96//Hs. 21635:Al417305

R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441

R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792

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R-MAMMA1001604
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R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]//1.9e-97:488:96//Hs.143263: AI057616

R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//Hs.121493:D25272

5 R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472:76//Hs.15519: AB018315

R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]//6.8e-15:168:73//Hs.115216:AA291074 R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377

R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606

10 R-MAMMA1001649

R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.7e-54:272:81// Hs.129735:AF010144

R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:89//Hs.155464:AF088219

R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248

15 R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation Inhibitor 1//0.066:196:62//Hs.159161:X69550 R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081

R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs. 67619:AB007957

R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294:89//Hs.3094:D31884

20 R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:N52088

R-MAMMA1001715//ESTs//1.2e-73:399:9311Hs.124620:Al082338

R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI084596

R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gallus gallus]//3.7e-110:552:96//Hs.6923: AI161158

25 R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59651

R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:Al285666

R-MAMMA1001744

R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817

R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:N25041

30 R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413

R-MAMMA1001757//ESTs//1.0e-9.8:488:96//Hs.45184:C14904

R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:Al142276

R-MAMMA1001764//ESTs//0.00012:434:58//Hs.120051:AA707847

R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3e-41:299:85//Hs.149323:AB002325

35 R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825

R-MAMMA1001771//ESTS, Moderately similar to semaphorin B [M.musculus]//7.6e-43:257:91//Hs.7634: AA481246

R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.6e-42:272:86//

40 R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238

R-MAMMA1001788//EST//0.95:108:62//Hs.145881:Al274644

R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744

R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60313

R-MAMMA1001812//ESTs//2.4e-93:446:98//Hs.129034:AA776892

45 R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:Al052659

R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-46:325:87//Hs.44106:D86979 R-MAMMA1001818

R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:Al281881

R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:75//Hs.32567:AF073519

50 R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140

R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:339:83//Hs.43681:AL022394

R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811

R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H47461

R-MAMMA1001854//Small inducible cytokine A5 (RANTES)//2.6e-38:280:83//Hs.155464:AF088219

55 R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:Al148840

R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete cds//7.8e-31:262:77//Hs.5737: AB007944

R-nnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA, complete cds//9.2e-06:450:58//Hs.132206:

AF039694

R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.9e-46:332:83// Hs.73614:U83460

R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.2e-46:429:78//Hs.2379:U23942

R-MAMMA1001880//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//7.6e-26:230:79//Hs.106008:AA147606

R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788

R-MAMMA1001907//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4))//6.7e-47:283:89//Hs.103458:X53795

10 R-nnnnnnnnnn//ESTs//0.043:134:65//Hs.145333:Al251374

R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801

R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete cds//1.4e-18:174:77//Hs.139648: AB014606

R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790

R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sapiens]//6.7e-24:331:71//Hs.140506: AA308018

R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734

R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W27084

R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:70//Hs.155464:AF088219

20 R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054

R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MART-1) mRNA//3.7e-45:370:80//Hs. 154069:U06452

R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223

R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:Al206412

25 R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:76//Hs.32567:AF073519

R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, complete cds//1.9e-37:316:74//Hs. 10458:AF088219

R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881

R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979

R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION [Bacillus subtilis]//4.0e-45:404:7811Hs/138596:N38806

R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:Al032875

R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds//1.7e-42:314:83//Hs.10887: AB013924

35 R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-46:308:87//Hs.40100:AB002390

R-MAMMA1002093//EST//0.89:213:60//Hs.151201:Al125907

R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347

R-MAMMA1002118

R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:D38081

40 R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.4e-58:396:78//
Hs.129735:AF010144

R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//1.4e-37:422:75//Hs.128834: AF035835

R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276

45 R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:371:69//Hs.97476:AB007886

R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548

R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frames//8.7e-39:506:69//Hs.23094:M19503 R-MAMMA1002156//Homo sapiens mRNA for putative lipoic acid synthetase, partial//2.9e-44:336:82//Hs.53531: AJ224162

50 R-MAMMA1002158//ESTs//3-0e-40:313:83//Hs.118273:AA626040

R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-37:370:77//Hs.29736:AB000509

R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:H52638

R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.2e-51:318:82//Hs. 92381:AB007956

55 R-MAMMA1002209//ESTs//9.2e-34:111:88//Hs.141575:AA211734

R-MAMMA1002215//ESTs//3.6e-101:530:94//Hs.26780:N50038

R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2e-45:283:88//Hs.153026: AB014540

R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U48696

R-MAMMA1002236

R-MAMMA1002243

R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299:87//Hs.113283:AF018080 R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript

KIAA0487//1.6e-54:207:81//Hs.92381:AB007956

R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283

R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772

10 R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141

R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751

R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203:81//Hs.154257: Al275982

R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881

15 R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454

R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153

R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]// 2.3e-58:346:91//Hs.140385:AA773359

R-MAMMA1002308

20 R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280:87//Hs. 154069:U06452

R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-70:503:81//Hs.23094:M19503 R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094

R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.3e-49:457:76//Hs.144563:

25 AF057280

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R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183

R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084

R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658

R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//Hs.91916:AF035317

30 R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897

R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618

R-MAMMA1002347//ESTS//1.5e-44:326:83//Hs.111723:H57439

R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127

R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259:92//Hs.43628:Y15228

R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:77//Hs.40100:AB002390

R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:Al085367

R-MAMMA1002356//Clathrin, light polypeptide (Lcb)//4.9e-31:217:88//Hs.73919:X81637

R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:483:84//Hs.113283:AF018080 R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475

40 R-MAMMA1002361//Homo sapiens X-raý repair cross-complementing protein 2 (XRCC2) mRNA, complete cds// 2.6e-30:244:81//Hs.129727:AF035587

R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:Al292236

R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542

R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs.155464:AF088219

45 R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061

R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305: 83//Hs.86188:D87845

R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294

R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs. 115325:D84488

R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588

R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477

R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475

R-MAMMA1002434//ESTS, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]// 2.5e-106:521:98//Hs.112152:AA487348

R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.7e-37:374:68//Hs.157142:U85996

R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323:81//Hs.

89121:AB007954

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R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076

R-MAMMA1002470//ESTs, Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.5e-104:544:93//Hs.94570:Al192106

5 R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31: 263:79//Hs.38687:AA744496

R-MAMMA10024807/ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-34: 159:79//Hs.133526:N21103

R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:560:97//Hs.155223: AF055460

R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293

R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331:58//Hs.37035: U07664

R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA806277

R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds// 3.9e-103:529:95//Hs.18858:AF065214

R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317:88//Hs.153468: AB011147

R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851

20 R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-12: 280:65//Hs.12725:T65058

R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681

R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693

R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433

25 R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371

R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:Al419258

R-MAMMA1002597//Cytochrome P450, subfamily IIB (phenobarbital-inducible), polypeptide 6//2.9e-21:177:75// Hs.1360:M29874

R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737

30 R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124:AF019369

R-MAMMA1002612//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//4.2e-46:424: 75//Hs.1361:M55053

R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389

R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185:73//Hs.108287:L27670

35 R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306

R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081

R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:Al281881

R-MAMMA1002625//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.3e-35:308:79//Hs. 93332:AA811920

40 R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-57:283:86//Hs. 115325:D84488

R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:89//Hs.40100:AB002390

R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:Al144421

R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915

45 R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776

R-MAMMA1002655

R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:75//Hs.97476:AB007886

R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:82//Hs.154326:D42087

R-MAMMA1002671//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//5.3e-108:544:

50 96//Hs.16464:W19606

R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213

R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.6e-109:544:96//Hs.3363: D86987

R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385

55 R-MAMMA1002698//ESTs//5.9e-43:292:85//Hs.144660:AA652675

R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F22510

R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-70: 353:96//Hs.138404:R70986

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R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69234
        R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858
        R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273:89//Hs.153563:AF011333
        R-MAMMA1002727//ESTs//2.9e-84:395:10011Hs.162826:AA679571
        R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266:88//Hs.155464:AF088219
5
         R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757
         R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907
         R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330:80//Hs.
        154069:U06452
         R-MAMMA1002754//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:
10
         369:77//Hs.105292:AA504776
         R-MAMMA1002758
         R-MAMMA1002764//ESTs//4.2e-103:486:99//Hs.159909:Al393281
         R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651
15
         R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:Al301272
         R-MAMMA1002780//ESTs//1.6e-52:292:92//Hs.135985:AA342750
         R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145
         R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812
         R-MAMMA1002807//Archain//1.4e-39:315:80//Hs.33642:X81198
         R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260
20
         R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:Al248319
         R-MAMMA1002833//EST//1.2e-48:306:88//Hs.149580:AI281881
         R-MAMMA1002835
         R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723
         R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395
25
         R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78160:AF010238
         R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081
         R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361:91//Hs.85155:X79067
         R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941
         R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:Al243592
30
         R-MAMMA1002880//ESTs//6.5e-100:506:96//Hs.163533:N52194
         R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:Al365871
         R-MAMMA1002886//Small inducible cytokine A5 (RANTES)//3.4e-36:228:88//Hs.155464:AF088219
         R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152l55:AA424811
         R-MAMMA1002890//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//4.2e-92:438:
35
         99//Hs.155871:AA533783
         R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:322:80//Hs.26929:AF008915
         R-MAMMA1002895//ESTs//2.7e-32:330:76//Hs.139132:AA211087
         R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF068179
         R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:76//Hs.90981:D80002
40
         R-MAMMA1002930//EST//4.9e-44:260:91//Hs.149580:Al281881
         R-MAMMA1002938
         R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1e-83:556:85//Hs.23094:M19503
         R-MAMMA1002947//ESTs//7.0e-22:222:80//Hs.103395:T79243
         R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:77//Hs.153014:AB002353
45
         R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081
         R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525:95//Hs.94396:AA399630
         R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H15835
         R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279
         R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//
50
         2.1e-41:402:67//Hs.133089:AF064019
         R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF068179
         R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:Al127857
         R-MAMMA1003007//ESTs//2.0e-47:404:80//Hs.146314:R99617
         R-MAMMA1003011//ESTs, Highly similar to HISTONE MACRO-H2A.1 [Rattus norvegicus]//1.4e-53:320:90//Hs.
55
         92023:AI022248
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R-MAMMA1003015//ESTs//1.5e-42:363:79//Hs.155184:AA573189 R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA251268

R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA897315

R-MAMMA1003031//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.5e-27:257:77//Hs.96337:AA225358

R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA603321

5 R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA552160

R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55940

R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:Al002941

R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12862

R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60//Hs.2510:X57348

10 R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:Al281881

R-MAMMA1003056//ESTs//0.99:107:66//Hs.30348:Al038559

R-MAMMA1003057//ESTs, Highly similar to hypothetical protein MD6 [M.musculus]//1.1e-102:545:93//Hs.13755: AA878911

R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322:83//Hs.66710:X96969

15 R-MAMMA1003089//ESTS, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.4e-34:421:70//Hs.161959:AA493652

R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59651

R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T51283

R-MAMMA1003113//EST//3.7e-29:457:70//Hs.123616:AA815366

20 R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA410788

R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA863125

R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:AI149537

R-MAMMA1003146//Wingless-type MMTV integration site 5A, human homolog//0.020:413:61//Hs.152213: L20861

25 R-nnnnnnnnnn

R-MAMMA1003166//ESTs, Moderately similar to PEANUT PROTEIN [Drosophila melanogaster]//2.0e-87:524:89// Hs.6884:W30736

R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:587:94//Hs.108112:AF070640

R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59312

30 R-NT2RM4000027

R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03663

R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:Al86169

R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z78379

R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds/4.0e-113:549:97//Hs.95665:

35 AF070639

R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA877817

R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H19708

R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:AI052312

R-NT2RM4000155//ESTs, Moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]

40 //1.9e-99:536:92//Hs.127810:Al246301

R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA676397

R-nnnnnnnnnn//ESTs//1.0:214:61//Hs.119370:W52962

R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:Al382160

R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//4.1e-99:542:93//Hs.6366:AA614113

45 R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA156723

R-NT2RM400019911ESTsl10.020:95:6511Hs.146203:Al254528

R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.126538:AA931876

R-NT2RM4000202//Small inducible cytokine A5 (RANTES)//4.3e-37:330:77//Hs.155464:AF088219

R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.7e-103:546:94//Hs.111138:

50 AB018255

R-NT2RM4000215

R-nnnnnnnnn//ESTs//7.1e-92:457:97//Hs.162074:AA477760

R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)//0.00020:174:66//Hs.235:X51602

55 R-NT2RM4000244//ESTs//6.6e-61:320:95//Hs.108646:AA613031

R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein)//0.63:219:62//Hs. 119498;AF000974

R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:Al378742

- R-NT2RM4000290//ESTs//4.0e-87:435:96//Hs.162592:AA594128
- R-NT2RM4000324//ESTs//2.2e-80:413:96//Hs.12313:R43673
- R-NT2RM4000327//Small inducible cytokine A5 (RANTES)//3.2e-45:286:87//Hs.155464:AF088219
- R-NT2RM4000344//Clathrin, light polypeptide (Lcb)//8.6e-60:452:84//Hs.73919:X81637
- 5 R-NT2RM4000349//ESTs, Weakly similar to KIAA0005 [H.sapiens]//2.5e-. 117:579:96//Hs.5216:AA534881
  - R-NT2RM4000354//ESTs//2.1e-85:406:99//Hs.126774:AI224479
  - R-NT2RM4000356//ESTs//7.9e-109:548:96//Hs.44278:AA418063
  - R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//2.8e-113:577:95//Hs.8152:AB014542 R-NT2RM4000368//ESTs//2.2e-61:310:97//Hs.143611:M78140
- 10 R-NT2RM4000386//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//1.0e-93:521:92//Hs.41793: AA775879
  - R-NT2RM4000395//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-99:524:94//Hs.5249:U55977
  - R-NT2RM4000414//EST//2.7e-06:196:64//Hs.136648:AA688285
- 15 R-NT2RM4000421//ESTs, Weakly similar to No definition line found [C.elegans]//5.4e-75:470:90//Hs.69235: AA192359
  - R-NT2RM4000425//H.sapiens mRNA for MACH-alpha-2 protein//0.17:112:69//Hs.19949:X98173
  - R-NT2RM4000433//ESTs//2.7e-100:479:98//Hs.24553:AI150687
  - R-NT2RM4000457//ESTs//5.1e-107:535:95//Hs.7579:AA775865
- 20 R-NT2RM4000471//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//6.0e-99: 492:96//Hs.21090:AA418587
  - R-NT2RM4000486//ESTs, Moderately similar to unnamed protein product [H.sapiens]//2.2e-102:493:97//Hs. 111279:W84558
  - R-NT2RM4000496
- 25 R-NT2RM4000511//EST//5.1e-43:326:81//Hs.157658:AI358465
  - R-NT2RM4000514//ESTS//1.7e-112:552:96//Hs.6686:AA205496
  - R-nnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN IN CPA2-ATP2 INTERGENIC REGION [Saccharomyces cerevisiae]//1.4e-60:343:93//Hs.16014:AA074879
  - R-NT2RM4000520//ESTs//2.7e-55:266:100//Hs.99838:AA204731
- 30 R-NT2RM4000531//ESTs//2.0e-88:502:91//Hs.13110:T67461
  - R-NT2RM4000532//ESTs//0.47:290:58//Hs.148753:T91777
  - R-NT2RM4000534//EST//0.00025:303:60//Hs.162809:AA632198
  - R-NT2RM4000585//EST//0.28:63:77//Hs.150024:Al291981
  - R-NT2RM4000590//ESTs//5.8e-65:320:98//Hs.116017:AA613437
- 35 R-NT2RM4000595//Homo sapiens KIAA0431 mRNA, partial cds//0.99:189:64//Hs.16349:AB007891
  - R-NT2RM4000603//ESTs//4.6e-68:356:96//Hs.48855:AA134589
  - R-nnnnnnnnnn//ESTs//1.5e-89:431:97//Hs.26117:W16697
  - R-NT2RM4000616//ESTs, Highly similar to ACETYL-COENZYME A SYNTHETASE [Escherichia coli]//1.4e-102: 519:96//Hs.14779:N64822
- 40 R-NT2RM4000674//ESTs//5.1e-78:398:97//Hs.8268:N70144
  - R-NT2RM4000689//ESTs, Weakly similar to T01G9.4 [C.elegans]//2.9e-115:550:98//Hs.11820:AA205531
  - R-NT2RM4000698//ESTs//2.0e-17:130:87//Hs.86420:AA927510
  - R-nnnnnnnnnnn
  - R-NT2RM4000712//EST//0.99:103:65//Hs.114039:AA701128
- 45 R-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus] //2.2e-103:519:95//Hs.6823:W18181
  - R-NT2RM4000733//ESTs//8.7e-88:429:98//Hs.72185:AA465311
  - R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.6e-105:536:95//Hs.137168: AB018303
- 50 R-NT2RM40007.41//ESTs//0.99:266:58//Hs.142718:AA034046
  - R-NT2RM4000751//ESTs//1.6e-20:351:66//Hs.43145:AA776988
  - R-NT2RM4000764
  - R-NT2RM4000778//EST//0.066:254:61//Hs.148232:AA904174
  - R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//9.3e-106:546:94//Hs.18586:
- 55 AB007920
  - R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.5e-40:424:73//Hs. 154069:U06452
  - R-NT2RM4000790//EST//9.0e-48:259:94//Hs.159694:Al417008

R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0:203:63//Hs.20991:D31891

R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:Al003520

R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//2.5e-28:158:96//Hs.118249: M21868

5 R-NT2RM4000813

R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539:97//Hs.99636:

R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448:99//Hs.20223:AA482031

R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864

10 R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:Al309597

R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:Al283343

R-nnnnnnnnnnn

R-NT2RM4000895//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.3e-96:450:99//Hs.142076:AA604514

15 R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262

R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887

R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647

R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414:96//Hs.115342: AA650126

20 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545:97//Hs.19542: AB018272

R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556:97//Hs.15711: AB014539

R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352

25 R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133:67//Hs. 32170:AB015132

R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300

R-nnnnnnnn//ESTs//3.4e-91:439:99//Hs.103177:W72798

R-NT2RM4001092//ESTs//1.4e-86:517:8911Hs.132969:Z78324

30 R-NT2RM4001116//EST//5.2e-57:275:100//Hs.131115:Al016962

R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276

R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311

R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848

R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:Al209085

35 R-NT2RM4001187//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//9.2e-43:273:91//Hs.109005:N31174

R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3.1e-32:274:70//Hs.2379:U23942 R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849

R-NT2RM4001203

40 R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307

R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410

R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677

R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184

R-NT2RM4001309

45 R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857

R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:Al128899

R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:Al042352

R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae]//1.9e-105:522:97//Hs. 18442:AI129307

50 R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339

R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476

R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA450211

R-NT2RM4001382

R-NT2RM4001384//ESTs//9.6e-91:445:98//Hs.55000:AA805507

55 R-NT2RM4001410//EST//0.13:50:82//Hs.157675:Al358790

R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adaptor protein Lnk [M.musculus]//4.0e-102:539: 94//Hs.15744:Al055859

R-NT2RM4001412

R-NT2RM4001414//ESTs//6.5e-35:226:88//Hs.121727:AA775895

R-NT2RM4001437//EST//0.017:169:67//Hs.13207:F10054

R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae]//7.4e-108:544:94//Hs.7558:AA526812

5 R-NT2RM4001454//ESTs//4.7e-108:517:98//Hs.32295:N32277

R-NT2RM4001455//EST//9.6e-81:395:97//Hs.127978:AA969739

R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324:85//Hs.22271:D26067

R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.0e-104:547:93//Hs.153121: AB014585

10 R-NT2RM4001519//Histatin 1//0.53:340:59//Hs.119101:M26664

R-NT2RM40015227/Small inducible cytokine A5 (RANTES)//8.4e-55:306:80//Hs.155464:AF088219

R-NT2RM40015577/ESTs, Weakly similar to F11A10.4 [C.elegans]//6.1e-21:165:83//Hs.29134:H43072

R-NT2RM4001565//ESTs//2.0e-103:483:99//Hs.121273:AA758027

R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-

Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.7e-43:446:72//Hs.4943:Z98046

R-NT2RM4001569//ESTs//3.6e-37:186:100//Hs.86959:AA888009

R-NT2RM4001582//ESTs//1.2e-96:459:98//Hs.114432:N52946

20 R-nnnnnnnnnn

15

R-NT2RM4001594//ESTs//1.6e-83:404:98//Hs.134740:AA282171

R-NT2RM4001597//ESTs//6.9e-111:558:96//Hs.11408:Al358871

R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.1e-112:565:95//Hs.23255: AB018334

25 R-NT2RM4001611//EST//5.9e-74:353:99//Hs.125318:AA837079

R-NT2RM4001629//ESTs//6.1e-95:453:99//Hs.115765:AA485957

R-NT2RM4001650

R-NT2RM4001662

R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.6e-36:230:70//Hs.7764:

30 AB007938

R-NT2RM4001682//EST//4.3e-68:393:90//Hs.157362:Al367496

R-NT2RM4001710//ESTs//4.3e-48:235:99//Hs.7299:AA203440

R-NT2RM4001714//ESTs//0.0014:568:58//Hs.50458:AA868686

R-nnnnnnnnn//ESTs//6.5e-104:487:99//Hs.153581:AA630465

35 R-NT2RM4001731//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-108:563:94//Hs.18510: AA522887

R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]//0.083:124:68//Hs. 120980:S83390

R-NT2RM4001746//ESTs//6.1e-90:420:100//Hs.139003:AA948200

40 R-NT2RM4001754//Human kpni repeat mma (cdna clone pcd-kpni-4), 3' end//5.4e-59:504:78//Hs.139107:K00629

R-NT2RM4001758//ESTs//8.9e-27:140:100//Hs.149973:Al290740

R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236:80//Hs.39871:AB018270

R-NT2RM4001783//ESTs//9.9e-30:156:99//Hs.115260:AA314956

R-NT2RM4001810//ESTs//1.3e-65;346:95//Hs.131915:W22567

45 R-NT2RM4001813//ESTs//5.7e-102:473:100//Hs.87574:Al089920

R-NT2RM4001823//ESTs//3.8e-62:324:95//Hs.124109:AA888839

R-NT2RM4001828//ESTs//1.3e-119:563:98//Hs.102397:AA706551 R-NT2RM4001836//ESTs//5.5e-16:92:100//Hs.26996:AA551070

R-NT2RM4001841//ESTs//1.3e-99:540:94//Hs.42322:AA082619

50 R-NT2RM4001842//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.1e-10: 274:62//Hs.161959:AA493652

R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//3.0e-43:292:86//Hs.14202:N46000

R-nnnnnnnnnn//ESTs//6.2e-104:495:98//Hs.118686:AA682280

55 R-NT2RM40018657/Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592:97//Hs.61628: Y17711

R-NT2RM4001876//ESTs//2.9e-98:532:92//Hs.100734:AA158252

R-NT2RM4001880//ESTs//2.5e-29:224:86//Hs.6193:AA045149

R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178 R-NT2RM4001922//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-105: 535:95//Hs.30991:AA994438 R-NT2RM4001930//ESTs//4.1-84:425:96//Hs.80042:N63143 R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:Al205893 5 R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:95//Hs.118631: AF098162 R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268 R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//5.7e-62:326:95//Hs.3385:N25917 R-nnnnnnnnnnn//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9e-21:121:98//Hs.8772:AA521097 10 R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265 R-NT2RM4001984 R-NT2RM4001987 R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:Al345528 R-NT2RM4002018 15 R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087 R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435 R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226 R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887 R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179 20 R-nnnnnnnnnnn//Homo sapiens OPA-containing protein mRNA, complete cds//5.5e-42:554:68//Hs.85313: R-NT2RM4002067//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.3e-43:468:73//Hs.139107:K00629 R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthetase [H.sapiens]//6.8e-57:290:96// 25 Hs.109274:AA193416 R-NT2RM4002075//ESTs//0.078:267:61//Hs.163563:AA641655 R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528 R-nnnnnnnnn//ESTs//1.0:95:69//Hs.25897:W65409 R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:Y13620 R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712 30 R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987 R-NT2RM4002146//ESTs//1.9e-93:43 9:99//Hs.119295:AA442090 R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535 R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:72//Hs.154103:AF061258 R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400 35 R-NT2RM4002194//EST//0.22:68:72//Hs.149104:Al244343 R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678 R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079 R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster] //5.1e-112:569:95//Hs.23900:U82984 40 R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase [C.elegans]//1.1e-100:544:93//Hs.27567:W72190 R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs.155464:AF088219 R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864 R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA128263 45 R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638 R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461 R-NT2RM4002294 R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164 R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498 50 R-nnnnnnnnn//ESTs//5.0e-59:283:100//Hs.125048:AA682913 R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:M77198 R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163: AB014549 R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594 55 R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884

R-NT2RM4002409//ESTs, Weakly similar to coded for by C. elegans cDNA yk52e10.5 [C.elegans]//1.3e-97:473:

R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328

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98//Hs.16464:W19606
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R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677

R-NT2RM4002446

R-NT2RM4002452//EST//1.0:164:60//Hs.1166l9:AA668142

5 R-NT2RM4002457

R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890

R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.6e-103:507:97//Hs. 8765:AF083255

R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172:98//Hs.94781:

10 AB014591

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R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884

R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:Al088029

R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA464464

R-nnnnnnnnnn//ESTs, Weakly similar to peroxisome targeting signal 2 receptor [H.sapiens]//1.4e-73:360:91//

15 Hs.31030:H50467

R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788

R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:Al417057

R-NT2RM4002567//ESTs//7.6e-41:272:87//Hs.7114:R24312

R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE [Bos

taurus]//2.3e-89:435:97//Hs.15830:AA165698

R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569

R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus] //9.6e-28:194:87//Hs.59346:Al126802

R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:N45096

25 R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:D38081

R-NT2RP2000008//Zinc finger protein 37a (KOX 21)//5.2e-25:366:67//Hs.54488:X69115

R-NT2RP2000027//ESTs//9.5e-74:377:96//Hs.96557:AA286713

R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7e-42:223:96//Hs.8309:AB018290

R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//

4.3e-64:309:98//Hs.6216:AF061749

R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798

R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:Al094910

R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//2.3e-35:199:94//Hs.41793: AA775879

35 R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [R.norvegicus]//1.4e-78:383:98//Hs.58254:W72881 R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097

R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379:97//Hs. 54877:AF050078

R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcript, partial//2.9e-21:232:75//Hs. 102576:AJ010230

R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8e-75:378:96//Hs.22926:AB018338 R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236:63//Hs.41:D90064

R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757 R-NT2RP2000098//ESTs//9.0e-53:279:94//Hs.87807:AA813827

45 R-NT2RP2000108//EST//1.5e-75:378:96//Hs.162105:AA524419

R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//5.8e-76:386:95//Hs.17706:AB018356 R-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//1.9e-19:153:86//Hs.5268:W22670

R-nnnnnnnn//ESTs//1.0e-55:293:95//Hs.14570:Al422099

50 R-nnnnnnnnnn//ESTs//0.24:354:59//Hs.157564:Al356513

R-NT2RP2000147//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//3.0e-89:457:95//Hs.3832:Al208601

R-NT2RP2000153//EST//0.0039:93:68//Hs.140386:AA773548

R-NT2RP2000157//ESTs//1.1e-53:322:91//Hs.6877:AA040820

R-NT2RP2000161//EST5//1.6e-99:492:97//Hs.21738:Al188190

R-NT2RP2000175//ESTs//1.4e-98:489:96//Hs.4849:AI143741

R-NT2RP2000183//ESTs//9.0e-72:358:96//Hs.4856:N51373

R-NT2RP2000195//ESTs//3.9e-92:439:98//Hs.145091:AA814510

R-NT2RP2000205//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-80:415:95//Hs.11807:T86897

R-NT2RP2000224//RNA polymerase II, polypeptide C (33kD)//1.1e-57:306:94//Hs.79402:AC004382 R-NT2RP2000232

R-NT2RP2000233//ESTs//1.1e-08:63:96//Hs.124861:Al090683

R-NT2RP2000239//ESTs//5.3e-87:427:96//Hs.86211:AA604379

R-NT2RP2000248//ESTs, Weakly similar to O-linked GlcNAc transferase [H.sapiens]//1.3e-95:454:99//Hs. 102057:AA649005

R-NT2RP2000257//ESTs//5.1e-58:282:99//Hs.122565:Al126840

10 R-NT2RP2000258//EST//1.0:67:68//Hs.61812:AA035649

R-NT2RP2000270//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]// 8.4e-59:298:96//Hs.16085:Al261382

R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635

R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865

15 R-NT2RP2000289

R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//9.8e-106:494:99//Hs.102951: AA574249

R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712

R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:

20 93//Hs.58218:U82381

R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSSs// 2.9e-71:342:98//Hs.87684:AL022398

25 R-NT2RP2000329//ESTs, Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus] //3.4e-69:371:94//Hs.43436:N32441

R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:Al276062

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.1e-47:262: 94//Hs.76556:U83981

30 R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103

R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09:93:83//Hs.808:L28010

R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:Al222324

R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140: 90//Hs.5819:AF102265

35 R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]//1.3e-65:362:93//Hs.22197:Al151425 R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-75:435:92//Hs.21938:W81045 R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:Al352013

R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078

R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:Al290215

R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.110:AB007896

R-nnnnnnnn//ESTs//9.9e-63:376:89//Hs.47546:AA181348

R-NT2RP2000523

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R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5e-30:167:97//Hs.14409:AB011144

R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72446

R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1e-66:335:96//Hs.7314:AB014514

R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222

R-NT2RP2000656//ESTs//1.0e-10:128:80//Hs.23977:AA115275

R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396

R-NT2RP2000668//ESTs//8.2e-40:255:88//Hs.113310:R16767

R-NT2RP2000678//ESTs//2.6e-53:271:9611Hs.23790:N99347

R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:AI261368

R-NT2RP2000715//EST//1.2e-87:418:9911Hs.139425:AA429279

R-NT2RP2000731//EST//5.3e-65:322:97//Hs.136754:AA713965

55 R-NT2RP2000758//ESTS//1.0:187:61//Hs.10545:N62642

R-NT2RP2000764//ESTs//5.8e-84:485:91//Hs.121816:AA775419

R-NT2RP2000809

R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745

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R-nnnnnnnnn//ESTs//6.3e-87:433:97//Hs.145479:AA969404
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R-NT2RP2000816//ESTS//0.45:100:69//Hs.147529:AA458918

R-NT2RP2000819

R-NT2RP2000841//ESTs//1.9e-73:351:99//Hs.116385:AI224511

5 R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6

PRECURSOR//4.6e-10:247:66//Hs.29352:M31165

R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:Al206552

R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345

R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//2.8e-43:277:89//Hs.3615:

10 AB018284

R-NT2RP2000892//ESTs//2.8e-50:25 8:96//Hs.119238:AA476267

R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266

R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTEIN ZK652.2 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-37:199:95//Hs.112318:AA186477

15 R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494:96//Hs.19822: AB018298

R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021

R-NT2RP2000970//EST//8-7e-06:255:62//Hs.149202:Al246481

R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGENIC

20 REGION [S.cerevisiae]//7.8e-92:468:95//Hs.12124:AA522537

R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521

R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643

R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA453660

R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108

25 R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665

R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068

R-NT2RP2001119

R-NT2RP2001127//Homa sapiens mRNA for HRIHFB2060, partial cds//1.5e-56:304:94//Hs.146282:AB015348 R-NT2RP2001137

30 R-NT2RP2001149//ESTs//5.1e-66:324:9711Hs.27475:AA704512

R-NT2RP2001168//ESTs//2.0e-98:539:92//Hs.77870:Al188145

R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490:96//Hs.26247: AB007949

R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287

35 R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510

R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:AI188402

R-NT2RP2001226//EST//0.0074:154:63//Hs.128612:AA909358

R-NT2RP2001233/TESTs, Highly similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538:80// Hs.44014:AA632298

40 R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92996

R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//1.5e-112:544:97//Hs.7531:AB018353

R-NT2RP2001277//ESTs//2.0e-81:387:99//Hs.13751:AA908229

R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA044775

R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.123854:AA412665

45 R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7961:AA401205

R-NT2RP2001327//ESTs, Moderately similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]// 2.3e-43:238:93//Hs.106632:N25679

R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:AI341138

R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA114178

50 R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50028

R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA444038

R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H. sapiens]//3.9e-74:411:93//Hs.47305:AA195153

R-NT2RP2001394//ESTs//9.5e-54:305:93//Hs.70256:R07875

F-NT2RP2001397//ESTs, Highly similar to G2/MITOTIC-SPECIFIC CYCLIN B2 [Mesocricetus auratus]//5.2e-97: 469:97//Hs.20483:AA522505

R-NT2RP2001420//ESTs//1.6e-49:228:88//Hs.163602:N32030

R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R35431

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R-NT2RP2001427//EST//1.7e-1 1:107:84//Hs.148584:Al201728
        R-NT2RP2001436//ESTs, Weakly similar to F02D8.3 [C.elegans]//2.9e-114:558:97//Hs.7627:Al341556
         R-NT2RP2001440//EST//0.17:192:58//Hs.133442;AI061394
         R-NT2RP2001445//ESTs//1.1e-43:215:100//Hs.145497:AA501453
         R-NT2RP2001449//ESTs//4.1e-08:234:61//Hs.134067:Al076765
5
         R-NT2RP2001450//ESTs//9.5e-65:356:94//Hs.61829:Al079539
         R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255:83//Hs.155464:AF088219
         R-NT2RP2001506//ESTs//2.9e-23:170:88//Hs.7147:T23513
         R-NT2RP2001511//ESTs//2.0e-08:59:100//Hs.57660:AA251146
         R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1//6.7e-106:545:95//Hs.4277:
10
         Y14494
         R-NT2RP2001526//ESTs//3.7e-23:295:72//Hs.8514:AF039240
         R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//
         1.9e-15:99:95//Hs.99742:AF035586
         R-NT2RP2001560//ESTs//2.2e-58:310:94//Hs.87454:AA732816
15
         R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.0e-76:387:96//Hs.
         67619:AB007957
         R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:193:60//Hs.119:D14661
         R-NT2RP2001581//ESTs//5.1e-08:107:78//Hs.157114:T58884
20
         R-NT2RP2001597//EST//5.2e-22:151:88//Hs.158613:Al369995
         R-NT2RP2001601//ESTs//1.5e-78:373:99//Hs.137558:Al393767
         R-NT2RP2001613
         R-NT2RP2001628//EST//0.99:195:60//Hs.144238:W52294
         R-NT2RP2001663//ESTs//4.0e-37:282:84//Hs.12319:W56090
         R-NT2RP2001677//ESTs//1.4e-44:232:96//Hs.159387:Al370845
25
         R-NT2RP2001678//ESTs//0.91:124:60//Hs.10593:Al201336
         R-NT2RP2001699//EST//0.0033:230:61//Hs.146544:Al125323
         R-NT2RP2001720//ESTs//1.8e-52:255:99//Hs.101064:AA290579
         R-NT2RP2001721//ESTs//7.0e-101:479:99//Hs.129750:AA987538
         R-NT2RP2001740//ESTs//3.3e-76:379:96//Hs.144704:AI147100
30
         R-NT2RP2001748//ESTs//1.4e-44:352:81//Hs.142259:AA828840
         R-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//2.1e-105:519:96//Hs.47504:
         AF091754
         R-NT2RP2001813//ESTs//6.3e-78:406:95//Hs.21902:R44037
35
         R-NT2RP2001861
         R-NT2RP2001869//EST//2.8e-21:173:82//Hs.130321:Al002941
         R-NT2RP2001876//ESTs//6.1e-102:526:95//Hs.4944:AA533088
         R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.elegans]//6.9e-110:556:95//Hs.23159:
         AA113849
         R-NT2RP2001900//ESTs//6.9e-85:442:95//Hs.154220:AA171724
         R-NT2RP2001907//ESTs//2.1e-82:432:94//Hs.142257:AA188423
         R-NT2RP2001926//EST//2.3e-24:299:71//Hs.135085:AI097268
         R-NT2RP2001936//ESTs//1.1e-45:265:92//Hs.112482:T66087
         R-NT2RP2001943//EST//1.4e-05:246:61//Hs.144096:Al032180
45
         R-NT2RP2001946//ESTs//3.6e-87:410:99//Hs.20242:W72594
         R-NT2RP2001947//ESTs//1.9e-55:338:88//Hs.58582:T72588
         R-NT2RP2001969
         R-NT2RP2001976//ESTs//1.2e-98:499:95//Hs.121028:AA902745
         R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1 [M.musculus]//8.3e-15:118:
50
         89//Hs.18760:AA166678
         R-NT2RP2002025//ESTs//2.1e-82:393:98//Hs.159488:Al378233
         R-NT2RP2002032//ESTs//4.4e-98:531:91//Hs.93836:AA813332
         R-NT2RP2002033//ESTs//3.5e-43:229:96//Hs.30563:AA102627
         R-NT2RP2002041
55
         R-NT2RP2002046//ESTs//1.6e-101:476:99//Hs.101107:AA825938
         R-NT2RP2002047//ESTs//9.1e-85:431:95//Hs.116750:AA629895
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R-NT2RP2002058//ESTs//1.3e-31:163:99//Hs.33085:AA258068 R-NT2RP2002066//ESTS//1.9e-87:459:93//Hs.118871:AA846091

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R-NT2RP2002070//ESTs//4.1e-63:332:96//Hs.156446:T92265
        R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26:178:87//Hs.11039:AF052183
        R-NT2RP2002079//ESTs//1.2e-79:389:97//Hs.135214:AI350524
        R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein//1.5e-60:376:89//Hs.155218:
5
        AJ007509
        R-NT2RP2002105//ESTs//8.4e-54:313:90//Hs.98702:Al123000
        R-NT2RP2002124//ESTs//6.6e-81:431:93//Hs.127326:AA525134
        R-NT2RP2002137//Deoxycytidine kinase//0.29:183:62//Hs.709:M60527
        R-NT2RP2002154//ESTs//9.6e-97:539:91//Hs.18624:AA523268
10
         R-NT2RP2002172//EST//0.69:53:75//Hs.156238:Al334495
        R-NT2RP2002185//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.4e-54:269:98//Hs.107201:W52859
        R-NT2RP2002192//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-
         15:245:71//Hs.87578:AI125363
         R-NT2RP2002193//ESTs//3.5e-79:45 3:90//Hs.76578:Al290672
         R-NT2RP2002208//ESTs//2.0e-72:347:99//Hs.164028:Al003946
15
         R-NT2RP2002219//EST//0.039:229:63//Hs.149830:AI287499
         R-NT2RP2002231//ESTs//3.3e-64:337:94//Hs.79828:AA642341
         R-nnnnnnnnnn//ESTs, Highly similar to co-repressor protein [M.musculus]//5.4e-48:238:99//Hs.22583:
         R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//1.6e-15:131:83//Hs.150595:
20
         AF005418
         R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99:548:91//Hs.92137:M19720
         R-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTEIN [H.sapiens]//4.8e-100:550:91//Hs.4029:Z78373
         R-NT2RP2002292//ESTs, Weakly similar to F13B12.1 [C.elegans]//3.2e-92:482:93//Hs.5570:Al377863
         R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//4.1e-103:527:94//
25
         Hs.24812:AF069532
         R-NT2RP2002316//ESTs//4.2e-91:425:100//Hs.3350:Al368015
         R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.2e-112:567:
         95//Hs.31034:AB015594
30
         R-NT2RP2002333//ESTs//1.9e-86:483:91//Hs.155198:AA767372
         R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//1.2e-103:600:
         89//Hs.109051:AF038958
         R-NT2RP2002394//ESTS//0.11:158:65//Hs.28792:AI343467
         R-NT2RP2002408//ESTs//1.5e-51:278:93//Hs.6044:W22815
         R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.7e-33:285:80//Hs.15731:
35
         AB011135
         R-NT2RP2002439//ESTS//3.2e-12:134:76//Hs.32246:AA464020
         R-NT2RP2002457//ESTs//4.7e-52:282:94//Hs.21968:H97521
         R-NT2RP2002464//ESTs//5.3e-27:148:98//Hs.115660:Al362230
         R-NT2RP2002475//ESTs//3.9e-85:439:94//Hs.9873:W27233
40
         R-nnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//9.9e-115:605:92//Hs.
         125856:AB005289
         R-NT2RP2002498//ESTs//6.3e-37:227:93//Hs.108779:N73180
         R-NT2RP2002503//ESTs//1.9e-54:358:86//Hs.57800:W60838
         R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.5e-107:583:91//Hs.23255:
45
         R-NT2RP2002520//ESTs//4.2e-99:509:94//Hs.32368:AA205305
         R-NT2RP2002537//ESTs//4.2e-105:552:93//Hs.154363:AA533090
         R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA//2.6e-109:570:93//Hs.49476:AF009314
         R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189:86//Hs.80961:U60325
50
         R-NT2RP2002591//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.5e-118:564:97//Hs.94549:
         AA149547
         R-NT2RP2002595//EST//1.4e-15:101:95//Hs.129528:AA994783
         R-NT2RP2002606//ESTs//4.5e-99:475:98//Hs.45046:N40170
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R-NT2RP2002609//ESTs//1.9e-104:568:92//Hs.9175:Al184220

R-NT2RP2002618//ESTs//0.014:493:57//Hs.96322:AA541615 R-NT2RP2002621//EST//4.4e-36:252:84//Hs.149580:AI281881 R-NT2RP2002643//ESTs//6.9e-32:247:74//Hs.33354:AA179944

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R-NT2RP2002672
         R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB//0.99:184:63//Hs.50727:U43572
        R-NT2RP2002706//EST//2.8e-41:148:86//Hs.161917:AA483223
         R-NT2RP2002710//EST//0.34:105:71//Hs.136747:AA749210
         R-NT2RP2002727//ESTs//8.7e-68:368:94//Hs.14366:T78626
5
         R-NT2RP2002736//ESTs//9.7e-98:457:99//Hs.74899:AA993300
         R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360:59//Hs.119139:AB011108
         R-NT2RP2002741//ESTs//3.1e-102:489:98//Hs.112024:Al042352
         R-NT2RP2002750//EST//3.6e-43:166:86//Hs.162404:AA573131
         R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:M62042
10
         R-NT2RP2002753//ESTs//1.7e-49:262:96//Hs.49005:W89124
         R-NT2RP2002769//ESTs//1.3e-59:376:88//Hs.4046:H03587
         R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341:94//Hs.17481:AF070537
         R-NT2RP2002800//ESTs//6.5e-08:79:84//Hs.153262:AA551124
         R-NT2RP2002839//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-
15
         100:501:97//Hs.136202:AA206578
         R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031
         R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870
         R-NT2RP2002880
20
         R-NT2RP2002891
         R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894
         R-NT2RP2002928//ESTs//3.9e-108:502:99//Hs.29105:AA574143
         R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096
         R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:Al308771
         R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:N57480
25
         R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:Al147060
         R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213
         R-NT2RP2002986//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//3.1e-119:578:97//
         Hs.106290:Al125291
         R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78:74//Hs.146395:AB002329
30
         R-NT2RP2002993//ESTS, Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE IH.
         sapiens]//2.4e-98:467:98//Hs.86337:AA149311
         R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642
         R-NT2RP2003034//ESTs//9.3e-87:408:96//Hs.164042:H12594
         R-NT2RP2003073//Human transporter protein (g17) mRNA, complete cds//0.95:259:61//Hs.76460:U49082
35
         R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328:81//Hs.89887:D38081
         R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512
         R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336:86//Hs.101996:AB002345
         R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA133355
         R-NT2RP2003125
40
         R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986
         R-NT2RP2003137//ESTs//2.1e-37:259:85//Hs.63169:N78506
         R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379
         R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8980:AA629067
         R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952
45
         R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156
         R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816
         R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074
         R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253
         R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661
50
         R-NT2RP2003243//ESTs//3.6e-53:300:92//Rs.18793:AA192438
          R-NT2RP2003265//ESTs, Highly similar to protein NGD5 [M.musculus]//3.3e-110:557:96//Hs.24994:AA236937
          R-NT2RP2003272//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228:89//Hs.107201:W52859
          R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.4e-111:565:95//Hs.1549l9:
55
          AB014525
          R-NT2RP2003280//ESTs//2.6e-101:541:94//Hs.6982:AA622427
          R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106
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R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458:74//Hs.154326:D42087

R-NT2RP2003295//Protein serine/threonine kinase stk2//0.31:321:57//Hs.1087:L20321

R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874

R-NT2RP2003308//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//4.8e-109:553:96//Hs.26089:AA195126

5 R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:Al424948

R-NT2RP2003339//ESTs//1.3e-85:441:96//Rs.24115:N32618

R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.155773:Al312825

R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA599014

R-NT2RP2003391//ESTs//2.8e-98:484:97//Hs.5842:AA534476

10 R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502

R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52249

R-NT2RP2003401//ESTs//6.1e-25:161:90//Hs.155360:AA984683

R-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.2e-106:508:98//Hs.131840:Al016073

15 R-NT2RP2003445//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.6e-21:161:70//Hs.43153:N22360

R-NT2RP2003446//ESTs, Weakly similar to C27H6.4 [C.elegans]//6.0e-105:529:96//Hs.8055:W60903

R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:Al277332

R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121

20 R-NT2RP2003499//ESTs, Weakly similar to elastin like protein [D.melanogaster]//7.0e-71:365:95//Hs.101056:

R-NT2RP2003506//ESTs, Weakly similar to ORF YPL207w [S.cerevisiae]//2.3e-115:577:96//Hs.16277:N36831 R-NT2RP2003511//ESTs//1.6e-22:182:85//Hs.28249:AA203733

R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//1.3e-108:566:94//Hs.78482:Y16270

25 R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)//4.9e-62:518:79//Hs.1976:M12783

R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170

R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101

R-NT2RP2003543//EST//1.0:80:68//Hs.65646:F13684

30 R-NT2RP2003559//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.8e-58:316:94//Hs.28891:W72439

R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696

R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719

R-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//4.7e-101:495:98//Hs.34627:

35 AA126463

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R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-103:501:97// Hs.58488:U97067

R-NT2RP2003629//EST//0.032:440:59//Hs.135297:Al038981

R-NT2RP2003643//ESTs, Weakly similar to HYPOTHETICAL 14.1 KD PROTEIN IN MURZ-RPON INTERGENIC

40 REGION [E.coli]//9.1e-62:359:92//Hs.12492:AA203188

R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951

R-NT2RP2003687//EST//5.9e-05:196:65//Hs.139064:AA135523

R-NT2RP2003691//ESTs, Weakly similar to F59C6.9 [C.elegans]//1.0:202:62//Hs.65539:Al148540

R-NT2RP2003702//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.3e-99:492:96//Hs. 93332:AA811920

R-NT2RP2003704//ESTs//1.0:155:63//Hs.104166:AA740246

R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.4e-47:265:93//Hs.78494:AB011097

R-NT2RP2003713//EST//0.81:210:59//Hs.14551:T79401

R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:Al365003

R-nnnnnnnnnnnnn//Human 19.8 kDa protein mRNA, complete cds//0.84:221:60//Hs.2384:U18914
R-NT2RP2003737//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Caenorhabditis el-

egans]//2.4e-50:302:90//Hs.19196:W74577

R-NT2RP2003751

R-NT2RP2003760//ESTs//2.6e-101:548:93//Hs.115987:AA483808

R-NT2RP2003764//ESTs//8.2e-25:134:98//Hs.64036:AA127709

R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606

R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds//6.0e-106:531:96//Hs.90436: AF047437

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R-NT2RP2003777//ESTs//2.6e-59:323:94//Hs.10101:Al381811
         R-NT2RP2003781//ESTs//2.0e-25:269:75//Hs.144951:N34836
         R-NT2RP2003793//ESTs//8.7e-94:466:97//Hs.93949:AA782955
         R-NT2RP2003840//ESTs//3.4e-97:533:93//Hs.16130:AA195077
         R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351:65//Hs.75196:X69838
. 5
         R-NT2RP2003859//ESTs//3.0e-07:96:81//Hs.153262:AA551124
         R-NT2RP2003871//ESTs//1.9e-102:509:97//Hs.25726:AA430167
         R-NT2RP2003885//ESTs//1.0e-102:502:97//Hs.36353:AA702341
         R-NT2RP2003912//EST//1.2e-38:336:76//Hs.134975:AI094611
         R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//0.90:190:60//Hs.
10
         75875:U49278
         R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568:97//
         Hs.35086:AB014458
         R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540:97//Hs.7302:
15
         AB007916
         R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568:96//Hs.7316:AB018347
         R-NT2RP2003984
         R-NT2RP2003986//ESTs//4.9e-36:272:82//Hs.158268:AA738087
         R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//3.2e-110:519:99//Hs.36093:
20
         AI149968
         R-NT2RP2004014//ESTs//8.4e-102:483:99//Hs.22867:Al417478
         R-NT2RP2004041
         R-NT2RP2004042//ESTs//1.5e-105:466:97//Hs.7296:N29706
         R-nnnnnnnnn//ESTs//1.4e-110:559:96//Hs.71916:AA219699
          R-NT2RP2004081//ESTs//3.7e-105:503:98//Hs.27542:AA977204
25
          R-NT2RP2004098//EST//7.3e-26:203:87//Hs.21897:R41461
          R-NT2RP2004124//ESTs//1.1e-83:435:95//Hs.43299:N23036
          R-NT2RP2004142//EST//1.3e-06:165:65//Hs.146742:Al147500
          R-NT2RP2004152//ESTs//7.0e-98:455:100//Hs.17731:Al342241
          R-NT2RP2004165//ESTs, Highly similar to DYNEIN BETA CHAIN, CILIARY [Anthocidaris crassispina]//1.0e-118:
30
          583:97//Hs.16520:Al224533
          R-NT2RP2004170//ESTs//6.7e-66:407:88//Hs.157138:Al348544
          R-NT2RP2004172//ESTs//1.5e-109:567:95//Hs.159091:AA033974
          R-NT2RP2004187//ESTs//3.6e-92:488:93//Hs.22954:W26589
35
          R-NT2RP2004194//ESTs//6.2e-114:585:95//Hs.18778:AA203167
          R-NT2RP2004196
          R-NT2RP2004207//ESTs//6.3e-102:488:98//Hs.22678:AA604756
          R-NT2RP2004226//ESTs//8.8e-18:252:71//Hs.11924:W26972
          R-NT2RP2004232//ESTs, Highly similar to protein kinase C mu [H.sapiens]//5.2e-105:499:98//Hs.143460:
 40
          R-NT2RP2004239//ESTs//1.2e-16:171:80//Hs.16134:AA203116
          R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds//3.4e-103:530:93//Hs.
          54900:AF039687
          R-NT2RP2004242//ESTs//1.3e-85:460:93//Hs.104535:AA211483
          R-NT2RP2004245//ESTs//6.4e-117:575:97//Hs.23744:AA035744
 45
          R-NT2RP2004270//ESTs//1.0:95:69//Hs.141371:H92187
          R-NT2RP2004300//ESTs//4.4e-80:379:99//Hs.130874:AA905056
          R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//4.7e-110:544:96//Hs.61152:
          AF000416
          R-NT2RP2004321//ESTs//2.1e-18:104:99//Hs.107207:AA044788
 50
          R-NT2RP2004339//EST//1.4e-47:309:86//Hs.161917:AA483223
          R-NT2RP2004347
          R-NT2RP2004364//ESTs//1.1e-113:566:96//Hs.25880:Al268173
          R-NT2RP2004365//ESTs//0.022:271:62//Hs.38897:AI129310
          R-NT2RP2004366//ESTs//9.5e-71:335:100//Hs.91867:Al218624
 55
          R-NT2RP2004373//ESTs//4.2e-25:172:87//Hs.83243:N32192
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R-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III

[Caenorhabditis elegans]//1.4e-11:108:82//Hs.30490:AA146916

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R-NT2RP2004392//ESTs//3.4e-81:427:94//Hs.5827:AA581646
        R-NT2RP2004396//EST//5.6e-06:100:77//Hs.138623:H92473
        R-NT2RP2004399//EST//0.98:337:59//Hs.118446:N67900
        R-NT2RP2004400//ESTs//2.1e-90:422:100//Hs.152460:AA602921
        R-NT2RP2004412//ESTS//1.4e-105:503:98//Hs.15929:AA403121
5
        R-NT2RP2004425//EST//0.00017:225:60//Hs.146935:Al168124
        R-NT2RP2004476//ESTs//1.4e-88:477:94//Hs.4859:N29695
        R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDK1) mRNA, complete cds//
        8.6e-34:143:98//Hs.154729:AF017995
        R-NT2RP2004512//ESTs//2.6e-91:426:100//Hs.94133:Al270700
10
        R-NT2RP2004523//ESTs//1.6e-74:377:97//Hs.14217:R61320
        R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:279:89//Hs.89887:D38081
        R-NT2RP2004551//ESTs//0.47:147:66//Hs.131519:Al024347
         R-NT2RP2004568//ESTs//1.3e-107:567:94//Hs.65234:AA195470
         R-NT2RP2004580//ESTs//5.9e-29:156:98//Hs.147801:AI221661
15
         R-NT2RP2004587//ESTs//1.0e-102:495:97//Hs.91662:AA781126
         R-NT2RP2004594//ESTs//4.1e-56:298:95//Hs.24641:AA954666
         R-NT2RP2004600//ESTs//4.8e-67:374:93//Hs.49762:N69862
         R-NT2RP2004602//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-07:
20
         149:76//Hs.12845:N28835
         R-NT2RP2004614//ESTs//1.0e-111:557:96//Hs.37892:N53497
         R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-118:587:96//Hs.5198:AJ006291
         R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.9e-107:520:96//Hs.29956:
         AB007929
         R-NT2RP2004675//ESTs//2.7e-82:407:97//Hs.116113:F18930
25
         R-NT2RP2004681//NUCLEOLIN//0.34:387:58//Hs.79110:M60858
         R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//5.0e-120:600:96//Hs.154919:
         AB014525
         R-NT2RP2004709//ESTs//1.1e-106:511:98//Hs.38034:Al149793
         R-NT2RP2004710//ESTs//9.9e-87:477:93//Hs.6834:AA203433
30
         R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//1.3e-118:594:96//Hs.4236:
         AB007947
         R-NT2RP2004743//ESTs//2.1e-48:327:88//Hs.43635:AA447015
         R-NT2RP2004767//EST//4.0e-57:328:81//Hs.142796:N51423
         R-NT2RP2004775//ESTs//9.4e-60:326:94//Hs.115339:AA136774
35
         R-NT2RP2004791//ESTs//3.2e-82:367:96//Hs.141911:N64013
         R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//
         8.0e-116:564:96//Hs.40820:AF058953
         R-NT2RP2004802//ESTs//6.5e-111:586:94//Hs.90375:W74579
         R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//8.7e-120:584:97//Hs.67052:
40
         R-NT2RP2004841//EST//3.8e-31:323:74//Hs.147714:AI219906
         R-NT2RP2004861//EST//0.92:147:63//Hs.23064:R20803
         R-NT2RP2004897//ESTs//1.7e-46:390:80//Hs.139225:H96567
45
         R-NT2RP2004936//EST//0.97:176:63//Hs.137436:AA280529
         R-nnnnnnnn//ESTs//0.059:137:64//Hs.144109:Al345543
         R-NT2RP2004961//ESTs//1.8e-87:409:100//Hs.138297:AA781941
         R-NT2RP2004962//ESTs//0.0021:292:59//Hs.145917:Al275458
         R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-51:506:75//Hs.154326:D42087
         R-NT2RP2004978//ESTs//0.95:138:63//Hs.13619:W93496
50
         R-NT2RP2004982//ESTs//7.8e-95:468:97//Hs.22545:R43910
         R-NT2RP2004985
         R-NT2RP2004999//ESTs//2.9e-94:450:98//Hs.128766:Al419902
         R-NT2RP2005000
         R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//9.6e-113:577:95//Hs.155972:
55
         AB014515
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R-nnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568:97//Hs.31575:AF100141

R-NT2RP2005003//EST//1.3e-75:387:96//Hs.140843:R42235

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R-NT2RP2005018//ESTs//7.5e-46:280:90//Hs.126857:AA932161
        R-NT2RP2005020//ESTs//1.6e-105:554:94//Hs.14846:AA148507
        R-NT2RP2005031//EST//3.1e-79:379:99//Hs.139709:AA227887
         R-NT2RP2005037//ESTs//5.3e-102:551:93//Hs.26516:AA195220
         R-NT2RP2005038//ESTs//5.8e-101:566:92//Hs.46964:N49757
5
         R-NT2RP2005108
         R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7e-105:518:97//Hs.22616:
         AB014564
         R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//4.6e-69:464:85//Hs.
10
         100555:X98743
         R-NT2RP2005139//ESTs//1.0e-108:545:95//Hs.21006:AA523383
         R-NT2RP2005140//ESTs//4.3e-90:422:99//Hs.62180Al341261
         R-NT2RP2005144//ESTs//0.91:162:62//Hs.52399:AI075744
         R-NT2RP2005147//ESTs//4.6e-100:502:96//Hs.27931:AA633438
         R-NT2RP2005159//ESTs//7.5e-105:533:95//Hs.109819:Al357582
15
         R-NT2RP2005162//ESTs//6.6e-83:419:96//Hs.113998:H50648
         R-NT2RP2005168//Homo sapiens mRNA for EIB-55kDa-associated protein//2.4e-101:513:95//Hs.155218:
         AJ007509
         R-NT2RP2005204//ESTs, Weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG [H.sapiens]//1.9e-
20
         115:577:96//Hs.7600:H98166
         R-NT2RP2005227//Homo sapiens UM protein mRNA, complete cds//1.0e-45:359:82//Hs.154103:AF061258
         R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:
         245:97//Hs.21090:AA418587
         R-NT2RP2005254//ESTs//3.3e-111:581:94//Hs.22549:AA524503
         R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III
25
         [Caenorhabditis elegans]//1.1e-79:412:95//Hs.23047:N66596
         R-NT2RP2005276//ESTs//4.6e-85:426:96//Hs.24550:AA316272
         R-NT2RP2005287//ESTs//1.7e-109:565:94//Hs.61976:Al279001
         R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594:98//
30
         Hs.27007:AF060219
         R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545:96//Hs.44766:AJ007590
         R-NT2RP2005293//ESTs//5.1e-116:538:99//Hs.62180:Al341261
         R-NT2RP2005315//ESTs//1.4e-82:415:97//Hs.155829:AA018338
         R-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds//2.5e-45:272:91//Hs.
35
         1569:U11701
         R-NT2RP2005336//ESTs//1.9e-93:444:99//Hs.110966:AA151699
         R-NT2RP2005 344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//0.011:463:
         58//Hs.150926:AF017445
         R-NT2RP2005354//ESTs//7.2e-22:148:91//Hs.153783:H14544
         R-NT2RP2005360//ESTs//0.048:225:60//Hs.7602:AA099247
40
         R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248:82//Hs.93121:AB018304
         R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461:88//Hs.
         70849:AA121697
         R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II
         [C.elegans]//8.1e-96:491:95//Hs.7194:AI185631
45
         R-NT2RP2005441//ESTs//1.1e-110:548:96//Hs.5209:AA780068
         R-NT2RP2005453//ESTs//0.94:352:58//Hs.25870:H14423
         R-NT2RP2005457//ESTs//2.1e-46:236:97//Hs.19522:AA975096
         R-NT2RP2005464//ESTS//1.8e-72:349:99//Hs.44045:N51307
         R-NT2RP2005465//ESTs//0.0058:322:58//Hs.127009:Al378936
50
         R-NT2RP2005472//ESTs//0.47:309:60//Hs.144838:Al222019
         R-NT2RP2005476//ESTS//5.1 e-40:205:9811Hs.101577:Al168526
         R-NT2RP2005490//ESTs//L3e-70:364:96//Hs.134382:AA083573
         R-NT2RP2005491//EST//0.012:220:60//Hs.144448:AA812455
         R-NT2RP2005495//ESTs//1.2e-86:501:91//Hs.99445:R93540
55
          R-NT2RP2005496//ESTs//3.2e-34:263:81//Hs.70279:AA757426
          R-NT2RP2005498//ESTS, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT,
          NEURONAL ISOFORM [Oryctolagus cuniculus]//2.3e-45:284:88//Hs.85752:Al138993
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R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:Al141755

R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME I [Schizosaccharomyces pombe]//8.2e-36:215:92//Hs.5298:AA725071

R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.2e-110:

5 570:9411Hs.119023:AF092563

R-NT2RP2005525//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.3e-84: 433:95//Hs.36942:AA524535

R-NT2RP2005531//EST//0.98:64:70//Hs.146573:Al139856

R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e-108:560:94//Hs.159597:

10 AJ012449

R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115:583:96//Hs.62515: AB007963

R-NT2RP2005549//EST//0.61:111:62//Hs.147482:Al215572

R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:Al357567

15 R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169

R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:H03240

R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733

R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060

R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:Al376788

20 R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229

R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:Al418211

R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740

R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173

R-NT2RP2005651//ESTS, Highly similar to XFIN PROTEIN [Xenopus laevis]//2.9e-103:525:96//Hs.70589:

25 AA868470

R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:60//Hs.162:X16302

R-NT2RP2005669//Homo sapiens nitrilase 1 (VIII) mRNA, complete cds//2.7e-14:87:100//Hs.146406:AF069987 R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//5.8e-91:434:98// Hs.25664:AF089814

30 R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229

R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:Al292236

R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:Al273643

R-NT2RP2005701//ESTs, Highly similar to BUTYROPHILIN PRECURSOR [Bos tauros]//2.8e-68:376:93//Hs. 9095:AA532630

35 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105:503:98//Hs.61638: AR018342

R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precursor [H.sapiens]//5.4e-105:500:98// Hs.14298:Al417523

R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA223982

40 R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455

R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:Al223153

R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258

R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:N78064

R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//4.3e-42:223:96//

45 Hs.159651:AF068868

55

R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//1.2e-104:494:98//Hs. 26285:AF082516

R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:Al362163

R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463

50 R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-112:559:96//Hs.14214:Al189379

R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108:544:96//Hs. 22151:Al214321

R-NT2RP2005781//ESTs//1.7e-43:217:99//Hs.144391:AA365664

R-NT2RP2005784//EST//0.0071:217:60//Hs.117332:AA699724

R-NT2RP2005804//ESTs//8.8e-107:512:98//Hs.15496:W44398

R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:AI298746

R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981

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R-NT2RP2005835//ESTs//1.5e-100;541;94//Hs.86813;N25122
        R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403
        R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:Al076062
        R-NT2RP2005857//ESTS//1.0e-115:576:96//Hs.30663:Al338462
        R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105
        R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133
        R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315
        R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:AI125268
        R-NT2RP2005908//ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]//2.4e-73:397:
        94//Hs.16667:T92427
10
        R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R.norvegicus]//2.8e-114:560:97//Hs.9082:AA873170
         R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:Al338419
         R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988
         R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080
         R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347
15
         R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II
         [C.elegans]//1.2e-50:278:94//Hs.7194:Al185631
         R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492
         R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA522714
         R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093
20
         R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26860:N56918
         R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031:254:62//
         Hs.46440:U21943
         R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365
         R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522
25
         R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17:255:72//Hs.154103:AF061258
         R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435
         R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1e-110:553:95//Hs.109299:
         AB014554
         R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.151293:U79276
30
         R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398
         R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.2e-94:532:90//Hs.153910:X96484
         R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:Al341312
         R-NT2RP2006238//ESTs, Highly similar to rA8 [R.norvegicus]//1.5e-29:183:91//Hs.4048:AA404253
         R-NT2RP2006258//ESTs//3.2e-87:462:94//Hs.141556:N49928
35
         R-NT2RP2006261//ESTs//3.4e-57:3 26:92//Hs.22523:W02999
         R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:481:97//Hs.3404:AF035262
         R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015
         R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapiens]//1.9e-89:460:96//Hs.21889:
40
         R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.61697:AI081771
         R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412
         R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:AI282321
         R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411
         R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//3.9e-48:403:
45
         77//Hs.1361:M55053
         R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27:155:76//Hs.
         115325:D84488
         R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092
         R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:AI341146
50
         R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63595
         R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109:524:97//Hs.72160:AJ006266
         R-NT2RP2006467//EST//0.99:140:61//Hs.146958:AI174478
         R-NT2RP2006472//ESTs//3.3e-92:473:95//Hs.29216:AA916679
         R-NT2RP2006534//ESTs//1.2e-83:394:99//Hs.162116:AA524947
55
         R-NT2RP2006554//ESTs//1.0e-87:460:95//Hs.47095:AA181474
          R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:Al299886
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R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622

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R-nnnnnnnnn//ESTs//2.0e-112:533:98//Hs.18685:Al393829
         R-NT2RP2006598//ESTs, Weakly similar to retinoid X receptor interacting protein [M.musculus]//4.1e-109:542:
         97//Hs.7889:Al337112
         R-NT2RP3000002//ESTs//1.3e-08:399:59//Hs.126044:Al301598
         R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-116:560:97//Hs.6764:
5
         AJ011972
        R-NT2RP3000046//Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs.155464:AF088219
         R-NT2RP3000047//EST//0.91:130:66//Hs.140208:AA702213
         R-NT2RP3000050//ESTs, Weakly similar to putative p150 [H.sapiens]//3.1e-41:249:90//Hs.156155:Al222202
         R-NT2RP3000055//EST//2.4e-19:146:86//Hs.160497:AI255095
10
         R-NT2RP3000072//ESTs//2.2e-82:424:96//Hs.21542:N49574
         R-NT2RP3000080//ESTs//2.1e-29:186:89//Hs.153372:AA424029
         R-NT2RP3000085//ESTs//4.5e-101:482:98//Hs.47649:AA838715
         R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:Al342241
         R-NT2RP3000134//EST//4.7e-106:497:99//Hs.125531:AA884000
15
         R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.2e-116:578:96//Hs.13273:
         AB011164
         R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N93418
         R-NT2RP3000186
         R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R51882
20
         R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA933091
         R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R61306
         R-NT2RP3000233//EST//7.8e-77:368:99//Hs.49075:N64817
         R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:AI032819
         R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA969239
25
         R-NT2RP3000251
         R-NT2RP3000252//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//2.0e-108:532:97//Hs.111086:Al379177
         R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA743073
         R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA534446
         R-NT2RP3000299//ESTs, Weakly similar to enhancer of filmentation 1 [H.sapiens]//3.6e-103:516:96//Hs.4894:
30
         R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:AI094117
         R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA192438
         R-NT2RP3000324
35
         R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:AA476267
         R-NT2RP3000341//ESTS//0.51:251:61//Hs.94090:AA777689
         R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:AI276225
         R-NT2RP3000350//ESTs, Weakly similar to Lpg15p [S.cerevisiae]//3.1e-110:556:96//Hs.111086:Al379177
         R-NT2RP3000359//EST//4.9e-61:340:92//Hs.126495:AA913741
         R-NT2RP3000361//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR PRP6 [S.cerevisiae]//4.8e-91:439:
40
         97//Hs.31334:AI144423
         R-NT2RP3000366//EST//0.20:392:57//Hs.149652:Al283303
         R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA855106
         R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//4.2e-111:529:98//Hs.28307:
45
         AF071185
         R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA682947
         R-NT2RP3000433
         R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26340
         R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA421254
         R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:Al379102
50
         R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA748492
         R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4pl6.3 DNA fragment//1.8e-23:347:70//Hs.
         114963:L34408
         R-NT2RP3000484//Heparin cofactor II//0.98:166:62//Hs.1478:M58600
         R-NT2RP3000487//ESTs//0.012:384:60//Hs.88684:AA885141
55
         R-NT2RP3000512//Homeo box B3//2.0e-69:377:93//Hs.49931:X16667
         R-NT2RP3000526//ESTS//1.6e-91:432:99//Hs.38042:AA187151
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R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:Al078161

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R-NT2RP3000531//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.95:85:71//Hs.5184:AA709151
        R-NT2RP3000542//ESTs//2.6e-53:375:84//Hs.44158:N30180
        R-NT2RP3000561//EST//1.1e-13:170:75//Hs.148421:Al198036
         R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds//0.97:141:68//Hs.79077:D87071
         R-NT2RP3000578//ESTs//2.6e-68:324:100//Hs.5445:AA779447
5
         R-NT2RP3000582//ESTS//2.1 e-25:131:80//Hs.152465:AA563785
         R-NT2RP3000584//ESTs//1.8e-97:460:99//Hs.120698:Al241511
         R-NT2RP3000590//ESTs//2.0e-97:453:100//Hs.105355:AA953817
         R-NT2RP3000592//ESTs//2.8e-91:432:99//Hs.144304:Al190916
         R-nnnnnnnnnnn//Human mRNA for KIAA0314 gene, partial cds//1.5e-09:447:58//Hs.155045:AB002312
10
         R-NT2RP3000599//ESTs//3.8e-93:437:99//Hs.23971:AA829880
         R-NT2RP3000605//ESTs//4.2e-111:554:96//Hs.40780:AA422049
         R-NT2RP3000622//ESTs//2.0e-100:473:99//Hs.11387:AI127394
         R-NT2RP3000624//ESTs, Weakly similar to KIAA0256 [H.sapiens]//5.4e-115:545:98//Hs.4857:AI090739
         R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete cds//4.3e-49:397:80//Hs.15519:
15
         AB018315
         R-NT2RP3000632//ESTs, Moderately similar to cyclin-selective ubiquitin carrier protein [H.sapiens]//6.3e-92:434:
         99//Hs.152517:AA719022
         R-NT2RP3000644//ESTs//1.0e-44:306:84//Hs.155498:W27084
         R-NT2RP3000661//ESTs//3.1e-95:470:97//Hs.126069:W76185
20
         R-NT2RP3000665//ESTs//3.3e-95:503:94//Hs.34313:W81185
         R-NT2RP3000685//ESTs//2.7e-99:515:94//Hs.9711:R60873
         R-NT2RP3000690//ESTs//3.3e-88:414:99//Hs.1465 89:AI085578
         R-NT2RP3000736
         R-NT2RP3000742//ESTs, Highly similar to 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODI-
25
         ESTERASE DELTA 1 [Rattus norvegicus]//1.8e-07:114:75//Hs.136065:W21960
         R-NT2RP3000753//ESTs//3.1e-99:461:100//Hs.150901:Al310447
         R-NT2RP3000759//ESTs//2.0e-74:384:95//Hs.104222:AA207243
         R-NT2RP3000815//ESTs//8.5e-97:455:99//Hs.158897:Al378583
         R-NT2RP3000825//EST//0.0089:343:59//Hs.42897:N20810
30
         R-NT2RP3000826//EST//3.4e-33:342:74//Hs.162236:AA551582
         R-NT2RP3000836//ESTs//6.8e-24:181:84//Hs.134464:AI151081
         R-NT2RP3000841//ESTs//4.5e-93:491:93//Hs.23618:H98082
         R-NT2RP3000845//ESTs//2.4e-88:473:93//Hs.8312:AA813022
         R-NT2RP3000847//ESTs//9.3e-89:460:95//Hs.154106:Al051657
35
         R-NT2RP3000850
         R-NT2RP3000852//Fibrillin 2//0.55:237:63//Hs.79432:U03272
         R-NT2RP3000859//ESTs//1.4e-96:509:94//Hs.7187:AA576895
         R-NT2RP3000865//EST//4.8e-23:461:66//Hs.162088:AA505741
         R-NT2RP3000868//ESTs//5.4e-78:430:93//Hs.102796:N70837
40
         R-NT2RP3000869//ESTs//8.5e-77:397:94//Hs.84484:Al014673
         R-NT2RP3000875//Mevalonate kinase//3.8e-78:531:84//Hs.75138:M88468
         R-NT2RP3000901//ESTs//2.1e-95:466:97//Hs.10647:AA428217
         R-NT2RP3000904//ESTs//1.6e-79:380:99//Hs.100850:AA479385
         R-NT2RP3000917//ESTs, Highly similar to mouse Dhml protein [M.musculus]//9.5e-113:566:96//Hs.5900:
45
         AA035728
         R-NT2RP3000919
         R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A/1.5e-25:375:71//Hs.2953:X84407
         R-NT2RP3000980//ESTs//3.3e-72:364:96//Hs.9536:AA114178
         R-NT2RP3000994//ESTs//3.5e 111:537:97//Hs.21146:AA683542
50
         R-NT2RP3001004//ESTs//9.6e-91:456:96//Hs.58974:W87405
         R-NT2RP3001007//ESTs//6.7e-99:482:97//Hs.117737:AI088029
         R-NT2RP3001055//ESTs//0.0012:294:60//Hs.66479:AA863044
          R-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]//5.6e-102:486:99//Hs.
55
          145956:AA007349
          R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD)//0.0012:447:58//Hs.2133:U18991
          R-NT2RP3001084//ESTs//4.3e-102:528:96//Hs.25277:W87874
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R-NT2RP3001096//ESTS//1.1e-110:540:96//Hs.42824:AA873182

R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832

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R-nnnnnnnnnn//DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325
         R-NT2RP3001111//ESTs, Weakly similar to Trf-proximal protein [D.melanogaster]//3.2e-104:543:95//Hs.93796:
         C06063
5
         R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575
         R-NT2RP3001115//0xytocin receptor//7.9e-30:505:67//Hs.2820:X64878
         R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779
         R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180
         R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166
         R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188
10
         R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761
         R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305
         R-NT2RP3001147//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]
         //9.6e-113:552:97//Hs.23900:U82984
15
         R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717
         R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266
         R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460
         R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139
         R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963
         R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196
20
         R-NT2RP3001232//ESTs//1.5e-101:5l8:94//Hs.21630:AA778399
         R-NT2RP3001236//ESTs, Highly similar to KIAA0377 [H.sapiens]//2.8e-89:462:95//Hs.116793:AA779588
         R-NT2RP3001239//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//5.2e-82:466:91//Hs.66048:
         AA524416
         R-NT2RP3001245//EST//0.53:237:62//Hs.161131:Al417631
25
         R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:Al222997
         R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135
         R-NT2RP3001268//Human Aac11(aac11) mRNA, complete cds//0.12:494:59//Hs.151031:U83857
         R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:Al383965
         R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.1113184:N25651
30
         R-NT2RP3001281//EST//3.1e-60;298;98//Hs.149230;Al247332
         R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691
         R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571
         R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98989
         R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete cds//0.22:199:63//Hs.159534:
35
         U35234
         R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.9e-114:566:96//Hs.18586:
         AB007920
         R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653
40
         R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798
         R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA993090
         R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA169778
         R-NT2RP3001384//ESTs, Weakly similar to A-kinase anchor protein 95, AKAP95 [R.norvegicus]//5.7e-92:522:90//
         Hs.96200:AA218942
         R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375
45
         R-NT2RP3001396//ESTS//3.7e-111:528:98//Hs.22612:AA152232
         R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:Al276628
         R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186
         R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898
50
         R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817
         R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:550:94//Hs.6957:AF052158
         R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692
         R-nnnnnnnnn//Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:533:91//Hs.85844:X66397
         R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374
         R-NT2RP3001447//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.1e-
55
         101:482:98//Hs.124135:AA910560
         R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994
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R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs.155464:AF088219

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R-NT2RP3001457//ESTS//1.5e-52:256:99//Hs.117982:AA644658
        R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA167280
        R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009
         R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783
         R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds//1.4e-61:338:93//Hs.519:U13395
5
         R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds//
         6.8e-112:549:9711Hs.28285:AF064801
         R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047
         R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA, complete cds//7.9e-59:427:83//Hs.5247:AF029750
         R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463
10
         R-NT2RP3001554//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//2.8e-76:392:95//Hs.66048:
         AA524416
         R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49477
         R-NT2RP3001587//Homa sapiens mRNA for HRIHFB2115, partial cds//1.8e-09:86:88//Hs.4311:AB015337
         R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194
15
         R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328
         R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:Al279798
         R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:Al193598
         R-NT2RP3001629
         R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:541:96//Hs.9899:AF099149
20
         R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915989
         R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709
         R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030
         R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:Al382189
         R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648
25
         R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:Al268225
         R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:Al222558
         R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:87//Hs.40100:AB002390
         R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:Al341312
         R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618
30
         R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669
         R-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]
         //4.1e-80:444:91//Hs.6823:W18181
         R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:Al422099
         R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923
35
         R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810
         R-NT2RP3001752//ESTS//6.1e-93:490:94//Hs.4210:AA740440
         R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968
         R-NT2RP3001764//ESTs, Weakly similar to protein-tyrosine phosphatase [H.sapiens]//1.2e-87:450:96//Hs.20281:
40
         R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725
         R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2e-113:549:97//Hs.28169:
         AB007928
         R-NT2RP3001792//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.1e-21:119:99//Hs.44268:AA455900
         R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.129780:X75962
45
         R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:Al291292
         R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117
         R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52900
         R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81792
         R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642
50
         R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180
         R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666
         R-NT2RP3001926//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.24709:
         AI123300
         R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA682781
55
         R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA534737
         R-NT2RP3001938//ESTs, Highly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]
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//1.3e-95:483:96//Hs.5771:W74591

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R-NT2RP3001943//ESTs//1.2e-23:169:88//Hs.103930:AA160990
        R-NT2RP3001944//ESTs//2.0e-90:439:97//Hs.103380:Al291325
        R-NT2RP3001969//ESTs//0.95:133:65//Hs.131669:AI025889
         R-NT2RP3001989//ESTS, Weakly similar to C01A2.4 [C.elegans]//8.9e-64:310:99//Hs.11449:Al201540
         R-NT2RP3002002//ESTs//2.1e-95:562:89//Hs.5997:AA897088
5
         R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.6e-42:335:82//Hs.75087:X86779
         R-NT2RP3002007//ESTs//0.12:184:66//Hs.94030:AA846729
         R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291:89//Hs.155464:AF088219
         R-NT2RP3002033
         R-NT2RP3002045//ESTs//1.0e-92:555:88//Hs.106411:W29081
10
         R-NT2RP3002054//EST//0.45:155:63//Hs.5656:D20426
         R-NT2RP3002056//ESTs//1.4e.95:504:93//Hs.17428:Al365221
         R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127:66//Hs.90438:D63486
         R-NT2RP3002062
         R-nnnnnnnnn//ESTs//2.1e-113:552:97//Hs.9591:AA069657
15
         R-NT2RP3002081//ESTs//5.5e-43:212:100//Hs.124852:AA969139
         R-NT2RP3002097//EST//2.3e-10:80:91//Hs.102717:N59148
         R-NT2RP3002102
         R-NT2RP3002108
         R-NT2RP3002146//ESTs//5.5e-58:296:97//Hs.65328:AA625385
20
         R-NT2RP3002147//EST//2.5e-53:387:81//Hs.147928:M249703
         R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [Homo sapi-
         ens]//6.2e-107:534:96//Hs.59523:AA602837
         R-NT2RP3002163//ESTs//2.7e-106:520:97//Hs.21258:AA412293
         R-NT2RP3002165//ESTs//7.4e-93:479:95//Hs.27299:AI074024
25
         R-NT2RP3002166//ESTs//1.0:261:59//Hs.132817:AA593713
         R-NT2RP3002173//ESTs//2.7e-93:512:92//Hs.23648:H07120
         R-NT2RP3002181//ESTs//1.0e-84:435:96//Hs.47378:Al193598
         R-NT2RP3002244//ESTs//2.7e-11:97:89//Hs.9412:W72446
         R-NT2RP3002248//ESTs//4.3e-90:459:95//Hs.9848:AA130588
30
         R-NT2RP3002255//ESTs//1.3e-45:289:88//Hs.9100:AA431672
         R-NT2RP3002273//ESTs//2.3e-100:489:97//Hs.8258:AA744743
         R-NT2RP3002276//ESTs//1.2e-50:306:91//Hs.16160:AA778171
         R-NT2RP3002303//ESTs//1.1e-67:323:99//Hs.129761:AA836898
         R-NT2RP3002304//ESTs//2.8e-86:405:99//Hs.29643:AA418500
35
         R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]
         //1.8e-19:136:87//Hs.106928:AI041737
         R-NT2RP3002343//ESTs//1.0e-42:260:93//Hs.7797:W25667
         R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0048:221:64//Hs.556:L41887
         R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//5.8e-105:516:94//Hs.6483:
40
         R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5e-103:524:95//Hs.12707:
         R-NT2RP3002484//Human APRT gene for adenine phosphoribosyltransferase//0.54:108:71//Hs.28914:Y00486
         R-NT2RP3002501//ESTs//2.7e-96:489:95//Hs.27335:N74185
45
         R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III
         [C.elegans]//3.2e-90:526:90//Hs.8083:AA521436
         R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN
         C2G11.03C [Schizosaccharomyces pombe]//3.8e-101:497:96//Hs.6650:AA843246
         R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.1e-83:438:94//Hs.19542:AB018272
50
         R-NT2RP3002549//ESTs//3.8e-98:493:96//Hs.7358:AA191673
         R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.14:
         184:63//Hs.89230:AF031815
         R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138:78//Hs.129883:AB007880
         R-NT2RP3002590//ESTs//2.9e-51:290:93//Hs.162942:AI243850
55
         R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58:100//Hs.76691:AF070673
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R-NT2RP3002603

R-NT2RP3002631//ESTs//4.8e-54:367:85//Hs.13109:AA192514

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R-NT2RP3002659//ESTs//5.3e-30:229:85//Hs.152114:AA401365
        R-NT2RP3002660//ESTs//1.9e-88:452:95//Hs.120146:AA708573
        R-NT2RP3002663//EST//3.2e-89:469:95//Hs.105767:AA525172
         R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [Drosophila melanogaster]//5.9e-109:537:
         97//Hs.19348:AA151678
5
        R-NT2RP3002682//ESTs//2.3e-98:541:91//Hs.75844:AA115502
        R-NT2RP3002687//ESTs//5.5e-103:498:97//Hs.72782:AA910871
         R-NT2RP3002688//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-101:
         524:95//Hs.32580:AI123601
         R-NT2RP3002701//EST//0.87:131:63//Hs.161916:AA483169
10
         R-NT2RP3002713//ESTs//4.7e-106:542:95//Hs.14479:AA160945
         R-NT2RP3002763//ESTs//1.3e-54:290:94//Hs.142031:AA809159
         R-NT2RP3002770//ESTs//0.047:275:61//Hs.122984:AA526973
         R-NT2RP3002785//ESTs//2.4e-52:255:99//Hs.132959:AI376958
         R-NT2RP3002799//EST//8.2e-61:321:94//Hs.140992:R71377
15
         R-NT2RP3002810//EST//0.19:116:68//Hs.121810:AA775240
         R-NT2RP3002818//ESTs//1.3e-109:531:98//Hs.58924:Al348080
         R-NT2RP3002861//ESTs//2.5e-84:429:95//Hs.23920:AA909678
         R-NT2RP3002869//EST//0.00011:116:71//Hs.161606:AA019641
         R-NT2RP3002876//ESTs//0.0024:182:63//Hs.117306:AA687262
20
         R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//
         8.1e-14:146:72//Hs.129727:AF035587
         R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5e-110:570:95//Hs.6162:AB018314
         R-NT2RP3002911//ESTs//3.6e-92:436:99//Hs.143917:Al206286
         R-NT2RP3002948//EST//1.0:102:65//Hs.144730:Al191975
25
         R-NT2RP3002953//ESTs//1.8e-107:513:98//Hs.119693:AI201698
         R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.23:563:56//Hs.127338:
         AB007961
         R-NT2RP3002969//ESTS, Weakly similar to LONG-CHAIN-FATTY-ACID--COA LIGASE 1 [Saccharomyces cere-
30
         visiael112.0e-56:387:86//Hs.144597:W20143
         R-NT2RP3002972//ESTs//1.7e-97:502:96//Hs.7274:AA476850
         R-NT2RP3002978//ESTs//8.6e-104:498:98//Hs.118923:AA252116
         R-NT2RP3002988//EST//1.2e-59:315:94//Hs.157743:Al360553
         R-NT2RP3003008//ESTs//1.4e-97:515:94//Hs.6544:AA524423
         R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Mus musculus]//
35
         3.0e-100:528:94//Hs.90353:N98551
         R-NT2RP3003059//ESTs//1.7e-76:398:95//Hs.102971:W05355
         R-NT2RP3003061//ESTs//4.9e-82:414:96//Hs.99603:AI141912
         R-NT2RP3003068//ESTs, Weakly similar to M18.3 [C.elegans]//5.9e-83:392:99//Hs.101364:AA534439
         R-NT2RP3003071//ESTs//6.3e-85:399:99//Hs.109755:AA180809
40
         R-NT2RP3003078//ESTs//1.0e-98:471:99//Hs.7995:AI359466
         R-NT2RP3003101//EST//0.032:235:60//Hs.147920:Al202441
         R-NT2RP3003121//ESTs//3.0e-47:238:97//Hs.43559:Al003520
         R-NT2RP3003133//EST//1.5e-77:395:96//Hs.142150:AA223982
         R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]//3.3e-107:535:96//Hs.
45
         27437:AA004208
         R-NT2RP3003139//ESTs//2.5e-106:504:98//Hs.106795:Al271632
         R-NT2RP3003150//ESTs//1.6e.99:539:91//Hs.46500:AA129774
         R-NT2RP3003157//ESTs//1.5e-114:563:97//Hs.58608:AA081007
         R-NT2RP3003185//ESTs//3.9e-93:443:98//Hs.9741:Al131226
50
         R-NT2RP3003193//ESTs//2.0e-37:428:71//Hs.33354:AA179944
         R-NT2RP3003197//ESTs//5.8e-56:312:94//Hs.7016:AA215796
         R-NT2RP3003203//EST//0.0073:212:63//Hs.161355:Al422634
         R-NT2RP3003204//ESTs//7.4e-52:253:99//Hs.120146:AA708573
         R-NT2RP3003212//ESTs//1.8e-76:401:95//Hs.29067:N26107
55
         R-NT2RP3003230//ESTs, Highly similar to CORONIN [Dictyostelium discoideum]//2.0e-40:229:93//Hs.17377:
         AI078151
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R-NT2RP3003242//ESTs//8.3e-97:458:99//Hs.23057:AI290343

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R-NT2RP3003251//ESTs//1.5e-60:320:95//Hs.36495:AA151628
        R-NT2RP3003264//ESTs//2.1e-103:521:95//Hs.4094:AA173960
        R-NT2RP3003278//ESTs//8.2e-109:536:96//Hs.23788:AA524061
        R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:550:93//Hs.11702:L36983
        R-NT2RP3003290//EST//4.3e-27:372:70//Hs.159131:AI384035
5
        R-NT2RP3003301//ESTs//4.4e-56:285:97//Hs.95370:AA601055
        R-NT2RP3003302//EST//7.2e-10:395:63//Hs.162554:AA584818
        R-NT2RP3003311//ESTs//4.2e-110:538:97//Hs.62180:Al341261
        R-NT2RP3003313//ESTs//2.1e-106:531:96//Hs.22630:C05931
        R-NT2RP3003327//ESTs//4.3e-102:518:95//Hs.120355:AA625445
10
        R-NT2RP3003330//ESTs//8.6e-104:497:97//Hs.72071:Al125289
        R-NT2RP3003344//ESTs//2.5e-105:494:99//Hs112188:AA872993
         R-NT2RP3003346//ESTs//1.0:123:69//Hs.116029:AA813102
         R-NT2RP3003353//EST//0.0014:162:68//Hs.149191:Al246155
15
         R-NT2RP3003377//EST//4.5e-15:119:85//Hs.148129:AA885567
         R-NT2RP3003384//EST//0.0057:86:74//Hs.127735:AA962272
         R-NT2RP3003385//ESTs//0.64:347:59//Hs.5646:W72721
         R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.2e-
         24:418:67//Hs.139488:AI124095
         R-NT2RP3003409//ESTs//5.3e-98:479:97//Hs.155198:AA767372
20
         R-NT2RP3003411//ESTs//4.8e-86:416:97//Hs.129059:AA126041
         R-NT2RP3003427//ESTs//7.4e-103:510:96//Hs.25303:AA641023
         R-NT2RP3003433//ESTs//3.5e-85:405:99//Hs.63131:AA664156
         R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//3.6e-97:479:96//Hs.14934:
25
         AF004828
         R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1e-102:527:93//Hs.26450:
         AB018268
         R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-106:549:94//Hs.7886:
         R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401:60//Hs.75307:U02556
30
         R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRNA//4.1e-33:217:88//Hs.
         8068:U00952
         R-NT2RP3003552//ESTs//3.1e-106:546:94//Hs.101754:Al123430
         R-NT2RP3003555//ESTs//3.4e-106:537:95//Hs.85550:AA187681
35
         R-NT2RP3003564
         R-NT2RP3003572//ESTs//1.2e-20:122:88//Hs.8253:N48721
         R-NT2RP3003576//ESTs//2.7e-71:394:94//Hs.151136:R99944
         R-NT2RP3003589//EST//0.58:242:59//Hs.130804:AA894759
         R-NT2RP3003625//ESTs//7.6e-41:349:80//Hs.140608:N53448
         R-NT2RP3003656//Human LIM protein (LPP) mRNA, partial cds//0.26:222:60//Hs.17217:U49957
40
         R-NT2RP3003659//ESTs//2.0e-113:547:97//Hs.23389:AA769310
         R-NT2RP3003665//ESTs//1.6e-80:415:95//Hs.141084:H11714
         R-NT2RP3003672
         R-NT2RP3003686//ESTs//6.8e-114:552:97//Hs.43299:N23036
         R-NT2RP3003701//ESTs//2.1e-16:282:66//Hs.115512:Al208768
45
         R-NT2RP3003716//ESTs//2.1e-45:195:91//Hs.41296:N71923
         R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//5.6e-103:492:97//Hs.48513:
         AB018300
         R-NT2RP3003746//ESTs//1.9e-85:411:98//Hs.54835:AI050863
         R-NT2RP3003795//EST//6.2e-97:459:99//Hs.134769:AI089747
50
         R-NT2RP3003799//ESTs//2.8e-62:337:94//Hs.124023:H18913
         R-NT2RP3003800//PROTO-ONCOGENE TYRO SINE-PROTEIN KINASE SRC//8.9e-108:551:95//Hs.115742:
         AF077754
         R-NT2RP3003805//ESTs//2.2e-103:490:99//Hs.9412:W72446
55
         R-NT2RP3003809//ESTs, Highly similar to SAV PROTEIN [Sulfolobus acidocaldarius]//3.4e-89:456:95//Hs.5555:
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R-NT2RP3003819//Interieukin 10//3.3e-43:173:89//Hs.2180:M57627 R-NT2RP3003825//ESTs//1.6e-66:485:80//Hs.7405:W27761

R-NT2RP3003828//ESTs, Weakly similar to unknown.[H.sapiens]//9.6e-98:511:95//Hs.26955:Al333224 R-NT2RP3003831//ESTs//2.2e-38:317:79//Hs.142173:AA757743 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300: AF070611 R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888 5 R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:Al332962 R-NT2RP3003870//ESTs//3.4e-82:449:92//Hs.122691:AA152298 R-NT2RP3003876//ESTs//1.9e-89:449:96//Hs.45046:N40170 R-NT2RP3003914//ESTs//1.3e-99:470:98//Hs.118966:AA926726 R-NT2RP3003918//ESTs//1.3e-79:417:94//Hs.5005:W25933 10 R-NT2RP3003932//ESTs//6.0e-83:427:94//Hs.93581:H50221 R-NT2RP3003989//ESTs//4.8e-76:403:93//Hs.127243:W80409 R-NT2RP3003992//ESTs//2.4e-88:508:90//Hs.134200:D19593 R-NT2RP3 004013//ESTs//3.7e-111:551:97//Hs.105108:AA781142 R-NT2RP3004016//ESTs//1.7e-81:394:98//Hs.63368:AA613714 15 R-NT2RP3004041 R-NT2RP3004051//ESTs//3.5e-69:386:93//Hs.51347:T72820 R-NT2RP3004070//ESTs//5.5e-108:552:9511Hs.23392:Al310139 R-NT2RP3004078//ESTs//3.3e-82:443:93//Hs.26407:W4537 R-NT2RP3004093//ESTs//4.4e-83:426:94//Hs,140932:Al262104 20 R-NT2RP3004095//ESTs//0.00013:93:78//Hs.36567:AA262045 R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]//3.5e-76:402:95//Hs.55847:W31092 R-NT2RP3004125//ESTs//9.3e-74:363:97//Hs.32988:C01696 R-NT2RP3004145//ESTs//2.6e-96:451:99//Hs.59584:AA587334 25 R-NT2RP3004148//ESTs//1.3e-10:77:92//Hs.135890:Al183425 R-NT2RP3004155//ESTS//1.7e-110:558:96//Hs.27003:AI279093 R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//1.8e-40: 200:100//Hs.26089:AA195126 R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M.musculus]//1.1e-41:266:89//Hs.6314:AA522619 30 R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]//3.7e-112:547:97//Hs.99819:Al346680 R-NT2RP3004215//ESTs//1.1e-103:541:95//Hs.124918:N64794 R-NT2RP3004242//ESTs//4.5e-105:524:96//Hs.29724:N46252 R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA884827 35 R-NT2RP3004253//EST//2.9e-88:454:94//Hs.127713:AA961628 R-NT2RP3004258//ESTs, Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]//1.6e-89: 468:95//Hs.5117:AA831530 R-NT2RP3004262//ESTs//4.1e-86:443:96//Hs.101393:T87623 R-NT2RP3004334//EST//0.00057:206:63//Hs.149388:AI273630 40 R-NT2RP3004341//EST//0.00042:151:68//Hs.148498:AI200264 R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds//5.9e-61:299:85//Hs.154103:AF061258 R-NT2RP3004349//EST//3.6e-42:175:88//Hs.161917:AA483223 R-NT2RP3004378//ESTs//0.27:294:60//Hs.66479:AA863044 R-NT2RP3004399//ESTs//5.8e-99:479:98//Hs.120234:AA732224 45 R-NT2RP3004424//EST, Highly similar to F21G4.6 [C.elegans]//0.30:253:58//Hs.97184:AA385934 R-NT2RP3004428//ESTs//2.8e-48:279:91//Hs.106826:W25985 R-NT2RP3004451//ESTs//4.8e-101:509:96//Hs.29725:W74621 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//9.3e-108:526:98//Hs.27349: 50 AB007917 R-NT2RP3004466//ESTs//0.25:51:90//Hs.7778:AA195616 R-NT2RP3004470//EST//0.032:70:71//Hs.147925:Al249332 R-NT2RP3004472//ESTs//0.0069:430:59//Hs.116651:AA993406 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//5.0e-107:521:97//Hs.5003:AB007925 55 R-NT2RP3004480 R-NT2RP3004490//ESTs//4.7e-68:354:95//Hs.163721:H42504 R-NT2RP3004498//ESTs, Moderately similar to ORF2: function unknown [H.sapiens]//3.4e-100:508:95//Hs.

47393:AA218858

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R-NT2RP3004503//ESTs//4.6e-90:478:93//Hs.133998:AA994735
        R-NT2RP3004504//ESTs, Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus]//
        1.8e-83:465:92//Hs.137064:AA318257
        R-NT2RP3004507//ESTs//1.5e-98:495:96//Hs.128905:AI051971
        R-NT2RP3004527//EST//1.6e-109:535:97//Hs.149481:Al279865
        R-nnnnnnnnnnnn
        R-NT2RP3004544//EST//0.035;226;60//Hs.99195;AA449232
        R-NT2RP3004566//ESTs//4.1e-86:455:95//Hs.13110:T67461
        R-NT2RP3004569//ESTs//2.9e-94:493:94//Hs.24948:AA977674
        R-NT2RP3004572//ESTs//1.1e-92:437:99//Hs.24846:Al420493
10
        R-NT2RP3004578//ESTs//0.98:166:64//Hs.124593:AA854456
        R-NT2RP3004594//EST//5.8e-89:426:98//Hs.134213:Al080213
        R-NT2RP3004617//ESTs//1.4e-40:226:85//Hs.15921:R71157
         R-NT2RP3004618//ESTs//1.8e-38:229:90//Hs.125153:AA453723
         R-NT2RP3004670//Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase
15
         (GicNAc6ST), complete cds//7.2e-57:291:95//Hs.8786:AB014680
         R-NT2RP4000008//ESTs//8.9e-119:561:98//Hs.25035:AI123335
         R-NT2RP4000023//EST//1.2e-34:271:80//Hs.98300:AA418560
         R-NT2RP4000035//Small inducible cytokine A5 (RANTES)//2.1e-68:320:82//Hs.155464:AF088219
         R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds//6.7e-60:289:82//Hs.51233:AF016266
20
         R-NT2RP4000051//ESTs, Weakly similar to protein B [H.sapiens]//8.3e-98:462:99//Hs.10114:Al345945
         R-NT2RP4000078//ESTs//0.00068:367:60//Hs.106090:AA457030
         R-NT2RP4000102//ESTs//9.7e-50:256:97//Hs.24266:R28287
         R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536:96//Hs.57929:AB011538
         R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//3.5e-112:554:97//Hs.64691:
25
         AB007952
         R-NT2RP4000147//ESTs//3.9e-11:122:80//Hs.25584:AA632014
         R-NT2RP4000150//EST//4.4e-84:510:88//Hs.144238:W52294
         R-NT2RP4000151//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III
         [C.elegans]//5.7e-93:515:92//Hs.8083:AA521436
30
         R-NT2RP4000159//ESTs//0.0019:209:65//Hs.161816:AA400295
         R-NT2RP4000167//ESTs//2.1e-113:549:97//Hs.109441:N66569
         R-NT2RP4000185//ESTs//0.65:232:59//Hs.144445:AA807257
         R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.5e-100:505:96//Hs.13999:
35
         AB014600
         R-NT2RP4000212//ESTs//8.5e-14:169:75//Hs.8520:AA081788
         R-NT2RP4000214//Human mRNA for KIAA0392 gene, partial cds//6.2e-43:272:90//Hs.40100:AB002390
         R-NT2RP4000218//ESTs//6.1e-10:335:64//Hs.105658:AA978185
         R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.9e-70:354:96//Hs.155481:
40
         AJ006470
         R-NT2RP4000246//ESTs//7.1e-26:154:94//Hs.14838:AA502757
         R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.3e-79:379:99//Hs.43728:
         AF091092
         R-NT2RP4000263
         R-nnnnnnnnnnn/ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]
45
         //4.7e-104:525:96//Hs.152069:AA548972
         R-NT2RP4000312//ESTs//8.2e-66:319:99//Hs.35091:Al271631
         R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513:99//Hs.13410:AF070524
         R-NT2RP4000323//ESTs//7.7e-109:534:97//Hs.34790:AA192760
         R-NT2RP4000355//ESTs//3.1e-44:320:83//Hs.141323:N80390
50
         R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//7.6e-111:520:99//Hs.107479:
         R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.8e-
         110:527:98//Hs.31323:AF044195
         R-NT2RP4000370//ESTs//8.9e-32:166:98//Hs.70488:Al301130
55
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R-NT2RP4000415//ESTs, Weakly similar to coded for by C. elegans cDNA yk30b3.5 [C.elegans]//3.9e-87:499:

R-NT2RP4000376//ESTs//6.8e-99:465:99//Hs.27182:AA604498 R-NT2RP4000381//ESTs//3.0e-50:280:93//Hs.8395:W27376

91//Hs.26156:AA630975 R-NT2RP4000417//ESTs, Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTER-GENIC REGION [Saccharomyces cerevisiae]//8.9e-95:468:96//Hs.93871:Al191318 R-NT2RP4000424//ESTs//3.7e-98:473:98//Hs.24945:Al189011 R-NT2RP4000448//ESTs//2.6e-79:446:91//Hs.25159:R60955 5 R-NT2RP4000449//ESTs//3.6e-98:468:98//Hs.31176:Al037953 R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.35:153:63//Hs.113286:U77783 R-nnnnnnnnnnn//ESTs//4.5e-89:455:96//Hs.62638:AA127740 R-NT2RP4000480//ESTs//4.9e-92:431:99//Hs.121072:Al204167 10 R-nnnnnnnnnnn R-NT2RP4000500//ESTs, Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [C.elegans]//1.2e-40:125:97//Hs.56124:Al424792 R-NT2RP4000515//EST//6.7e-30:183:90//Hs.150710:Al122713 R-NT2RP4000517//Aldehyde dehydrogenase 7//7.5e-28:183:76//Hs.83155:U10868 15 R-NT2RP4000518//EST//0.091:178:58//Hs.133031:Al049874 R-NT2RP4000519 R-NT2RP4000524//ESTS, Highly similar to rsec8 [R.norvegicus]//3.4e-93:496:93//Hs.107394:H07126 R-NT2RP4000528//EST//0.84:130:66//Hs.140208:AA702213 R-NT2RP4000541//EST//5.2e-63:337:94//Hs.156337:AI337328 20 R-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//8.2e-92:448:98//Hs. 25597:H93026 R-NT2RP4000588//ESTs//3.8e-94:445:98//Hs.44077:N28840 R-NT2RP4000614//ESTs//6.5e-18:159:83//Hs.24549:N57263 R-NT2RP4000638//ESTs//2.5e-46:296:87//Hs.132722:AA618531 25 R-NT2RP4000648//ESTs//2.6e-103:559:93//Hs.23794:W80393 R-NT2RP4000657//ESTs//1.0:189:60//Hs.87073:AA972704 R-NT2RP4000704//ESTs//2.8e-101:509:96//Hs.84824:AA935651 R-NT2RP4000724//ESTS//1.5e-83:442:94//Hs.142114:AA205615 R-NT2RP4000728//ESTs//0.84:61:75//Hs.145334:Al251399 30 R-NT2RP4000739//ESTs//8.8e-80:418:94//Hs.42959:N21211 R-NT2RP4000781//ESTs//1.4e-79:376:99//Hs.135458:AI081312 R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//3.1e-106:550:94//Hs.25132: AB007939 R-NT2RP4000833//ESTs//5.8e-46:309:85//Hs.163979:AA828834 35 R-NT2RP4000837//ESTs//1.7e-112:539:97//Hs.97718:AI334028 R-NT2RP4000855//ESTs//1.1e-95:486:95//Hs.5345:AA988104 R-NT2RP4000865//EST//6.2e-68:412:89//Hs.142196:AA258356 R-NT2RP4000878//ESTs//1.9e-80:417:95//Hs.104716:AI023185 R-NT2RP4000879//ESTs//1.8e-42:211:99//Hs.89991:AI374617 40 R-nnnnnnnnn//ESTs//1.2e-89:453:97//Hs.100182:N92594 R-nnnnnnnnnn//EST//9.4e-06:197:63//Hs.145970:Al277106 R-NT2RP4000925//ESTs, Weakly similar to KIAA0405 [H.sapiens]//5.9e-17:134:85//Hs.14146:W92235 R-nnnnnnnnnn//ESTs//4.3e-14:84:100//Hs.155360:AA984683 R-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//8.2e-108:548:95// 45 Hs.24812:AF069532 R-NT2RP4000929//ESTs//1.3e-119:567:98//Hs.62717:AA044905 R-NT2RP4000955//ESTs//3.5e-10:I 19:78//Hs.42946:N21111 R-NT2RP4000973//ESTs//2.8e-05:93:69//Hs.155126:AA563986 R-NT2RP4000975//ESTs//4.4e-58:324:95//Hs.126070:AA045179 50 R-NT2RP4000979//ESTs//3.5e-42:468:73//Hs.106210:Al193017 R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequence//8.7e-120:570:98//Hs.12457:AF052123 R-NT2RP4000989//ESTs//1.3e-122:581:98//Hs.10499:AA528018 R-NT2RP4000996//ESTs//9.2e-113:579:94//Hs.23762:N26620

R-NT2RP4001004//ESTs//3.6e-78:389:98//Hs.156290:Al016769
R-NT2RP4001006//ESTS, Moderately similar to ORF2: function unknown [H.sapiens]//6.6e-124:574:99//Hs.

R-NT2RP4000997//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-28:439:68//Hs.

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129735:AF010144

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47393:AA218858
        R-NT2RP4001010//EST//2.8e-31:194:90//Hs.161186:Al418635
        R-NT2RP4001029//ESTs//4.4e-111:523:99//Hs.28423:Al336292
        R-NT2RP4001041//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cer-
        evisiae]//3.6e-114:569:96//Hs.6762:AA088424
5
        R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds//2.0e-51:282:94//Hs.100955:AB007859
        R-NT2RP4001064//ESTs, Weakly similar to protein B [H.sapiens]//2.1e-103:485:99//Hs.10114:AD45945
         R-NT2RP4001078
         R-NT2RP4001079//Homo sapiens mRNA for putative Ca2+-transporting ATPase, partial/1.7e-119:569:98//Hs.
10
         106778:AJ010953
         R-NT2RP4001080//ESTs//7.6e-10:65:100//Hs.131694:AA927668
         R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds//5.9e-121:548:95//Hs.13273:AB011164
         R-NT2RP4001095//ESTs//1.5e-113:563:96//Hs.118732:Al344055
         R-NT2RP4001100//ESTs//2.0e-46:413:79//Hs.146314:R99617
         R-NT2RP4001117//EST//7.4e-51:294:92//Hs.7260:T23737
15
         R-NT2RP4001122//ESTs//5.4e-109:509:99//Hs.16390:AI052357
         R-NT2RP4001126//EST//0.97:169:61//Hs.148107:AA693476
         R-NT2RP4001138//ESTs//3.0e-110:543:97//Hs.57655:AI056890
         R-NT2RP4001143//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC
         REGION [Saccharomyces cerevisiae]//5.4e-113:573:96//Hs.5249:U55977
20
         R-NT2RP4001148//ESTs//3.1e-103:490:98//Hs.121282:Al091453
         R-NT2RP4001149//EST//1.7e-50:281:93//Hs.101727:H16171
         R-NT2RP4001150//ESTS//1.9e-90:422:100//Hs.125490:Al138884
         R-NT2RP4001159
         R-NT2RP4001174//ESTs//2.5e-110:526:98//Hs.116555:AA639278
25
         R-nnnnnnnnnn//ESTs//1.1 e-25:140:97//Hs.83756:Al002822
         R-NT2RP4001207//ESTs//4.4e-70:432:89//Hs.13109:AA192514
         R-NT2RP4001210//ESTs//1.4e-108:509:99//Hs.27021:Al359495
         R-NT2RP4001213//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//4.4e-123:624:95//Hs.
30
         22744:AI379892
         R-NT2RP4001219//ESTs//0.0043:142:65//Hs.6733:AI160750
         R-NT2RP4001228//ESTs//4.9e-101:482:98//Hs.62684:AA806103
         R-NT2RP4001235//ESTs//3.7e-105:571:93//Hs.37706:AA005120
         R-NT2RP4001256//ESTs//1.1e-12:189:74//Hs.20621:W28255
35
         R-NT2RP4001260//EST//6.9e-05:313:61//Hs.116438:AA648430
         R-NT2RP4001274//EST//0.0020:246:63//Hs.149955:Al289933
         R-nnnnnnnnn//ESTs//2.9e-34:213:91//Hs.43100:AA186588
         R-NT2RP4001313
         R-NT2RP4001315//EST//6.1e-38:217:93//Hs.97832:AA400892
         R-NT2RP4001339//ESTs//3.8e-91:430:99//Hs.34840:Al279612
40
         R-NT2RP4001345//ESTs//5.3e-89:443:96//Hs.6770:AA972732
         R-NT2RP4001351//ESTs//6.0e-78:394:97//Hs.102796:N70837
         R-NT2RP4001353//ESTs//4.8e-06:90:82//Hs.7778:AA195616
         R-NT2RP4001373//ESTs, Weakly similar to HYPOTHETICAL 48.8 KD PROTEIN IN TRK2-MRS4 INTERGENIC
45
         REGION [Saccharomyces cerevisiae]//1.7e-108:546:96//Hs.32271:AA203680
         R-NT2RP4001375//ESTs//2.4e-19:155:87//Hs.62119:AA043299
         R-NT2RP4001379//EST//4.4e-29:288:72//Hs.157848:Al362501
         R-NT2RP4001389//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN IN PAP1-MRPL13 INTERGENIC
         REGION [Saccharomyces cerevisiae]//3.8e-79:438:93//HS.21938:W81045
50
         R-NT2RP4001407//ESTs//8.3e-112:541:97//Hs.22587:AA743132
         R-NT2RP4001414//ESTs//8.6e-18:117:90//Hs.90789:W27649
         R-NT2RP4001433//ESTs, Moderately similar to PROHIBITIN [H.sapiens]//1.6e-102:498:97//Hs.62386:AA512948
         R-NT2RP4001442//ESTs//8.8e-104:489:99//Hs.101619:Al339433
55
         R-NT2RP4001447
         R-NT2RP4001474
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R-NT2RP4001483//ESTs//2.1e-100:528:92//Hs.17860:AA706655 R-NT2RP4001498//ESTs//1.1e-97:470:98//Hs.95744:Al392846

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R-NT2RP4001502//ESTs//6.7e-73:382:96//Hs.11874:N93511
         R-NT2RP4001507//ESTs//2.6e-57:302:96//Hs.65328:AA625385
        R-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//2.9e-107:546:96//Hs.5570:Al377863
         R-NT2RP4001529//ESTs//3.3e-112:524:99//Hs.28423:Al336292
         R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Paramecium
5
         tetraurelia1//2.8e-120:566:98//Hs.108530:AA523928
         R-nnnnnnnnnnn//ESTs, Weakly similar to CELL DIVISION CONTROL PROTEIN 68 [S.cerevisiae]//1.4e-26:184:
         88//Hs.136189:AA133224
         R-NT2RP4001555//ESTs//1.1e-95:445:100//Hs.134403:AA677552
         R-NT2RP4001567//ESTs//2.8e-106:506:98//Hs.102708:AA292285
10
         R-NT2RP4001568//ESTs//6.4e-55:300:94//Hs.57442:N63437
         R-NT2RP4001571//ESTs//1.3e-114:556:97//Hs.30340:AA521251
         R-NT2RP4001574//ESTs//0.0035:120:67//Hs.96339:AA225906
         R-NT2RP4001575
         R-NT2RP4001592//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL[S.cerevisiae]
15
         //8.7e-112:557:97//Hs.7558:AA526812
         R-NT2RP4001610//ESTs//6.2e-77:382:96//Hs.21543:AA166776
         R-NT2RP4001614//ESTs//2.8e-117:565:98//Hs.9591:AA069657
         R-NT2RP4001634//ESTs//2.0e-39:213:96//Hs.32360:AA534737
         R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds//1.7e-116:559:97//Hs.5332:
20
         AF007151
         R-NT2RP4001644//ESTs, Moderately similar to MNK1 [H.sapiens]//5.3e-36:192:97//Hs.5662:AA868361
         R-NT2RP4001656//ESTs, Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II
         [Caenorhabditis elegans]//1.1e-104:525:96//Hs.20472:W28734
         R-NT2RP4001677//ESTs//1.8e-106:522:97//Hs.106390:AA156805
25
         R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//5.7e-118:583:96//Hs.
         15562:U96629
         R-NT2RP4001725//ESTs//2.0e-11:141:74//Hs.117589:N25941
         R-nnnnnnnnnnn//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRE-
         CURSOR [D.melanogaster]//3.4e-73:362:97//Hs.152332:Al141922
30
         R-NT2RP4001739//ESTs//6.6e-59:340:91//Hs.122293:AA843692
         R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113:552:96//Hs.2481:X78926
         R-NT2RP4001760//ESTs//2.5e-94:453:98//Hs.122579:AA766315
         R-NT2RP4001790//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//2.0e-62:326:94//Hs.110839:
35
         W28098
         R-NT2RP4001803
         R-NT2RP4001822//ESTs//4.4e-98:526:92//Hs.96908:AI161133
         R-NT2RP4001823//ESTs//1.7e-72:357:97//Hs.144900:Al218434
         R-NT2RP4001828//ESTs//3.3e-101:536:92//Hs.18851:AA857826
         R-NT2RP4001838//ESTs//4.2e-58:344:90//Hs.48723:N66663
40
         R-NT2RP4001849//EST//0.24:105:71//Hs.136747:AA749210
         R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34:212:88//Hs.154326:D42087
         R-NT2RP4001893//ESTs//3.0e-58:321:95//Hs.158787:W79602
         R-NT2RP4001896//EST//3.8e-15:108:92//Hs.160835:Al345528
         R-NT2RP4001901//ESTs//1.2e-110:536:97//Hs.31443:Al018606
45
         R-NT2RP4001927//ESTs//2.1e-105:546:93//Hs.73291:Al417099
         R-NT2RP4001938//ESTs//2.8e-40:235:78//Hs.163641:R61848
         R-NT2RP4001946//ESTs//1.3e-29:175:93//Hs.43703:AA088436
         R-NT2RP4001950//ESTs//4.6e-95:458:98//Hs.150890:AI341793
         R-NT2RP4001953//Clathrin, light polypeptide (Lcb)//2.3e-62:310:82//Hs.73919:X81637
50
         R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//8.3e-87:457:94//Hs.41793:
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R-NT2RP4002018
R-NT2RP4002047//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//4.7e-09: 90:86//Hs.41127:AA555184
R-NT2RP4002052//ESTs//0.054:353:60//Hs.117510:AA903738
R-NT2RP4002058//EST//7.8e-26:151:94//Hs.124617:AA855106

R-NT2RP4001975//ESTs//1.9e-52:281:94//Hs.7704:W58252

AA775879

R-NT2RP4002071//ESTs//6.9e-99:475:98//Hs.29216:AA916679

R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:AI284198

R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sapiens]//1.6e-61:464:82//Hs. 144228:N99507

5 R-nnnnnnnnnn/ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II [C.elegans]//2.3e-56:271:100//Hs.6185:AA428565

R-NT2RP4002083//ESTs//2.0e-108:548:96//Hs.6120:W80407

R-NT2RP4002408//ESTs//2.6e-77:391:96//Hs.14014:AA745592

R-NT2RP4002791//ESTs//7.9e-101:527:93//Hs.22394:N32555

10 R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//1.9e-65:373:92// Hs.31532:H18272

R-NT2RP4002905//ESTs//1.5e-107:517:98//Hs.40460:N36090

R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8e-115:605:94//Hs.108258: AB007934

15 R-OVARC1000004

R-OVARC1000006//ESTs//1.5e-19:139:89//Hs.143034:AI126929

R-OVARC1000013//ESTs//5.9e-98:531:93//Hs.16470:AA121635

R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273

R-OVARC1000017

20 R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:AI078286

R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-46:331:83//Hs.96247:X95073

R-OVARC1000060//EST//2.8e-28:348:71//Hs.141728:W73041

R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367

R-OVARC1000071//ESTs//2.5e-60:321:96//Us.25010:R6787

25 R-OVARC1000085//Proteasome component C5//8.6e-67:366:92//Hs.75748:AL031259

R-nnnnnnnnnn//ESTs//1.0e-111:526:98//Hs.129020:Al380703

R-OVARC1000091//ESTS, Weakly similar to HOST CELL FACTOR CI [H.sapiens]//3.9e-112:596:94//Hs.20597: W58370

R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:Al289942

30 R-OVARC1000106

R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//8.3e-102:495:97//Hs.3688:AF069250

R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:489:74//Hs.101238:Y11312

R-OVARC1000133//EST//0.00028:284:61//Hs.30547:H05482

35 R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:Al333214

R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090

R-OVARC1000151

R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023

R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629

40 R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339:81//Hs.154103:AF061258 R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93 [H.sapiens]//1.1e-32:196:92//Hs. 64322:AA142864

R-OVARC1000212//EST//0.20:178:61//Hs.133031:AI049874

R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958

45 R-OVARC1000241//EST//0.00018:115:68//Hs.150728:Al123130

R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.3e-74:403:93//Hs.108117:Al097079

R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476

R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MOV10 [Mus musculus]//2.9e-

50 37:191:98//Hs.20725:AI027777

R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449

R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743

R-OVARC1000326//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//1.3e-98:488: 96//Hs.125749:Al377682

55 R-OVARC1000335//ESTs//3.0e-115:565:97//Hs.54835:AI050863

R-OVARC1000347//EST//0.0018:145:65//Hs.136945:AA765672

R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA203423

R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:C05928

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R-OVARC1000411//ESTs//3.2e-82:395:98//Hs.104747:AA406219
         R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-27:211:79//Hs.108287:L27670
         R-OVARC1000420//EST//2.8e-38:255:74//Hs.138525:R99237
         R-OVARC1000427//EST//2.6e-58:302:96//Hs.122914:AA767034
5
         R-OVARC1000431//ESTs//4.9e-108:551:96//Hs.11668:AI123426
         R-OVARC1000437
         R-OVARC1000440//ESTs//2.9e-91:456:96//Hs.93701:Al018671
         R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.3e-45:320:84//
         R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.6e-79:418:94//Hs.12334:
10
         AB014583
         R-OVARC1000461//ESTs//3.1e-62:342:93//Hs.23241:R46582
         R-OVARC1000465//ESTs//1.7e-67:349:95//Hs.127238:AA477576
         R-OVARC1000466//ESTs//1.9e-66:337:95//Hs.5212:AI421211
         R-OVARC1000473//ESTs//5.4e-89:320:99//Hs.29173:AA134926
15
         R-OVARC1000479//ESTs, Highly similar to TIP120 [R.norvegicus]//1.1e-102:514:96//Hs.11833:AI299947
         R-OVARC1000486//ESTs//3.9e-78:405:95//Hs.98312:AA424983
         R-OVARC1000496
         R-OVARC1000520//ESTs//1.2e-20:145:88//Hs.87456:AA434484
         R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47:217:87//Hs.155464:AF088219
20
         R-OVARC1000533//ESTs, Moderately similar to integrase [H.sapiens]//8.5e-48:264:92//Hs.49860:AA702248
         R-OVARC1000543//ESTs//5.7e-74:410:94//Hs.62817:AA047021
         R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27:202:85//Hs.90859:X85106
         R-OVARC1000557//EST//2.8e-18:169:79//Hs.149101:AI244285
25
         R-OVARC1000564//EST//2.3e-34:199:92//Hs.146637:Al141587
         R-OVARC1000573//Interleukin 10//4.7e-42:300:83//Hs.2180:M57627
         R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58:392:84//Hs.155464:AF088219
         R-OVARC1000588//EST//1.8e-41:174:85//Hs.163333:AA879053
         R-OVARC1000605
         R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.4e-47:417:77//Hs.
30
         159897:AB007970
         R-OVARC1000640//H.sapiens mRNA for translin associated protein X//1.9e-28:366:72//Hs.96247:X95073
         R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31:162:100//Hs.111862:
35
         R-OVARC1000678//EST//0.92:199:60//Hs.122025:AA778480
         R-nnnnnnnnnn//ESTs//0.94:416:59//Hs.130754:AA279522
         R-OVARC1000681//EST//9.2e-21:179:80//Hs.132635:AI032875
         R-OVARC1000689//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.053:160:64//Hs.108447:AJ000517
         R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09:141:73//Hs.32511:AB007901
         R-OVARC1000703//ESTs//1.7e-46:298:87//Hs.138856:H47461
40
         R-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:
         R-OVARC1000746//ESTs//0.16:366:60//Hs.136969:AA830918
         R-OVARC1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//4.6e-
45
         28:430:69//Hs.42457:AA523306
         R-OVARC1000771//ESTs//1.3e-87:461:94//Hs.22399:AA531016
         R-OVARC1000781//ESTs//8.3e-119:572:97//Hs.41972:AA626793
         R-OVARC1000787//ESTs//7.4e-18:115:93//Hs.164036:AA845659
         R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19:119:95//Hs.3069:L11066
         R-OVARC1000802//ESTs//2.2e-41:383:78//Hs.161228:Al419764
50
         R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.2e-106:536:95//Hs.61628:
         R-OVARC1000846//Clathrin, light polypeptide (Lcb)//1.6e-66:282:87//Hs.73919:X81637
         R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115:579:96//Hs.18910:AF045584
         R-OVARC1000862//EST//4.3e-14:129:81//Hs.150663:AA923096
55
         R-OVARC1000876//ESTs//1.0e-115:573:96//Hs.87287:Al150674
         R-OVARC1000883//ESTs//3.5e-109:523:98//Hs.28423:Al336292
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R-OVARC1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE IN ROCC-PTA INTERGENIC

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REGION [Bacillus subtilis]//7.9e-98:525:93//Hs.10366:W21953
        R-OVARC1000886//ESTs//8.2e-79:417:94//Hs.7729:AA830777
        R-OVARC1000891//ESTs//6.8e-75:401:94//Hs.5833:H15401
        R-OVARC1000897//ESTs//3.5e-91:440:98//Hs.125264:AA873350
5
        R-OVARC1000912
        R-OVARC1000915//ESTs//1.0e-45:328:82//Hs.163980:AA715814
        R-OVARC1000924//ESTs//1.0e-100:501:96//Hs.30204:AA497127
        R-OVARC1000936//EST//3.0e-74:367:98//Hs.145098:AA421696
         R-OVARC1000937//EST//1.1e-53:290:95//Hs.162846:AA631215
         R-OVARC1000945//ESTs//4.9e-51:301:89//Hs.20100:W25794
10
         R-OVARC1000948//ESTs//3.7e-67:332:98//Hs.112570:AA621971
         R-OVARC1000959//Small inducible cytokine A5 (RANTES)//7.2e-44:283:86//Hs.155464:AF088219
         R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80//Hs.43681:AL022394
         R-OVARC1000971//EST//6.2e-05:126:70//Hs.160491:AI254909
         R-OVARC1000984//ESTS, Weakly similar to No definition line found [C.elegans]//3.5e-68:346:96//Hs.25544:
15
         AA532784
         R-OVARC1000996//EST//0.12:92:71//Hs.117141:AA678811
         R-OVARC1000999/Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73//Hs.127649:AB007874
         R-OVARC1001000//ESTs//1.8e-22:198:80//Hs.140608:N53448
         R-OVARC1001004//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.7e-28:181:77//Hs.139107:K00629
20
         R-OVARC1001010//EST//2.1e-09:92:85//Hs.147893:AI223270
         R-OVARC1001011//EST//2.4e-14:200:75//Hs.149290:AI248117
         R-OVARC1001032//EST//2.7e-29:304:73//Hs.141733:W80630
         R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-09:
25
         137:74//Hs.77579:AF013263
         R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1e-101:501:96//Hs.9899:AF099149
         R-OVARC1001040//ESTs//2.9e-87:415:99//Hs.132812:Al032046
         R-OVARC1001044//ESTs//1.1e-83:432:96//Hs.55043:N94384
         R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12962
30
         R-OVARC1001055//ESTs//2.4e-23:238:76//Hs.141421:H99231
         R-OVARC1001062//ESTs//3.4e-92:469:96//Hs.34658:N98652
         R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//7.3e-97:463:98//Hs.3426:
         AF082657
         R-OVARC1001072//ESTs//1.3e-34:227:89//Hs.126704:W95844
         R-OVARC1001074
35
         R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//Hs.103126:U57029
         R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337,
         LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.4e-96:325:98//Hs.21753:AJ005897
         R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//3.3e-75:386:95//Hs.26584:
40
         AF051782
         R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete cds//3.9e-37:283:84//Hs.
         46468:U45984
         R-OVARC1001118//ESTs//5.3e-99:485:97//Hs.130815:AA936548
         R-OVARC1001129//ESTs//9.8e-66:351:95//Hs.18616:T99312
         R-OVARC1001l61//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//2.2e-
45
         66:346:95//Hs.53263:AA173226
         R-OVARC1001162//EST//1.5e-44:376:80//Hs.161917:AA483223
         R-OVARC1001167//ESTs//4.7e-110:548:96//Hs.35254:Al133727
         R-OVARC1001169//ESTs//0.22:152:68//Hs.149424:AI274200
         R-OVARC1001170//Small inducible cytokine A5 (RANTES)//1.8e-42:305:84//Hs.155464:AF088219
50
         R-OVARC1001173//EST//2.5e-35:182:84//Hs.161917:AA483223
         R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.6e-64:247:
         80//Hs.97203:U83171
         R-OVARC1001188//ESTs//4.1e-18:296:69//Hs.139197:AA228343
55
         R-OVARC1001200//ESTs//2.0e-28:207:85//Hs.35121:AA877826
         R-OVARC1001232//ESTs//3.2e-61:358:91//Hs.6449:W95025
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R-OVARC1001240//ESTs//6.7e-45:316:85//Hs.121675:AA629668 R-OVARC1001243//ESTs//2.3e-86:409:99//Hs.163091:AA742361

R-OVARC1001261//ESTs//0.63:125:64//Hs.155743:Al344166

R-OVARC1001268//ESTs//8.1e-20:113:98//Hs.109477:AA477929 R-OVARC1001270//ESTs//1.5e-107:530:97//Hs.62905:AA460708 R-OVARC1001271//ESTs//4.5e-36:401:72//Hs.20190:AA525532 5 R-OVARC1001282//EST//4.0e-91:428:99//Hs.145599:Al263113 R-OVARC1001296//ESTs//2.6e-63:301:100//Hs.125753:AA740885 R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8e-70:334:100//Hs.23763: AB011090 R-OVARC1001329//Clathrin, light polypeptide (Lcb)//1.3e-68:304:83//Hs.73919:X81637 R-OVARC1001330//Proline arginine-rich end leucine-rich repeat protein//1.0:147:63//Hs.76494:U41344 10 R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452:76//Hs.155464:AF088219 R-OVARC1001341//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//6.9e-85:464:93//Hs.23651:AA650356 R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568:95//Hs.118690:X67247 R-OVARC1001344//EST//3.6e-44:341:81//Hs.162197:AA535216 15 R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250:93//Hs.3337:M90657 R-OVARC1001360//ESTs//5.2e-110:534:98//Hs.24743:AA843844 R-OVARC1001369//ESTs//1.7e-98:478:97//Hs.7729:AA830777 R-OVARC1001372//ESTs//2.6e-97:456:99//Hs.153648:Al341415 R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.1e-53:344:72//Hs.153468: 20 AB011147 R-OVARC1001381//ESTs//5.1e-19:200:66//Hs.114031:AA700958 R-OVARC1001391 R-nnnnnnnnnn//ESTs//0.003 9:48:95//Hs.117964:N20913 R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:561:95//Hs.21586:AB006651 25 R-OVARC1001425//EST//5.7e-20:395:66//Hs.159707:Al393136 R-OVARC1001436//ESTs//9.6e-90:427:99//Hs.6982:AA622427 R-OVARC1001442//ESTs//1.1e-66:317:100//Hs.18437:Al206345 R-OVARC1001453//ESTs//2.0e-20:163:84//Hs.133503:AA628592 30 R-OVARC1001476//EST//0.23:125:66//Hs.71444:AA131700 R-OVARC1001480//ESTs//3.1e-56:181:97//Hs.40109:AA928694 R-OVARC1001489//ESTs//1.0:297:58//Hs.86723:AA393089 R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//3.0e-117:585:96//Hs.6534: AF016507 35 R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283:90//Hs.155464:AF088219 R-OVARC1001525//EST//0.80:170:60//Hs.157398:AI364539 R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds//1.6e-111:566:95//Hs.6396:AB016492 R-OVARC1001547//ESTs//5.7e-105:564:93//Hs.68835:AA088388 R-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA7/4.4e-20:150:89//Hs.155160: 40 AF031166 R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282:72//Hs.154326:D42087 R-OVARC1001610//ESTs//4.6e-108:555:95//Hs.44295:N32019 R-OVARC1001611//ESTs//0.0021:117:71//Hs.135568:AA972965 R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114:78//Hs.5158:AB007869 45 R-OVARC1001668//ESTs//1.0:127:69//Hs.153290:AI022659 R-OVARC1001702//ESTs//4.8e-44:225:97//Hs.96855:AA346854 R-OVARC1001703//ESTs//2.3e-89:426:99//Hs.27099:W60080 R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784 R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [Xenopus laevis]//1.2e-27:236:81//Hs.15485: 50 AA046954 R-OVARC1001731//Tropomyosin4(fibroblast)//7.9e-74:422:90//Hs.102824:X05276 R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//1.7e-62:300:83//Hs.144563: AF057280 R-nnnnnnnnnnn//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//6.8e-100: 55 540:92//Hs.117741:AA903456 R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//

1.1e-109:567:94//Hs.155377:U97670

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R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds//2.0e-109:529:97//Hs.15869:
AB014575
R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127
R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604
R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978
R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276:81//Hs.153563:AF011333
R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688
R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831
R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1e-15:519:63//Hs.25639:AB011110
R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W52705
R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:Al374621
R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:Al242160
R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31809
R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence/1.9e-105:571:91//Hs.25300:
R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476
R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.2e-49:302:90//Hs.153468:
AB011147
R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310
R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//
1.6e-87:346:90//Hs.6216:AF061749
R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435
R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855
R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842
R-OVARC1001928
R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//2.5e-39:
253:88//Hs.117741:AA903456
R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637
R-OVARC1001949//ESTs, Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//8.3e-96:498:94//Hs.
22744:AI379892
R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:AI032875
R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:AI183729
R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887
R-OVARC1002044//ESTS//3.4e-45:303:85//Hs.132722:AA618531
R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:
AB007934
R-OVARC1002066//ESTs//8.5e-97:455:99//Hs.135477:AI088556
R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:
AB018315
R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860
R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:AI347130
R-OVARC1002138//ESTs, Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME
III [Caenorhabditis elegans]//1.7e-102:485:98//Hs.137516:AA805691
R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825
R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA478923
R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA908631
R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160
R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478
R-PLACE1000004//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//
7.5e-32:164:99//Hs.144194:AA706337
R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920
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R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:100:97//Hs.109268:AF070557

R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223

R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870

55 R-PLACE1000040//ESTs//0.00017:316:59//Hs.23342:AI310440

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R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frames//4.8e-79:519:86//Hs.23094:M19503

R-PLACE100005011ESTs//9.7e-90:453:96//Hs.27410:N25612

R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:L06499

94//Hs.30026:Al356771

R-PLACE1000081

R-PLACE1000078//ESTs//2.6e-30:212:85//Hs.89312:AA167659

R-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-61:331:

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R-PLACE1000094
         R-PLACE1000133//ESTs//4.4e-87:448:94//Hs.93748:AA884505
         R-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H.sapiens]//5.5e-103:538:94//Hs.9670:
         AA632135
         R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//4.1e-114:594:94//Hs.
         151017:AF058291
10
         R-PLACE1000185//ESTs, Weakly similar to No definition line found [C.elegans]//2.0e-19:114:95//Hs.7036:
         W22072
         R-PLACE1000213//ESTs//9.4e-99:494:96//Hs.24398:Al262946
         R-PLACE1000214//ESTs//5.3e-98:466:98//Hs.28661:AA805916
         R-PLACE1000236//Human BENE mRNA, partial cds//1.7e-19:162:84//Hs.85889:U17077
15
         R-PLACE1000246//EST//0.026:134:66//Hs.135611:Z21545
         R-PLACE1000292//ESTs//2.5e-80:418:96//Hs.138233:N57912
         R-PLACE1000332//EST//1.7e-82:422:96//Hs.118637:T61940
         R-PLACE1000347//ESTs//8.5e-36:180:100//Hs.6377:AA632424
         R-PLACE1000374//ESTs//2.8e-90:434:98//Hs.161785:AI423126
20
         R-PLACE1000380//ESTs//1.0e-81:399:97//Hs.47105:Al334994
         R-PLACE1000383//ESTs//3.7e-75:405:94//Hs.23200:AA203708
         R-PLACE1000401//ESTs//1.4e-16:212:72//Hs.151665:AA020959
         R-PLACE1000406//ESTs//2.1e-51:259:97//Hs.129651:N53089
         R-PLACE1000420//ESTs//7.7e-92:471:95//Hs.144407:AA737799
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         R-PLACE1000421//ESTs//2.9e-14:282:67//Hs.142068:AA176125
         R-PLACE1000424//EST//2.9e-35:453:70//Hs.162404:AA573131
         R-PLACE1000435//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete
         cds//1.6e-47:472:77//Hs.113259:AF023456
         R-PLACE1000444//ESTs, Moderately similar to platelet glycoprotein IIb precursor [H.sapiens]//2.0e-58:410:81//
30
         Hs.97579:AA398118
         R-PLACE1000453//ESTs//2.3e-85:442:95//Hs.9725:AA039793
         R-PLACE1000481//ESTS, Weakly similar to Ndr protein kinase [H.sapiens]//3.2e-109:549:95//Hs.19074:U69566
          R-PLACE1000492//ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [R.norvegicus]//3.5e-83:
          435:94//Hs.26510:AA700425
35
          R-PLACE1000540//ESTs//3.2e-58:281:99//Hs.118270:AA844729
          R-PLACE1000547//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.2e-32:208:88//Hs.153026:
          R-PLACE1000562//ESTs, Weakly similar to HYPOTHETICAL 23.0 KD PROTEIN IN IXR1-TFA1 INTERGENIC
          REGION [Saccharomyces cerevisiae]//1.9e-26:220:81//Hs.163791:W25348
40
          R-PLACE1000564//ESTs//1.1e-54:302:92//Hs.158520:Al380485
          R-PLACE1000583//Human mRNA for KIAA0355 gene, complete cds//5.5e-43:404:75//Hs.153014:AB002353
          R-nnnnnnnnnnn//Guanylate binding protein 1, interferon-inducible, 67kD//6.1e-79:542:82//Hs.62661:M55542
          R-PLACE1000596//ESTs//0.0028:364:59//Hs.106090:AA457030
          R-PLACE1000599//Human mRNA for KIAA0118 gene, partial cds//4.3e-49:295:90//Hs.154326:D42087
 45
          R-PLACE1000610//ESTs//0.0010:104:74//Hs.17413:N45301
          R-PLACE1000636//ESTs//1.8e-64:340:95//Hs.100895:AA479308
          R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:
          96//Hs.5819:AF102265
          R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and
 50
          LLNLc110F1857Q7 (RZPD Berlin))//1.4e-102:559:92//Hs.29595:AJ005896
          R-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//2.8e-10:281:
          64//Hs.128763:AF009353
          R-PLACE1000712//ESTs//7.8e-60:317:95//Hs.8245:AA115485
 55
          R-PLACE1000716
          R-PLACE1000748//ESTs//8.9e-87:466:93//Hs.25245:AA176701
          R-PLACE1000749//EST//0.019:186:61//Hs.135443:AI077396
          R-PLACE1000755//ESTs, Weakly similar to HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III [C.el-
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egans1//3.9e-40;224;94//Hs.87889;AA262008
        R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence//6.5e-27:531:66//Hs.133342:AF070536
        R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//8.5e-103:513:96//Hs.31921:
        AB014548
        R-PLACE1000786//ESTs//5.2e-93:449:97//Hs.58389:W74482
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        R-nnnnnnnnnn//H.sapiens mRNA for chemokine HCC-1//0.88:201:60//Hs.20144:AF088219
        R-PLACE1000798//ESTs//1.1e-97:508:94//Hs.139119:N32189
        R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory protein [H.sapiens]//7.7e-31:220:86//Hs.
         117576:R33135
         R-nnnnnnnnn//ESTs//1.8e-87:459:94//Hs.43100:AA186588
10
         R-PLACE1000856//ESTs//0.0084:224:59//Hs.145906:Al275039
         R-PLACE1000863//ESTs, Highly similar to PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W [Saccharomyces
         cerevisiae]//2.2e-92:467:95//Hs.6118.-Al141558
         R-PLACE1000909//ESTs//4.7e-89:435:97//Hs.95744:Al392846
         R-PLACE1000931//EST//1.9e-28:261:73//Hs.135545:AI097091
15
         R-PLACE1000948//ESTs//0.034:329:58//Hs.114851:AA608697
         R-PLACE1000972//EST//3.3e-24:264:74//Hs.130321:Al002941
         R-PLACE1000977//EST//0.085:153:65//Hs.131646:AI025689
         R-PLACE1000979
         R-PLACE1001000//ESTs//4.7e-56:284:96//Hs.117978:AA810725
20
         R-PLACE1001007//ESTs, Moderately similar to MNK1 [H.sapiens]//5.2e-63:343:93//Hs.5662:AA868361
         R-PLACE1001010//EST//0.96:53:71//Hs.96973:AA351146
         R-PLACE1001015//Oxytocin receptor//2.8e-25:308:71//Hs.2820:X64878
         R-PLACE1001024//ESTs//5.0e-12:79:96//Hs.97910:AA404736
         R-PLACE1001036//ESTs//4.0e-15:301:65//Hs.137947:Al025762
25
         R-PLACE1001062//ESTs//5.2e-15:199:73//Hs.138982:AA056120
         R-PLACE1001076//ESTs//3.9e-84:406:98//Hs.115455:AA678124
         R-PLACE1001088//ESTs//3.0e-106:518:97//Hs.158964:AA639580
         R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.035:259:59//Hs.31575:AF100141
         R-PLACE1001104//ESTs//6.1e-115:582:95//Hs.10972:AA164268
30
         R-PLACE1001118//ESTs//6.9e-81:440:93//Hs.5383:AA913610
         R-PLACE1001136//ESTs//7.4e-41:168:83//Hs.95115:AA206594
         R-PLACE1001168//ESTs//3.9e-21:116:99//Hs.5897:AA148834
         R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H.sapiens]//0.91:77:71//Hs.
         115211:AA287527
35
         R-PLACE1001185//ESTs//1.5e-65:330:96//Hs.26368:AA789297
         R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//1.9e-99:512:
         94//Hs.24884:AA176812
         R-PLACE1001241//ESTs//1.1e-81:446:93//Hs.42278:Al073464
         R-PLACE1001257//EST//6.4e-46:298:87//Hs.162404:AA573131
40
         R-PLACE1001272//ESTs//0.31:158:61//Hs.42960:N95371
         R-PLACE1001279//ESTs//1.8e-77:376:97//Hs.29276:AA427780
         R-PLACE1001280//ESTs//1.1e-30:134:89//Hs.163492:Al334460
         R-PLACE1001294//ESTs, Moderately similar to GAMETOGENESIS EXPRESSED PROTEIN GEG-154 [M.mus-
         culus1//2.7e-22:181:84//Hs.48320:AA149548
45
         R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]//4.2e-34:195:92//Hs.86276:
         W27601
         R-PLACE1001311//ESTs//9.1e-91:438:97//Hs.41055:Al339056
         R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds//5.5e-44:215:86//
50
         Hs.50984:U01160
         R-PLACE1001351//ESTs//2.4e-101:494:97//Hs.23944:Al097077
         R-PLACE1001366//Small inducible cytokine A5 (RANTES)//8.7e-43:284:85//Hs.155464:AF088219
         R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//2.3e-81:431:93//Hs.152005:
         R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence/1.0e-36:192:97//Hs.12342:AF055030
55
         R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//1.0e-86:
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456:94//Hs.21301:AF093419

R-PLACE1001387//ESTs//6.0e-74:383:94//Hs.55016:Al298280

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R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555
         R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348
        R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45:242:95//Hs.110404:
         AF091087
         R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800
5
         R-PLACE1001440
         R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115.
         R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:AI017547
         R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:Al248625
         R-PLACE1001502//ESTs//8.1e-31:161:99//Hs.126264:AA455617
10
         R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361
         R-PLACE1001517//Homo sapiens hGAAI mRNA, complete cds//2.1e-57:339:90//Hs.4742:AB006969
         R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:AI042153
         R-PLACE1001545/TESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-22:
         170:85//Hs.155456:AA707265
15
         R-PLACE1001551//ESTs//1.5e-39:202:98//Hs.139269:AA894431
         R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249
         R-PLACE1001602//EST//0.33:297:57//Hs.149839:Al287601
         R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904
         R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608683
20
         R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217:97//Hs.75258:
         AF054174
         R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458:91//Hs.
         114547:AA167095
         R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:Al168526
25
         R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61640
         R-PLACE10016727/ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.98:
         141:62//Hs.153060:AA195804
         R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-
         113:545:97//Hs.3688:AF069250
30
         R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA679124
         R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:Al374903
         R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA983667
         R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA010993
         R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA282171
35
         R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113
         R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA644266
         R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA236479
         R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:AI423937
         R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//4.1e-93:540:89//Hs.4812:
40
         AF061243
         R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N64662
         R-PLACE1001761
         R-PLACE1001771//ESTs//0.92:165:62//Hs.473 87:N51980
         R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA081236
45
         R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA807352
         R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA; partial cds//
          1.3e-93:463:95//Hs.40820:AF058953
          R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328:75//Hs.155464:AF088219
50
          R-PLACE1001845
          R-PLACE1001869//EST//1.0:207:62//Hs.137298:W32868
          R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H50009
          R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA789098
          R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363:97//Hs.17839:
          AF099936
          R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.85:130:66//Hs.151406:
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R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA007313

AB014523

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R-PLACE1001989//ESTs//1.3e-88:453:95//Hs.132717:AA171941
        R-PLACE1002046
        R-PLACE1002052//ESTs//1.7e-79:428:94//Hs.6737:N32595
        R-PLACE1002066//ESTs//2.8e-82:427:94//Hs.132972:AA543094
        R-PLACE1002072//ESTs//0.27:108:66//Hs.123163:AA809619
5
        R-PLACE1002073//EST//5.5e-70:369:95//Hs.132339:AI028552
        R-PLACE1002090//ESTs//6.3e-73:361:96//Hs.134469:AA731632
        R-PLACE1002115//ESTs//4.6e-34:233:88//Hs.163443:R23311
        R-PLACE1002119//ESTs//1.2e-88:444:96//Hs.15725:AA521293
10
        R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W91937
        R-PLACE1002150//ESTs//4.0e-96:465:98//Hs.7312:Al167614
        R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG[H.sapiens]//3.6e-
        39:400:76//Hs.162172:AA534189
        R-PLACE1002163//ESTs//3.2e-83:428:95//Hs.137011:Al185965
15
        R-PLACE1002171//ESTs//5.3e-68:392:90//Hs.62273:AA143745
         R-PLACE1002205//ESTS//1.5e-39:211:95//Hs.28338:N48793
        R-PLACE1002213//ESTs//5.1e-38:290:83//Hs.146811:AA410788
        R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N49892
        R-PLACE1002256//ESTs//2.4e-100:484:98//Hs.9343:AI004257
        R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//5.8e-67:501:81//Hs.23094:M19503
20
        R-PLACE1002319//ESTs//1.4e-28:17 8:92//Hs.7353:AA209308
        R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6e-95:501:93//Hs.18277:AB018271
         R-PLACE1002395//ESTs//3.6e-25:248:77//Hs.3853:AA034291
         R-PLACE1002399//ESTs//1.5e-27:238:78//Hs.13014:W26381
         R-PLACE1002433//ESTs//4.3e-108:511:98//Hs.98324:AA621959
25
         R-PLACE1002437//EST//1.2e-06:158:61//Hs.159833:T24110
         R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60//Hs.83715:X69804
         R-PLACE1002450//ESTs//1.5e-89:432:98//Hs.47371:AA136333
         R-PLACE1002465//ESTS//1.6e-92:488:93//Hs.78110:AA741320
         R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:166:85//Hs.19368:U69263
30
         R-PLACE1002477//ESTs//2.5e-62:305:98//Hs.88605:AA421132
         R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds//3.6e-
         55:307:91//Hs.17200:AF042273
         R-PLACE1002499//ESTs//7.4e-72:373:96//Hs.128221:AA972429
         R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296:83//Hs.5158:AB007869
35
         R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-
         14:217:69//Hs.152230:Al140609
         R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582:85//Hs.88756:AB018256
         R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19:116:93//Hs.99348:AC004774
         R-PLACE1002537//ESTs//4.8e-93:440:99//Hs.164005:AA766491
40
         R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555:
         95//Hs.23259:AA532437
         R-PLACE1002578//EST//1.9e-40:337:81//Hs.162404:AA573131
         R-PLACE1002583//EST//1.2e-07:264:65//Hs.156414:Al339738
         R-PLACE1002591//ESTs//2.3e-67:372:94//Hs.143046:N73778
45
         R-PLACE1002598//ESTs, Highly similar to PROTEIN HI1715 [Haemophilus influenzae]//1.2e-44:228:97//Hs.
         7527:AA843208
         R-PLACE1002604//ESTs//3.3e-106:532:96//Hs.86828:AA632147
         R-PLACE1002625//EST//3.8e-13:173:74//Hs.138597:H77749
         R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)//1.0:189:58//Hs.75703:J04130
50
         R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:
         390:97//Hs.124903:AF068180
         R-PLACE1002714//ESTs//8.2e-63:340:93//Hs.7973:H19830
         R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]//6.8e-75:445:90//Hs.
55
         29202:R71586
         R-PLACE1002768//ESTs//1.2e-70:359:95//Hs.132600:H12865
         R-PLACE1002772//ESTs//8.1e-49:362:82//Hs.141254:Al334099
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R-PLACE1002782//ESTs//2.4e-58:284:98//Hs.143545:AI149014

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R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593
        R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955
        R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:Al304392
         R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916
        R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-42:233:94//Hs.
5
         61518:AA167094
        R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142
        R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:Al096756
         R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539
10
         R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:Al066762
         R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:Al249332
         R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995
        R-PLACE1002962
         R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202
         R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941
15
         R-PLACE10029937/ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//1.3e-86:
         502:89//Hs.32232:AA604268
         R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:AI144268
         R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:AI151499
         R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:156r60//Hs.82042:D87075
20
         R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:
         R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777
         R-PLACE1003100//ESTs, Highly similar to NODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:491:93//Hs.
25
         6318:AI131178
         R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359
         R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//Hs.49346:U51920
         R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757
         R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467
         R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924
30
         R-PLACE1003176
         R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:Al091453
         R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017
         R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:H44802
         R-PLACE100323 8//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:436:94//Hs.58561:W79123
35
         R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-44:313:84//
         Hs.73614:U83460
         R-PLACE1003256//EST//9.6e-46:284:88//Hs.162404:AA573131
         R-PLACE1003258//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//8.3e-102:
40
         551:92//Hs.52431:AA625326
         R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986
         R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.
         29147:AA883993
         R-PLACE1003334//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.3e-94:463:
45
         97//Hs.155050:AA908765
         R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438
         R-PLACE1003343//EST//0.0087:412:58/Hs.159963:AA977701
         R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete
         cds//1.1e-99:469:98//Hs.6564:U92715
         R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:Al199636
50
         R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234
         R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans]//3.5e-18:109:95//Hs.27670:Al051591
         R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941
          R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:Al039909
          R-PLACE1003383//ESTs//0.00084:177:64//Hs.120695:Al377755
55
          R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020
          R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840
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R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697

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R-PLACE1003478//EST//1.0:162:63//Hs.147003:AI184671
         R-PLACE1003493//ESTs//1.2e-73:383:95//Hs.28852:R64270
         R-PLACE1003516//ESTs//3.2e-23:206:80//Hs.138632:H97952
         R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236:79//Hs.2853:Z29505
5
         R-PLACE1003521//ESTs//5.8e-74:371:96//Hs.30818:AA194980
         R-PLACE1003528//ESTs//1.1e-40:219:82//Hs.138856:H47461
         R-PLACE1003537//ESTs, Weakly similar to multispanning membrane protein [H.sapiens]//7.4e-69:338:98//Hs.
         110439·N93209
         R-PLACE1003553//ESTs//2.2e-87:438:97//Hs.132022:AI040321
10
         R-PLACE1003566//ESTs//1.2e-62:298:92//Hs.30799:AI052591
         R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145:80//Hs.
         92381:AB007956
         R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//1.5e-14:264:65//Hs.158253:
         R86178
15
         R-PLACE1003584
         R-PLACE1003592//ESTs//1.3e-15:213:69//Hs.139507:T77542
         R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5.8e-75:459:89//Hs.23884:AD77106
         R-PLACE1003596//ESTs//0.011:273:61//Hs.71719:AA142875
         R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576:88//Hs.56851:D83200
20
         R-PLACE1003605//ESTs//3.7e-86:407:99//Hs.136057:AA988299
         R-nnnnnnnnnn//ESTs//1.0:78:71//Hs.101248:T26446
         R-PLACE1003618//ESTs//6.8e-30:281:79//Hs.114455:AA411943
         R-PLACE1003625//ESTs//7.2e-78:377:98//Hs.102708:AA292285
         R-PLACE1003638//ESTs//6.7e-38:274:82//Hs.138852:AA284247
25
         R-PLACE1003669//ESTs//9.7e-83:418:95//Hs.4842:AI342607
         R-PLACE1003704//ESTs//3.0e-13:99:89//Hs.81648:W26521
         R-PLACE1003709//ESTs//0.019:178:60//Hs.32100:N59866
         R-PLACE1003711//ESTs//0.99:126:63//Hs.47005:N98639
         R-PLACE1003723//ESTS//1.7e-89:448:96//Hs.157222:AA766987
30
         R-PLACE1003738//ESTs//2.5e-36:182:100//Hs.122162:AI057087
         R-PLACE1003760//Human globin gene//L9e-98:538:91//Hs.100090:M69023
         R-PLACE1003762//EST//2.9e-15:125:85//Hs.162083:AA487512
         R-PLACE1003768//Human P042 gene, complete cds//3.1e-18:300:69//Hs.158302:U88965
         R-PLACE1003771//ESTs//1.2e-09:64:100//Hs.23799:Al003798
35
         R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans]//3.8e-38:199:97//Hs.115197:AA215757
         R-PLACE1003784//ESTs//3.7e-87:428:97//Hs.157985:Al366909
         R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.2e-36:236:88//Hs.153468:
         AB011147
         R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//8.5e-
40
         62:313:96//Hs.121020:AA526092
         R-PLACE1003850//ESTs//4.0e-67:351:96//Hs.159303:T91059
         R-PLACE1003858//ESTs//0.96:87:66//Hs.107112:AA679058
         R-nnnnnnnnnnn
         R-PLACE1003870//EST//2.9e-34:281:79//Hs.160895:AI365871
45
         R-nonnonnonnon
         R-PLACE1003886//ESTs//6.7e-85:410:97//Hs.25129:W93595
         R-PLACE1003888//ESTs//0.0085:165:64//Hs.96739:AA441915
         R-PLACE1003900//EST//2.4e-05:129:69//Hs.127931:AA969259
         R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.5e-54:282:96//Hs.58553:
50
         AA100804
        R-PLACE1003915//EST//0.87:55:76//Hs.145930:Al275760
        R-PLACE1003923//ESTs//1.7e-89:456:95//Hs.14125:AA156236
        R-PLACE1003932//ESTs//3.0e-50:340:84//Hs.151208:Al126110
        R-PLACE1003936//EST//1.8e-08:208:65//Hs.162656:AA603567
55
        R-PLACE1003968//ESTs//7.4e-49:301:90//Hs.93850;AA115330
         R-PLACE1004104//ESTs//1.9e-46:254:94//Hs.96802:AA443231
         R-PLACE1004114//ESTs//1.2e-64:322:97//Hs.28928:AI052052
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R-PLACE1004118//ESTs//1.0e-83:404:98//Hs.112764:AA609770

- R-PLACE1004128//ESTs//5.3e-80:415:95//Hs.11835:AA040244
- R-PLACE1004149//ESTs//7.2e-25:331:72//Hs.141084:H11714
- R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56:491:76//Hs.113283:AF018080 R-PLACE1004161//ESTs//2.0e-59:355:88//Hs.13830:AA918601
- 5 R-PLACE1004183//Homo sapiens cytochrome c oxidase assembly protein COX11(COX11) mRNA, complete cds//
  4.7e-78:434:91//Hs.153504:AF044321
  - R-PLACE1004197
  - R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds// 1.5e-105:501:98//Hs.24640:AF069493
- 10 R-PLACE1004242//ESTs//1.0e-71:364:87//Hs.138632:H97952
  - R-PLACE1004256//EST//0.0011:347:61//Hs.131385:AI022630
  - R-PLACE1004257//EST//0.027:99:71//Hs.97587:AA398209
  - R-PLACE1004258//KERATIN. TYPE I CYTOSKELETAL 14//0.72:180:63//Hs.117729:100124
  - R-PLACE1004270//ESTS//0.011:264:59//Hs.110044:AA181800
- R-PLACE1004274//Human retinoic acid receptor-beta associated open reading frame, complete sequence//0.28: 121:66//Hs.1938:S82362
  - R-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds//1.4e-107:581: 91//Hs.127007:AF084830
  - R-PLACE1004284//ESTs//5.0e-22:187:82//Hs.23141:W92114
- 20 R-PLACE1004289//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-28: 279:77//Hs.38687:AA744496
  - R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]//8.2e-61:313:95//Hs. 71435:Al253099
  - R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115:590:94//Hs.11171:Y11588
- 25 R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//6.7e-69:572: 77//Hs.1361:M55053
  - R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//7.7e-72: 379:93//Hs.16232:AF100153
  - R-PLACE1004376//ESTs//0.49:362:59//Hs.138086:AI056309
- 30 R-PLACE1004384//EST//1.0:47:76//Hs.128546:AA905556
  - R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//1.3e-98:572:90//Hs.14202:N46000
  - R-PLACE1004405//ESTs//3.4e-99:507:95//Hs.28792:Al343467
  - R-PLACE1004425//ESTs//2.7e-85:442:95//Hs.12544:N53665
- 35 R-PLACE1004428//ESTs//1.0e-07:114:78//Hs.140225:AA704101
  - R-PLACE1004437//Human NAD\*-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.4e-90:516:88//Hs.155410:U49283
    R-PLACE1004451
  - R-PLACE1004460//ESTs//5.4e-14:338:64//Hs.97464:AA662980
- 40 R-PLACE1004467//ESTs//3.3e-85:467:92//Hs.9527:W52721
  - R-PLACE1004471//ESTs//3.0e-73:389:94//Hs.23240:R46578
  - R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101:510:95//Hs.16986:W89194
  - R-PLACE1004491//Human mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23: 278:61//Hs.89663:L13286
- 45 R-PLACE1004506//ESTs//2.5e-98:559:90//Hs.19447:AI057117
  - R-PLACE1004510//ESTs//1.5e-91:436:98//Hs.24846:AI420493
  - R-PLACE1004516//EST//1.7e-66:344:96//Hs.99303:AA453164
  - R-PLACE1004518//ESTs//5.2e-79:410:94//Hs.27091:AA436553
  - R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40:332:72//Hs.
- 50 115325:084488
  - R-PLACE1004550
  - R-PLACE1004564//ESTs//5.5e-76:367:98//Hs.49683:AA564742
  - R-PLACE1004629//ESTs, Weakly similar to OS-9 precurosor [H.sapiens]//8.1e-40:272:87//Hs.7100:W07181
  - R-PLACE1004645//ESTs//6.3e-14:83:100//Hs.17270:AA701903
- 55 R-PLACE1004646//ESTs//3.7e-22:231:76//Hs.141250:N29734
  - R-PLACE1004658//ESTs//2.0e-12:109:84//Hs.23508:AA101113
  - R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0714 protein, partial cds//7.8e-23:129:99//Hs.123129:AB018257 R-PLACE1004672//ESTs//2.0e-50:256:98//Hs.136367:AI144254

R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//L8e-90:510:91//Hs. 80019:AF035606

R-PLACE1004681//EST//2.1e-08:283:62//Hs.99543:AA461482

R-PLACE1004686

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R-PLACE1004691//EST//7.3e-42:305:82//Hs.141833:AA021552

R-PLACE1004693//ESTs//0.014:135:64//Hs.145333:Al251374

R-PLACE1004716//ESTs, Weakly similar to No definition line found [C.elegans]//3.4e-80:413:94//Hs.23528: Al279571

R-PLACE1004722//EST//0.14:165:63//Hs.18213:T97997

R-PLACE1004736//ESTs//1.0e-72:385:94//Hs.10657:N6391

R-PLACE1004740//ESTs//1.0:267:58//Hs.101661:AA416619

R-nnnnnnnnnn//EST//0.45:94:69//Hs.147174:Al192195

R-PLACE1004751//EST//9.8e-32:174:83//Hs.147901:AI223374

R-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds//2.7e-89:437:96//Hs.104715:AF084367

15 R-PLACE1004777//ESTs//7.4e-68:351:94//Hs.23395:AA398548

R-PLACE1004793//ESTs//1.3e-53:290:78//Hs.142375:AA398619

R-nnnnnnnnnn//Homo sapiens mRNA for KIAA0606 protein, partial cds//1.9e-99:580:88//Hs.38176:AB011178

R-PLACE1004813//ESTs//7.6e-86:433:96//Hs.85640:AA535856

R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.1e-108:358:99//Hs.3688:AF069250

R-PLACE1004815//EST//4.7e-50:333:84//Hs.142196:AA258356

R-PLACE1004824//Protein kinase, interferon-inducible double stranded RNA dependent//4.8e-46:450:76//Hs. 73821:M35663

R-PLACE1004827//ESTs//2.3e-48:250:96//Hs.138766:AA342185

25 R-PLACE1004836//ESTs//2.7e-39:222:94//Hs.78661:AA195299

R-PLACE1004838//EST//0.056:198:60//Hs.129589:AA995901

R-PLACE1004840//ESTs, Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae] //6.5e-71:381:93//Hs.8383:AA013272

R-PLACE1004868//ESTs//4.9e-70:367:94//Hs.100895:AA479308

R-PLACE1004885//Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds//1.8e-37:330:78//Hs.113259:AF023456

R-PLACE1004900//EST//1.2e-46:306:86//Hs.149580:AI211881

R-PLACE1004902//Sucrase-isomaltase//0.87:254:61//Hs.2996:X63597

R-nnnnnnnnnn//ESTs//4.5e-75:375:96//Hs.91115:Al221563

35 R-PLACE1004918//ESTs//2.6e-103:519:95//Hs.143607:Al424948

R-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//6.6e-102:532:93//Hs. 17839:AF099936

R-PLACE1004934//EST//0.035:156:67//Hs.162071:AA478980

R-PLACE1004937//ESTs, Weakly similar to F55B12.3 [C.elegans]//6.4e-80:409:95//Hs.31945:AA702l66

40 R-PLACE1004969//ESTs//9.8e-18:101:99//Hs.112837:N78013

R-PLACE1004972//ESTs//1.3e-65:337:95//Hs.75798:H29106

R-PLACE1004979//EST//1.2e-96:475:96//Hs.120158:AA708789

R-PLACE1004982//ESTs//1.0e-98:471:98//Hs.106496:Al291776

R-PLACE1004985//ESTs//2.1e-88:456:93//Hs.135050:Al420335

45 R-PLACE1005026

R-PLACE1005027//ESTs, Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R.norvegicus]//0.72:145:66//Hs.11215:N56719

R-PLACE1005046//Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297:88//Hs.153468: AB011147

R-PLACE1005052//ESTs, Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase [C.elegans]//1.2e-106:543:95//Hs.18625:AI074605

R-PLACE1005066//ESTs//3.9e-92:459:96//Hs.62684:AA806103

R-PLACE1005077//Human triadin mRNA, complete cds//1.8e-05:121:69//Hs.68731:U18985

R-PLACE1005085//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.6e-49:314:74//Hs.113283:AF018080

55 R-PLACE1005086//ESTs//1.2e-73:379:94//Hs.110128:AA584364

R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end ofcds//8.0e-99:531:92//Hs.75437:L40401

R-PLACE1005102//ESTs//7.2e-68:493:84//Hs.10593:AI201336

R-PLACE1005108//Human DNA fragmentation factor-45 mRNA, complete cds//9.2e-40:232:82//Hs.155344:

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U91985
        R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356:AA493225
        R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093:AA203423
        R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896:AA777349
        R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838:Al089013
5
        R-nnnnnnnnnn//ESTs//5.4e-75:366:97//Hs.48119:AA454227
        R-PLACE1005181//EST//0.012:172:66//Hs.147107:Al190589
        R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577:Al022830
        R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792:H45211
        R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552:R99532
10
         R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310:R16767
         R-PLACE1005261//ESTs//0.19:175:62//Hs.124337:AA829524
         R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146:AA699633
         R-PLACE1005277//ESTs//1.5e-29:314:72//Hs.163710:AA024516
         R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282:AA970322
15
         R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855:Al197937
         R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239:AA215797
         R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368:AA206614
         R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537:94//Hs.136309:AB007960
         R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291:Al189343
20
         R-PLACE1005335//ESTs, Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442:97//Hs.70202:AA732975
         R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901
         R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344:80//Hs.43681:AL022394
         R-PLACE1005409//EST//0.43:174:59//Hs.162077:AA479978
         R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306:AA555304
25
         R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257:AA188423
         R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-88:561:86//Hs.23094:M19503
         R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549:83//Hs.78935:U29607
         R-PLACE1005480//EST//0.99:39:82//Hs.157275:Al364046
         R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635:Al032875
30
         R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319:59//Hs.62705:AB000220
         R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277:98//Hs.28307:
         AF071185
         R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304:AA443325
         R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.9e-20:321:69//Hs.155481:
35
         R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380:Al291325
         R-PLACE1005550//ESTs, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III
         [Caenorhabditis elegans]//5.2e-95:458:98//Hs.38114:N62927
         R-PLACE1005554//ESTs//8.8e-36:267:86//Hs.98288:AA203555
40
         R-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR
         [Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:W81261
         R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771:R99835
         R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050:AA724612
         R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079:Al276023
45
         R-PLACE1005603//ESTs//8.2e-99:533:93//Hs.96357:AI026927
         R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941:AA261857
         R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382:AA808964
         R-PLACE1005630
         R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975:W72452
50
         R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585:93//Hs.8765:
         R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054:AA528169
         R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//
         3.3e-24:401:66//Hs.129727:AF035587
55
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R-PLACE1005698//ESTs//0.00013:82:79//Hs.116331:AA629355 R-PLACE1005727//EST//0.15:206:63//Hs.105002:AA449332 R-PLACE1005730//EST//0.0014:129:70//Hs.127931:AA969259

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R-PLACE1005739//ESTs, Moderately similar to unknown intracellular protein [M.musculus]//1.3e-42:236:94//Hs.
        23889:AI341137
        R-PLACE1005755//ESTs//2.8e-32:308:80//Hs.159821:AA524070
        R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds//3.3e-47:268:87//Hs.154326:D42087
        R-PLACE1005799//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III
5
        [Caenorhabditis elegans]//7.7e-15:88:98//Hs.109857:AA088385
        R-PLACE1005802//ESTs//2.8e-19:208:76//Hs.9271:W30941
        R-PLACE1005803//ESTs//2.6e-75:417:92//Hs.71414:AA131327
        R-PLACE1005804//EST//6.5e-20:182:70//Hs.149844:Al287693
        R-PLACE1005828//ESTs//3.0e-15:194:77//Hs.106236:N50058
10
        R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.040:435:58//Hs.75770:L41870
        R-PLACE1005845//EST//5.0e-61:294:99//Hs.133202:AI050965
        R-PLACE1005850//ESTs//3.4e-82:425:96//Hs.7966:AI203471
        R-PLACE1005851//ESTs//2.9e-21:165:84//Hs.23607:N98305
        R-PLACE1005876//ESTs//0.48:296:57//Hs.39140:AI041842
15
        R-PLACE1005884//ESTs//0.0027:177:66//Hs.150295:AA570558
        R-PLACE1005898//ESTs//1.7e-98:467:98//Hs.159475:Al339981
        R-PLACE1005921//ESTs//5.8e-96:480:95//Hs.30822:AA885501
        R-PLACE1005923//ESTs//1.8e-66:333:96//Hs.150890:Al341793
         R-PLACE1005925//Human Line-1 repeat mRNA with 2 open reading frames//2.8e-27:382:70//Hs.23094:M19503
20
        R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]//1.1e-70:377:93//Hs.5662:AA868361
         R-PLACE1005934//ESTs//1.0e-42:251:91//Hs.25092:AA922142
         R-PLACE1005936//ESTs//1.2e-88:461:94//Hs.94125:N62913
         R-PLACE1005951//ESTs//1.4e-83:533:86//Hs.21148:Al183729
         R-PLACE1005953
25
         R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN-IN CDC12-ORC6 INTERGENIC
         REGION [Saccharomyces cerevisiae]//2.2e-83:494:88//Hs.108117:Al097079
         R-PLACE1005966//ESTs//1.1e-95:465:97//Hs.98510:Al016239
         R-PLACE1005968//EST//0.26:103:66//Hs.161300:AI420897
         R-PLACE1005990
30
         R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds//2.0e-45:481:74//Hs.153014:AB002353
         R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROTEIN IN APE1/LAP4-CWP1 INTER-
         GENIC REGION [Saccharomyces cerevisiae]//3.1e-112:593:93//Hs.111449:Al192946
         R-PLACE1006011//ESTs, Moderately similar to NAD(+) ADP-RIBOSYLTRANSFERASE [D.melanogaster]//5.7e-
         100:596:88//Hs.24284:AA595596
35
         R-PLACE1006017//ESTs//4.2e-18:296:68//Hs.133350:Al056276
         R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C.elegans]//4.1e-102:491:98//Hs.61164:Al096332
         R-PLACE1006040//ESTs//1.2e-92:443:98//Hs.111680:N93765
         R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-
40
         26:213:77//Hs.139007:H74314
         R-PLACE1006119//ESTs//0.14:257:61//Hs.113149:AA908904
         R-PLACE1006129//ESTs//3.8e-54:285:97//Hs.18827:W68002
         R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC
         REGION [Saccharomyces cerevisiae]//2.6e-99:560:91//Hs.5249:U55977
         R-PLACE1006143//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glyco-
45
         gen storage disease type III)//0.038:463:59//Hs.904:U84010
         R-PLACE1006157//ESTs//0.014:341:58//Hs.121773:Al357886
         R-PLACE1006159//EST//0.00036:247:61//Hs.140054:AA668925
         R-PLACE1006164//ESTs//2.6e-31:362:73//Hs.141024:H07128
         R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//5.8e-54:286:94//Hs.152894:AC005239
50
         R-nnnnnnnnnnn//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//2.7e-79:393:96//Hs.19121:
         R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597:95//Hs.30464:AF091433
         R-PLACE1006195//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.8e-94:
55
         532:91//Hs.105216:AI361807
         R-PLACE1006196//ESTs//3.2e-66:382:90//Hs.18665:T99507
         R-PLACE1005205//EST//1.7e-89:448:96//Hs.116665:AA669114
         R-PLACE1006223//Human RNaseP protein p38 (RPP38) mRNA, complete cds//0.90:304:58//Hs.94986:U77664
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R-PLACE1006225//ESTs//7.2e-96:474:97//Hs.91165:Al079555
        R-PLACE1006236//ESTs//8.8e-105:535:95//Hs.7919:AI341472
        R-nnnnnnnnnnn//Homo sapiens BAC clone RG118D07 from 7q31//3.2e-99:497:95//Hs.3781:AC004142
        R-PLACE1006246//ESTs, Weakly similar to CMP-sialic acid transporter [M.musculus]//1.3e-104:532:95//Hs.
        41151:AI301961
        R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97:499:95//Hs.31921:AB014548
        R-PLACE1006262//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.6e-
        07:321:62//Hs.53057:W67839
        R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100:605:88//Hs.2060:L06132
        R-PLACE1006318//ESTs//2.4e-102:536:94//Hs.8109:AA005265
10
        R-PLACE1006325//ESTs//5.2e-105:518:96//Hs.102319:AI246503
         R-PLACE1006335//ESTs//5.1e-45:254:93//Hs.153585:R70900
         R-PLACE1006357//EST//6.5e-09:309:62//Hs.132493:AA923168
         R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097:381:58//Hs.154797:D42044
         R-PLACE1006368//ESTs//7.9e-85:412:97//Hs.150587:Al079284
15
         R-PLACE1006371//ESTs//7.7e-74:442:88//Hs.143671:W61053
        R-PLACE1006382
         R-PLACE1006385//ESTs//5.3e-06:346:61//Hs.163706:AA515748
         R-PLACE1006412//EST//7.7e-46:306:86//Hs.149580:Al281881
         R-PLACE1006414//Homo sapiens UM protein mRNA, complete cds//4.1e-43:551:69//Hs.154103:AF061258
20
         R-PLACE1006438//ESTs//1.1e-77:284:86//Hs.24545:Al278629
         R-PLACE1006445//ESTs//4.4e-53:259:99//Hs.24481:AA573139
         R-PLACE1006469//ESTs//9.4e-102:482:98//Hs.7218:AA936961
         R-PLACE1006470//ESTs//1.0:271:57//Hs.144517:AA938297
         R-PLACE1006482//ESTs//4.0e-61:354:92//Hs.51305:T47418
25
         R-PLACE1006492//EST//1.8e-09:48:91//Hs.144451:AA827722
         R-PLACE1006506//ESTs//0.012:161:61//Hs.145333:AI251374
         R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15:415:63//Hs.48824:D87717
         R-PLACE1006531//ESTs//5.6e-31:213:87//Hs.125153:AA453723
         R-PLACE1006534//ESTs//6.5e-101:512:95//Hs.27763:W46368
30
         R-PLACE1006540//ESTs//7.3e-40:320:79//Hs.121659:H02532
         R-PLACE1006552//EST//0.38:418:56//Hs.140470:AA765214
         R-PLACE1006598//ESTs//4.0e-80:409:95//Hs.142868:AI128443
         R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//
         9.3e-118:590:95//Hs.155377:U97670
35
         R-PLACE1006617//ESTs//8.1e-31:246:83//Hs.139128:AA205322
         R-PLACE1006626//ESTs//0.90:98:68//Hs.96322:AA541615
         R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33:315:78//Hs.101359:AB002384
         R-PLACE1006640//ESTs//3.7e-26:137:100//Hs.32672:W16522
         R-PLACE1006673//Interleukin 10//8.4e-47:330:83//Hs.2180:M57627
40
         R-PLACE1006678//ESTs//1.1e-13:87:98//Hs.34035:D87736
         R-PLACE1006704//ESTs//2.6e-65:394:89//Hs.30582:D12214
         R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence/1.9e-102:486:98//Hs.12472:AF038172
         R-PLACE1006754//EST//1.0e-61:381:89//Hs.14727:T83861
45
         R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73:394:93//Hs.7252:AF070622
         R-PLACE1006779//ESTs//1.4e-69:405:90//Hs.136235:AA262658
         R-PLACE1006782//EST//1.8e-25:197:86//Hs.137257:N33234
         R-PLACE1006792//ESTs//1.8e-43:317:84//Hs.139190:N55515
         R-PLACE1006795//ESTs//6.4e-68:350:95//Hs.11092:AA916335
         R-PLACE1006800//ESTs//1.9e-55:268:100//Hs.126695:AA917989
50
         R-PLACE1006805//ESTs//6.6e-91:484:93//Hs.94262:AA768847
         R-PLACE1006815//ESTs//2.1e-49:364:83//Hs.142031:AA809159
         R-PLACE1006819//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//
         1.0e-87:481:92//Hs.141263:H64113
         R-PLACE1006829//ESTs//5.7e-43:332:83//Hs.19906:AA456933
55
         R-PLACE1006860//ESTs//0.96:138:63//Hs.136649:AA-828359
         R-PLACE1006867//ESTs//1.4e-98:478:97//Hs.10299:N35008
         R-PLACE1006878//EST//8.4e-48:243:97//Hs.54970:N93536
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R-PLACE1006883//EST//3.1e-46:300:88//Hs.162404:AA573131
        R-nnnnnnnnnn//ESTs//3.0e-95:496:94//Hs.47546:AA181348
        R-PLACE1006904//ESTs//5.8e-18:304:68//Hs.125816:AA806089
        R-PLACE1006917//Endothelin receptor type B//0.00012:451:60//Hs.82002:D13168
        R-PLACE1006932//ESTs//4.6e-56:285:96//Hs.114727:Al379514
5
        R-PLACE1006935//ESTs//3.6e-12:157:73//Hs.161714:AA229078
        R-nnnnnnnnnnn/Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494:63//Hs.36927:D86956
        R-PLACE1006961//Tyrosine aminotransferase//2.5e-46:471:74//Hs.2999:X52520
        R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//9.0e-29:324:68//Hs.154257:Al275982
         R-PLACE1006966//ESTs//4.5e-99:470:99//Hs.46913:Al017636
10
         R-PLACE1006989//ESTs//2.2e-68:353:97//Hs.14394:R61257
         R-PLACE1007014//ESTs//3.4e-86:457:94//Hs.129819:AA838366
         R-PLACE1007021//ESTs//1.6e-93:539:90//Hs.7111:U55971
         R-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//6.6e-83:584:82//Hs.23094:M19503
         R-PLACE1007053//ESTs//4.2e-85:550:88//Hs.7984:AI202575
15
         R-PLACE1007097//ESTs//6.4e-78:493:86//Hs.56406:N91027
         R-PLACE1007105//ESTs//5.3e-70:381:91//Hs.22605:N74202
         R-PLACE1007111//ESTs//8.6e-75:358:99//Hs.145629:AA398646
         R-PLACE1007112//ESTs//6.9e-69:371:94//Hs.71922:AA148417
         R-PLACE1007132//ESTs//1.2e-36:373:69//Hs.10762:W28948
20
         R-PLACE1007140//ESTs//1.7e-70:360:96//Hs.56179:W56794
         R-PLACE1007178//EST//0.68:85:65//Hs.147010:AI184765
         R-PLACE1007226//ESTs//3.1e-78:452:90//Hs.8033:N94998
         R-PLACE1007238//ESTs//5.2e-70:362:95//Hs.85636:AA740619
         R-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//6.3e-93:534:
25
         89//Hs.80598:D50495
         R-PLACE1007242//ESTS//1.2e-80:390:98//Hs.117325:AA699450
         R-PLACE1007243//ESTs, Weakly similar to transporter protein [H. sapiens]//3.7e-73:357:98//Hs.18272:N78499
         R-PLACE1007257//Homo sapiens mRNA for dia-156 protein//4.3e-85:487:91//Hs.121556:Y15909
         R-PLACE1007274//ESTs//4.3e-79:430:93//Hs.146023 Al275071
30
         R-PLACE1007276//ESTs//1.5e-33:338:74//Hs.142850:R38419
         R-PLACE1007282//ESTs//4.8e-98:532:93//Hs.10071:AA100812
         R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518:74//Hs.154326:D42087
         R-PLACE1007301
         R-PLACE1007317
35
          R-PLACE1007342
          R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.2e-66:367:
          91//Hs.76596:AF096870
          R-PLACE1007367//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-98:
          488:96//Hs.24359:AA699594
 40
          R-PLACE1007375//ESTs//2.3e-67:375:92//Hs.33368:AA206614
          R-PLACE1007386//ESTs//0.020:242:62//Hs.42768:AI129945
          R-PLACE1007402//ESTs//1.6e-91:441:97//Hs.26243:AA455877
          R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//2.4e-113:590:94//
          Hs.14387:AF093771
 45
          R-PLACE1007416//ESTs, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens]//3.8e-115:579:95//Hs.
          72165:AI243857
          R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:
          80//Hs.97203:U83171
          R-PLACE1007452//EST//2.5e-42:386:77//Hs.140562:AA826514
 50
          R-PLACE1007460//ESTs//4.9e-87:434:95//Hs.28472:Al028230
          R-PLACE1007478
          R-PLACE1007484//ESTs//6.8e-08:64:92//Hs.100251:AA535975
          R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164,
          DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.26:411:60//Hs.79012:M18533
 55
          R-PLACE1007507//ESTs//2.2e-11:136:76//Hs.128815:AA678072
          R-PLACE1007511//ESTs, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens]//1.5e-41:261:
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89//Hs.9029:W57657

- R-PLACE1007524//ESTs//5.8e-45:297:87//Hs.154923:AA491377
- R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422:75//Hs.154326:D42087
- R-PLACE1007544//ESTs//8.4e-59:327:93//Hs.27410:N25612
- R-PLACE1007547//EST//0.00010:107:71//Hs.146867:Al161404
- 5 R-PLACE1007557//ESTs//1.6e-43:356:79//Hs.44702:Al148840
  - R-PLACE1007583//ESTs//1.7e-41:214:97//Hs.155071:AA584257
  - R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:554:93//Hs.21838:AF038179
  - R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)//0.54:l61:65//Hs.76506:J02923
  - R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537:94//Hs.151046:AF038176
- 10 R-PLACE1007632

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- R-PLACE1007645//ESTs//0.99:187:62//Hs.163453:AI344106
- R-PLACE1007649//ESTs//2.2e-108:561:94//Hs.24398:Al262946
- R-PLACE1007677//ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]// 9.0e-37:190:97//Hs.23437:AA707331
- 15 R-PLACE1007688//ESTs//7.5e-79:409:95//Hs.6166:Al376944
  - R-PLACE1007690//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum] //3.4e-61:384;89//Hs.92918:AA133274
  - R-PLACE1007697//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//1.8e-84:501:88//Hs. 91251:U66685
- 20 R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds//0.43:307:59//Hs.54481:D86407 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//5.7e-75:374:96//Hs.4812: AF061243
  - R-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-39:253:88//Hs.108797: AA476815
- 25 R-PLACE1007729//ESTs//2.7e-44:392:79//Hs.142375:AA398619
  - R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.7e-94:556:89//Hs.153121: AB014585
  - R-PLACE1007737//ESTs//1.1e-41:345:80//Hs.114671:N39322
  - R-PLACE1007743//ESTs//2.8e-17:98:100//Hs.124258:AA976778
- 30 R-PLACE1007746//ESTs//5.3e-69:413:90//Hs.5297:AA156903
  - R-PLACE1007791//ESTS, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]// 8.6e-27:143:98//Hs.144194:AA706337
  - R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9e-45:428:76//Hs.23094:M 9503 R-PLACE1007810//ESTs//5.9e-15:143:82//Hs.126257:Al279044
- 35 R-PLACE1007829//ESTs//2.2e-22:190:84//Hs.142707:W24050
  - R-PLACE1007843//ESTs//5.3e-110:556:95//Hs.107287:Al308839
  - R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525:91//Hs.23094:M19503 R-PLACE1007852//ESTs//4.5e-14:174:75//Hs.153419:N52017
  - R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574:94//Hs.28020:
    - R-PLACE1007866//EST//1.8e-48:262:96//Hs.141009:H01178
    - R-PLACE1007877//ESTs//1.2e-94:478:96//Hs.5999:Al207832
    - R-PLACE1007897//ESTs//2.3e-92:437:99//Hs.122843:Al189060
    - R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460:95//Hs. 92381:AB007956
  - R-PLACE1007946//ESTs//2.8e-28:172:78//Hs.126784:AA521510
    - R-PLACE1007954//ESTs//6.1e-72:366:95//Hs.27842:AI217966
    - R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509:96//Hs. 5671:AF084530
- 50 R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89: 465:93//Hs.78106:AF079529
  - R-PLACE1007969//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534:99//Hs.44268:AA455900
  - R-PLACE1007990//ESTs, Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster) //3.8e-97:493:95//Hs.6141:U69564
- 55 R-PLACE1008000//ESTs//0.00013:241:65//Hs.44369:AI206835
  - R-PLACE1008002//ESTs//2.2e-83:397:98//Hs.28780:Al263612
  - R-PLACE1008044//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus] //2.0e-115:575:95//Hs.92395:AA779854

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R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935
        R-PLACE1008080//EST//0.27:118:65//Hs.144110:AI054269
        R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469
        R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:Al309334
        R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028617
5
        R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511
        R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381
        R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:Al028266
        R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267
10
        R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107
        R-nnnnnnnnn/Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6e-104:551:93//Hs.10801:AB011102
        R-PLACE1008209//ESTs//L2e-72:366:96//Hs.92308:AI052701
        R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R80871
         R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990
         R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808
15
         R-nnnnnnnnnnn
         R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:Al338705
         R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852
         R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.53:206:62//Hs.79070:K02276
         R-PLACE1008330//ESTs, Weakly similar to EOSINOPHIL LYSOPHOSPHOLIPASE [H.sapiens]//8.6e-79:297:91//
20
         Hs.146477:Al128445
         R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656
         R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1e-99:556:90//Hs.5734:AB014579
         R-PLACE1008368//EST//0.0027:198:63//Hs.160868:Al359052
         R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009
25
         R-PLACE1008392//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-
         41:448:72//Hs.139007:H74314
         R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169:AA156242
         R-PLACE1008401//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-81:
30
         536:87//Hs.7570:W31010
         R-nnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds//5.1e-103:521:95//Hs.7763:D86326
         R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440
         R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:Al379778
         R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757
35
         R-PLACE1008429//ESTs//2.1e-12;188;71//Hs.140769;AA931562
         R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA001928
         R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761
         R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387
         R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:Al299636
         R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180
40
         R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816
         R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560
         R-PLACE1008532
         R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850
         R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:Al423223
45
         R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064
         R-PLACE1008621//ESTS, Weakly similar to line-1 protein ORF1 [H.sapiens]//8.6e-67:483:82//Hs.140416:
         AA778649
         R-nnnnnnnnnnn
         R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454
         R-PLACE1008627//ESTS//1.6e-90:475:93//Hs.102401:Al004972
         R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512
         R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:Al279612
         R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:79//Hs.153014:AB002353
         R-PLACE10086507/Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//7.9e-90:434:97//Hs.
55
         147967:AF044333
         R-PLACE1008693//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.51048:X68830
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R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.7e-51:316:

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76//Hs.1361:M55053
         R-PLACE1008715//EST//0.63:114:64//Hs.121353:AA758600
         R-PLACE1008748//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//2.3e-40:281:
         83//Hs.142209:AA873303
         R-PLACE1008757//ESTs//1.4e-45:226:99//Hs.22822:H06408
5
         R-PLACE1008790//ESTs//0.035;67;76//Hs.153554;Al286313
         R-PLACE1008798//ESTs//4.9e-59:285:99//Hs.49018:N79930
         R-PLACE1008807//ESTs//1.7e-82:413:96//Hs.130745:AA573217
         R-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//1.1e-98:499:
10
         95//Hs.7179:AF011905
         R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans cDNA cm10e3 [C.elegans]//4.2e-92:490:93//
         Hs.110454:H11810
         R-PLACE1008851//ESTs//2.4e-84:421:95//Hs.158893:AI378428
         R-nnnnnnnnnnnn
         R-PLACE1008867//ESTs//1.1e-77:400:95//Hs.44198:Al093502
15
         R-PLACE1008887//0xytocin receptor//1.1e-43:601:67//Hs.2820:X64878
         R-PLACE1008902//ESTs//0.023:208:61//Hs.154164:Al246893
         R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6e-56:344:89//Hs.62318:AB018308
         R-PLACE1008925//ESTs//0.17:294:57//Hs.105113:AA457018
         R-PLACE1008934//ESTs//2.0e-61:339:92//Hs.100448:AA622653
20
         R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]//
         1.3e-19:488:63//Hs.15780:U66680
         R-PLACE1008947//ESTs//1.3e-81:385:99//Hs.71574:Al376573
         R-PLACE1009020//ESTs//2.9e-79:419:94//Hs.121816:AA775419
         R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434:94//Hs.34780:AJ003112
25
         R-PLACE1009039//ESTs//2.8e-83:448:92//Hs.129179:AA988520
         R-PLACE1009045//ESTs//1.6e-64:318:97//Hs.103423:AA814195
         R-PLACE1009048//ESTs//2.7e-17:403:63//Hs.149343:Al249139
         R-PLACE1009050//ESTs//2.0e-88:475:92//Hs.122925:AA909008
         R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME
30
         III [Caenorhabditis elegans]//1.2e-112:555:96//Hs.9663:AA527142
         R-PLACE1009090//ESTs//5.0e-13:175:75//Hs.140608:N53448
         R-PLACE1009094//Human splicing factor SRp30c mRNA, complete cds//0.98:161:63//Hs.77608:AL021546
         R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.037:63:84//Hs.39943:AA203136
         R-PLACE1009110//EST//5.8e-17:307:65//Hs.117264:AA682549
35
         R-PLACE1009111//ESTs//1.9e-57:349:90//Hs.11260:N98983
         R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapiens]//6.5e-97:501:94//Hs.11123:
         R-PLACE1009150//LAMIN B1//0.064:393:60//Hs.89497:L37747
         R-PLACE1009155/TESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.5e-36:163:82//Hs.
40
         93332-AA811920
         R-PLACE1009158//ESTs//0.30:149:65//Hs.155796:R80005
         R-PLACE1009166//ESTs//3.3e-34:292:77//Hs.140255:AA708322
         R-PLACE1009172//EST//8.9e-21:364:67//Hs.142557:AA464948
         R-PLACE1009174//ESTs//2.9e-18:274:70//Hs.139241:AA283707
45
         R-PLACE1009183//ESTs//2.3e-44:297:87//Hs.136839:H93717
         R-PLACE10091867/ESTs, Weakly similar to No definition line found [C.elegans]//1.5e-109:572:94//Hs.54943:
         R-PLACE1009190//ESTs//2.6e-53:318:90//Hs.25245:AA176701
         R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33:195:92//Hs.104247:X98248
50
         R-PLACE1009230//ESTs//3.0e-31:153:92//Hs.124116:AA772680
         R-PLACE1009246//ESTs//2.7e-90:488:92//Hs.10706:AA909018
         R-PLACE1009308//ESTs//0.022:46:97//Hs.36545:AA075423
         R-PLACE1009319//ESTs//7.7e-99:533:92//Hs.109654:N91279
         R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//7.3e-82:578:82//Hs.23094:M19503
55
         R-PLACE1009335//EST//1.3e-64:311:99//Hs.130558:AI004397
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R-PLACE1009338//ESTs//6.0e-70:386:93//Hs.3542:AI015782 R-PLACE1009368//ESTs//1.4e-18:107:98//Hs.133303:W04760

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R-PLACE1009375//ESTs//8.9e-36:313:76//Hs.24608:AA161260
        R-PLACE1009388//EST//4.4e-11:101:83//Hs.147074:Al188883
        R-PLACE1009398//ESTs//5.7e-63:335:93//Hs.149003:AI243186
        R-nnnnnnnnnnnn//ESTs//3.6e-94:452:98//Hs.103177:W72798
        R-PLACE1009410//ESTs//2.2e-112:553:96//Hs.61779:AA195255
5
        R-PLACE1009434//EST//3.4e-15:109:74//Hs.103742:U48632
        R-PLACE1009443//EST//7.5e-61:302:98//Hs.157787:Al361269
        R-PLACE1099444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//6.6e-85:479:90//Hs.76987:AF012872
        R-PLACE1009459//ESTs//9.3e-86:437:95//Hs.104871:Al161427
        R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//1.3e-42:266:89//Hs.155049:
10
        AC004531
        R-PLACE1009477//ESTs//2.0e-50:367:82//Hs.152788:AA630925
        R-PLACE1009493//ESTs//4.5e-14:150:78//Hs.143918:AA699596
         R-PLACE1009524//ESTs//2.9e-97:454:99//Hs.7189:AA767698
         R-PLACE1009539//ESTs//9.1e-94:454:97//Hs.154706:AI262131
15
         R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.4e-10:
         289:63//Hs.77579:AF013263
         R-PLACE1009571//ESTs//2.1e-23:125:100//Hs.41767:AA732326
         R-PLACE1009581//ESTS, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHAIN PRECURSORS [H.
         sapiens]//0.0012:56:91//Hs.12151:AA001818
20
         R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.0e-42:547:70//Hs.69157:
         AB014535
         R-PLACE1009596//ESTs//1.9e-102:588:90//Hs.142395:Al374735
         R-PLACE1009607//ESTs//0.0093:107:70//Hs.70932:AA126482
         R-PLACE1009613//ESTs//7.5e-101:488:97//Hs.5905:AA946680
25
         R-PLACE1009621//EST//0.99:261:60//Hs.149030:Al243338
         R-PLACE1009622//ESTs//8.0e-93:508:92//Hs.20967:Al422858
         R-PLACE1009637//EST//8.7e-90:442:97//Hs.121372:AA758701
         R-PLACE1009639//EST//8.5e-49:279:93//Hs.117447:R27213
         R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.3e-109:589:92//Hs.21862:
30
         R-PLACE1009665//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//9.9e-62:483:79//Hs.140416:
         R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:310:97//Hs.109590:AF062534
         R-PLACE1009708//ESTs//3.Oe-94:471:96//Hs.40091:N48582
35
         R-PLACE1009721//ESTs, Weakly similar to MSF1 PROTEIN [S.cerevisiae]//4.2e-98:529:92//Hs.3945:AA004210
         R-PLACE1009731/TESTs, Weakly similar to immune associated protein 38 [M.musculus]//6.8e-85:489:89//Hs.
         R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:598:95//Hs.154320:AF046024
         R-PLACE1009794//ESTs//7.9e-102:529:95//Hs.42927:N20989
40
         R-nnnnnnnnnnn/Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubi-
         quinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene
         Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene
         similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//1.1e-
45
         113:549:97//Hs.16411:AL030996
         R-PLACE1009845//ESTs//9.5e-106:560:93//Hs.117751:AI056868
         R-PLACE1009879//ESTs//1.8e-61:399:86//Hs.141012:R68748
         R-PLACE1009886//EST//0.54:153:64//Hs.144281:AA081328
         R-PLACE1009888//ESTs//2.7e-105:520:97//Hs.108646:AA613031
         R-nnnnnnnnnnn//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//1.6e-114:594:94//Hs.67466:
50
         AI219740
         R-PLACE1009921//ESTs//7.6e-05:291:60//Hs.124786:AA825563
         R-PLACE1009924//EST//1.2e-42:216:98//Hs.31742:H20276
         R-PLACE1009925//ESTs//5.4e-30:154:100//Hs.114605:AI04317
         R-PLACE1009935//ESTs//1.4e-83:417:97//Hs.131755:AA496543
55
         R-PLACE1009947//Keratin 9//1.0:273:61//Hs.2783:Z29074
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R-PLACE1009971//ESTs//1.5e-87:424:98//Hs.13781:Al160540 R-PLACE1009992//ESTs//1.3e-87:531:87//Hs.55044:AA460698

R-PLACE1009995//ESTs//1.3e-103:575:91//Hs.71218:C75347

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R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286:86//Hs.155464:AF088219
        R-PLACE1010023//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:
        AI141736
        R-PLACE1010031//ESTs//0.22:191:62//Hs.127787:AA832204
5
        R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spur [M.musculus]//
        7.6e-104:546:94//Hs.8215:AA521150
        R-PLACE1010069//ESTs//0.99:173:59//Hs.21415:Al150905
        R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.5e-88:543:88//Hs.
10
         11183AF065482
        R-PLACE1010076//ESTs//3.4e-106:530:95//Hs.28005:AA604375
         R-PLACE1010083//ESTs//4.1e-65:395:88//Hs.6103:AA496424
         R-PLACE1010089//ESTs//1.6e-70:348:97//Hs.9011:AA418615
        R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//2.8e-104:565:92//Hs.11469:
         U69567
15
         R-PLACE1010102//ESTs//7.7e-50:311:89//Hs.5518:AI052015
         R-PLACE1010105//ESTs//6.0e-94:483:94//Hs.62684:AA806103
         R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens]//1.6e-107:575:93//Hs.48301:AA122270
         R-PLACE1010134//EST//8.5e-59:314:94//Hs.135005:AI095130
         R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79//0.52:351:56//Hs.48714:M90359
20
         R-PLACE1010152//ESTS//1.9e-40:240:90//Hs.17054:AI139897
         R-PLACE1010181//ESTs//3.6e-64:307:99//Hs.154163:AJ003313
         R-PLACE1010194//ESTs//2.7e-70:366:96//Hs.5301:T58466
         R-PLACE1010202//ESTs//0.57:120:67//Hs.58873:W95037
25
         R-PLACE1010231
         R-PLACE1010261//EST//6.9e-50:251:98//Hs.148208:AA897478
         R-PLACE1010270//ESTs//1.9e-87:430:96//Hs.25252:Al079545
         R-PLACE1010274//ESTs//1.9e-57:439:81//Hs.30078:H04535
         R-PLACE1010293//ESTs//8.1e-41:310:81//Hs.146811:AA410788
         R-PLACE1010321//ESTs//5.7e-50:246:99//Hs.151445:AA351081
30
         R-PLACE1010324//ESTs//0.00025:377:60//Hs.97430:AA398568
         R-PLACE1010329//Small inducible cytokine A5 (RANTES)//2.4e-40:300:82//Hs.155464:AF088219
         R-PLACE1010341//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.9e-
         32:190:77//Hs.152369:AA504818
         R-PLACE1010362//ESTs//8.2e-86:404:99//Hs.25625:AA669327
35
         R-PLACE1010364//ESTs//1.5e-105:556:93//Hs.12229:AA149594
         R-PLACE1010383//Homo sapiens mRNA for putative lipoic acid synthetase, partial//4.9e-35:166:86//Hs.53531:
         R-PLACE1010401//ESTs//2.3e-85:450:93//Hs.23193:AA418152
         R-PLACE1010481//ESTs//0.012:280:59//Hs.5579:Al392816
40
         R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//2.4e-89:438:96//Hs.13313:
         AF039081
         R-PLACE1010492
         R-PLACE1010522//EST//0.43:82:68//Hs.89303:AA284031
         R-nnnnnnnnnn//ESTs//3.4e-36:228:89//Hs.128724:AA215455
45
         R-PLACE1010562//ESTs//4.8e-68:408:90//Hs.17244:W86306
         R-PLACE1010579//EST//0.015:193:63//Hs.67093:C14033
         R-PLACE1010580//ESTs//2.4e-93:445:98//Hs.127325:AA234116
         R-PLACE1010599
         R-PLACE1010616//ESTs//2.9e-101:497:97//Hs.142197:AA573418
50
         R-PLACE1010622//ESTs//7.1e-23:157:91//Hs.159877:N57895
         R-PLACE1010624//ESTs//1.4e-89:428:98//Hs.116561:AA658475
         R-PLACE1010628//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.4e-74:
          391:95//Hs.163495:W57637
         R-PLACE1010629//ESTs//5.8e-75:359:99//Hs.123630:AI250805
55
          R-PLACE1010630//ESTs//9.5e-101:519:94//Hs.77873:AA731719
          R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//8.3e-94:497:93//Hs.10801:AB011102
          R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN PBS13 [Mus musculus]//4.8e-83:467:
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91//Hs.22383:R51067
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R-PLACE1010662//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//8.3e-103:538:94//Hs.105794:AA701659

R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152//4.8e-46:531:71//Hs.55452:AC003973

5 R-PLACE1010714//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.0074:351:60//
Hs.46440:U21943

R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.2e-56:300: 95//Hs.50758:AF092564

R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189

10 R-PLACE1010743

R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-94:442:96//Hs.3688:AF069250

R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024

R-PLACE1010786//ESTs, Highly similar to MYOSIN HEAVY CHAIN IB [Acanthamoeba castellanii]//7.6e-111:575:

15 94//Hs.10260:Al126627

R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558

R-PLACE1010802//ESTs//0.00021:428:5 8//Hs.70258:Al091203

R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896

R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472

20 R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048

R-PLACE1010857//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.4e-71:326:92//Hs.3385:N25917

R-PLACE1010870//ESTs//5.8e-57:303:96//1Hs.30503:H05090

R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087: AB011182

25 R-PLACE1010891

R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983

R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023

R-PLACE1010916//Plasminogen activator inhibitor, type II (arginine-serpin)//0.25:190:61//Hs.75716:Y00630

R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093

30 R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:Al125479

R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126 R-nnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds//8.9e-82:441:93//Hs.66392: AF064244

R-PLACE1010944

35 R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519

R-PLACE1010954//Small inducible cytokine A5 (RANTES)//8.8e-51:278:93//Hs.155464:AF088219

R-PLACE1010960//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.0e-103:565: 92//Hs.23259:AA532437

R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580

40 R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:Al199846

R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867

R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249

R-nnnnnnnnnnn/Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4e-102:563:91//Hs.41143:AB011153 R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135

45 R-PLACE1011056//Small inducible cytokine A5 (RANTES)//3.5e-38:285:82//Hs.155464:AF088219

R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537

R-PLACE1011090//ESTS. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-54: 398:84//Hs.108740:W20094

R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:Al149478

50 R-PLACE101111 4//ESTs//5.4e-90:475:94//Hs.69331:AA099587

R-PLACE1011133//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//3.0e-105:552:93//Hs.31257:

R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795

R-PLACE1011160//Homa sapiens mRNA for HRIHFB2038, partial cds//7.7e-97:534:91//Hs.28719:AB015333

55 R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:Al374673

R-PLACE1011185//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.4e-85:442: 95//Hs.136910:AA810782

R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438

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R-PLACE1011219//ESTs//7.6e-96:504:93//Hs.124834:Al138671
        R-PLACE1011221//ESTs//5.2e-23:241:78//Hs.26761:AA203299
         R-PLACE1011229//ESTs//1.9e-90:461:95//Hs.132288:AI027693
         R-PLACE1011263//ESTs//6.6e-56:321:93//Hs.158787:W79602
         R-PLACE1011273//ESTs//0.016:131:65//Hs.140466:AA766772
5
         R-PLACE1011291//EST//8.7e-47:267:91//Hs.158806:AI376913
         R-PLACE1011296//EST//2.7e-38:225:92//Hs.160934:Al376849
         R-PLACE1011310//ESTs//9.1e-37:196:96//Hs.39328:H71807
         R-PLACE1011325//Human clone 23721 mRNA sequence//0.0012:486:58//Hs.83572:U79291
         R-PLACE1011332//ESTs//8.4e-44:217:99//Hs.101365:R60578
10
         R-PLACE1011340//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//3.4e-
         92:452:97//Hs.144194:AA706337
         R-PLACE1011375//ESTs//2.2e-35:195:96//Hs.106486:H11376
         R-PLACE1011399//ESTs//0.00096:224:67//Hs.151643:AA001194
         R-PLACE1011419//ESTs//4.9e-50:267:95//Hs.7045:AA167337
15
         R-nnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//4.8e-114:600:94//Hs.10801:
         AB011102
         R-PLACE1011452//Homo sapiens mRNA for KIAA0707 protein, partial cds//3.7e-32:310:76//Hs.138488:
         AB014607
         R-PLACE1011465//ESTs//4.5e-86:471:93//Hs.144519:R70887
20
         R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//2.6e-104:515:96//Hs.111138:
         R-PLACE1011492//ESTs//1.7e-96:488:95//Hs.116555:AA639278
         R-PLACE1011503//Homo sapiens clone 23597 mRNA sequence//1.0:193:60//Hs.28197:AF035294
         R-PLACE1011520//ESTs//6.8e-99:477:97//Hs.85077:AA968576
25
         R-PLACE1011563//ESTs//1.4e-94:514:92//Hs.16471:AA206421
         R-PLACE1011567//EST//2.8e-89:417:100//Hs.149770:AI285985
         R-PLACE1011576//Zinc finger protein 91 (HPF7, HTF10)//4.7e-55:267:81//Hs.8597:L11672
         R-PLACE1011586//Myosin, heavy polypeptide 11, smooth muscle//0.98:168:61//Hs.78344:AF001548
         R-PLACE1011635//ESTs//2.5e-67:332:98//Hs.108194:AA780067
30
         R-PLACE1011641//ESTs//2.5e-71:J38:100//Hs.153085:AA993965
         R-PLACE1011643//EST//1.9e-18:181:78//Hs.160879:Al361900
         R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence//2.5e-73:414:91//Hs.78019:AF070535
         R-PLACE1011650//EST//5.8e-18:118:92//Hs.124486:AA846036
          R-PLACE1011664//Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)//0.50:178:
35
         62//Hs.31638:X64838
         R-PLACE1011675
         R-PLACE1011682//ESTs//2.4e-90:465:94//Hs.57830:Al312025
          R-PLACE1011719//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-57:410:83//Hs.23094:M19503
          R-PLACE1011725//ESTs//2.0e-70:340:98//Hs.161725:AA251392
40
          R-PLACE1011729//ESTs//7.5e-19:180:79//Hs.119516:AA443426
          R-PLACE1011749//Myelin oligodendrocyte glycoprotein {alternative products}//7.3e-40:361:77//Hs.53217:
         Z48051
          R-PLACE1011762//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-60:319:76//Hs.103948:K00627
          R-PLACE1011778//ESTs//8.0e-70:372:94//Hs.46765:AA521080
45
          R-PLACE1011783//Calcium modulating ligand//8.4e-41:279:85//Hs.13572:AF068179
          R-PLACE1011858//ESTs//2.6e-69:396:91//Hs.55220:D11563
          R-PLACE1011874//Human mRNA for KIAA0033 gene, partial cds//1.2e-53:439:80//Hs.22271:D26067
          R-PLACE1011875//ESTs//9.0e-88:420:98//Hs.70897:AA987648
          R-PLACE1011891//ESTs//3.9e-17:97:100//Hs.84698:AA725913
50
          R-PLACE1011896//ESTs//2.8e-23:176:84//Hs.121540:Al275497
          R-PLACE1011922//ESTs//6.6e-35:415:73//Hs.10972:AA164268
          R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//2.3e-99:546:92//Hs.3838:
          R-PLACE1011962//ESTs//3.3e-49:294:90//Hs.106800:AI031969
 55
          R-PLACE1011964//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.6e-
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06:284:63//Hs.124102:AA701285

R-PLACE1011982//ESTs//2.9e-51:291:93//Hs.20792:R14890

- R-PLACE1011995//ESTs//4.5e-39:304:81//Hs.138852:AA284247
- R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0e-106:540:95//Hs.88756: AR018256
- R-PLACE2000003//ESTs//2.0e-103:488:98//Hs.8341:AA490069
- 5 R-PLACE2000007//ESTs//2.4e-110:564:95//Hs.65135:W89120
  - R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//4.8e-105:524:95//Hs.21811:
  - R-PLACE2000015//ESTs//7.1e-111:543:96//Hs.32178:AA083211
  - R-PLACE2000017//EST//8.2e-46:404:79//Hs.133006:Al049504
- 10 R-PLACE2000021//EST//4.5e-19:221:71//Hs.150830:Al302868
  - R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.6e-43:355:79//Hs. 154069:U06452
  - R-PLACE2000034//ESTs//2.2e-21:314:70//Hs.107697:W29013
  - R-PLACE2000039//H.sapiens mRNA for translin associated protein X//2.9e-45:514:72//Hs.96247:X95073
- R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//4.1e-45:358:81//Hs.159523:AF001622
  - R-PLACE2000050//ESTs//4.5e-65:322:98//Hs.155820:N67652
  - R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.2e-41:429:72//Hs.153468:
- 20 R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296:86//Hs.40100:AB002390 R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6.2e-111:550:95//Hs.9443: AF027219
  - R-PLACE2000097//Calcium modulating ligand//6.2e-47:372:80//Hs.13572:AF068179
  - R-PLACE2000100//ESTs//8.8e-42:281:86//Hs.150727:Al292236
- 25 R-PLACE2000103//ESTs//4.7e-97:518:93//Hs.118727:W26941
  - R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00043:127:71//Hs. 42400:AF022789
  - R-PLACE2000115//ESTs//7.8e-93:458:96//Hs.104520:AA481662
  - R-PLACE2000132//ESTs//3.8e-69:409:91//Hs.98502:AA433988
- 30 R-PLACE2000136//ESTs//6.2e-05:274:61//Hs.114067:AA701558
  - R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.7e-44:302:85//Hs.118401: AB011134
  - R-PLACE2000164//ESTs//6.3e-106:506:98//Hs.16390:AI052357
  - R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326:79//Hs.155464:AF088219
- 35 R-PLACE2000172//ESTs//9.6e-43:232:94//Hs.6709:Al379778
  - R-PLACE2000176//EST//1.6e-24:154:91//Hs.157734:Al360292
  - R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292:90//Hs.22271:D26067
  - R-PLACE2000216//ESTS//0.0041:166:64//Hs.159476:Al382378
  - R-PLACE2000223//ESTs//0.49:171:60//Hs.86154:AA207191
- 40 R-PLACE2000235//ESTs//2.9e-39:264:85//Hs.136839:H93717
  - R-PLACE2000246//NAD(P)H:menadione oxidoreductase//4.0e-44:331:82//Hs.80706:M81600
  - R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds/4.0e-38:311:81//Hs.84123:AB002363
  - R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H.sapiens]//1.9e-87:422:98//Hs.9740: Al004779
- 45 R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//
  4.8e-68:380:92//Hs.107365:AA720664
  - R-PLACE2000305//ESTs//2.6e-43:413:75//Hs.I18732:AI344055
  - R-PLACE2000317//ESTs//2.8e-92:501:92//Hs.28432:R83380
  - R-PLACE2000335//ESTs//4.3e-32:300:77//Hs.163035:AA748058
- 50 R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00071:117:73//Hs. 42400:AF022789
  - R-PLACE2000347//ESTs//1.6e-30:214:86//Hs.135272:Al347618
  - R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288:86//Hs.140090:U09848
  - R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:392:82//Hs.89887:D38081
- 55 R-PLACE2000371//ESTs//3.6e-81:409:97//Hs.155138:AA158731
  - R-PLACE2000373//Homo sapiens mRNA for KIAA0734 protein, partial cds//0.89:186:62//Hs.101516:AB018277
  - R-PLACE2000379//ESTs//3.4e-10:228:64//Hs.57842:W63781
  - R-PLACE2000394//ESTs//6.7e-41:462:74//Hs.107657:AA126814

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R-PLACE2000398//ESTs//4.2e-33:373:74//Hs.155184:AA573189
        R-PLACE2000399
        R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC [Saccharomyces cer-
        evisiae]//4.2e-109:540:96//Hs.6762:AA088424
        R-PLACE2000411//ESTs//1.6e-89:459:95//Hs.117589:N25941
5
        R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [C.elegans]//1.6e-97:436:95//Hs.24647:W19739
        R-PLACE2000425//Homo sapiens PEC-205 mRNA, complete cds//2.2e-44:287:88//Hs.153563:AF011333
        R-PLACE2000427//ESTs, Weakly similar to coded for by C. elegans cDNA CEESI42F [C.elegans]//3.0e-113:543:
        97//Hs.16933:AA976002
        R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523
10
        R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.90964:AA393986
        R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:Al279887
         R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:74//Hs.40100:AB002390
        R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714
         R-PLACE2000458//ESTs//6.8e-92:473:96//Hs.115897:AA156638
15
         R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79228
         R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642
         R-PLACE3000004//ESTs//9.1e-114:558:97//Hs.13035:AA151838
         R-PLACE3000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.3e-64:350:86//Hs.153468:
20
         R-PLACE3000059//EST//0.028:175:61//Hs.159873:R92763
         R-PLACE3000070//ESTs//3.8e-16:200:74//Hs.138771:N70979
         R-PLACE3000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.51048:X68830
         R-PLACE3000119//ESTs//1.2e-45:330:83//Hs.35254:Al133727
         R-PLACE3000124//EST//3.1e-75:391:96//Hs.161515:N71739
25
         R-PLACE3000136//ESTs//8.3e-18:152:84//Hs.10043:D81792
         R-PLACE3000142//ESTs//0.047:183:62//Hs.43102:AA131369
         R-PLACE3000147//ESTs//6.6e-53:310:90//Hs.8230:W07142
         R-PLACE3000148//EST//1.9e-16:184:76//Hs.146570:Al139815
         R-PLACE3000155//ESTS//1.2e-19:192:79//Hs.131350:AA805223
30
         R-PLACE3000156//ESTs, Highly similar to ENV POLYPROTEIN [Avian spleen necrosis virus]//4.8e-36:262:88//
         Hs.31532:H18272
         R-PLACE3000157
         R-PLACE3000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs.155464:AF088219
35
         R-PLACE3000160
         R-PLACE3000169//ESTs//1.5e-64:329:97//Hs.129864:R20798
         R-PLACE3000194
         R-PLACE3000197//ESTs//1.4e-3 8:197:98//Hs.146341:Al269930
         R-PLACE3000199//ESTs, Highly similar to APOLIPOPROTEIN E PRECURSOR [Sus scrofa]//0.018:261:61//Hs.
40
         131370:AA927516
         R-PLACE3000207//EST//1.3e-15:154:78//Hs.136617:AA630476
         R-PLACE3000208//ESTS//1.6e-18:151:82//Hs.155498:W27084
         R-PLACE3000218//ESTs//1.8e-85:463:93//Hs.7849:AI129964
         R-PLACE3000220//ESTs//6.4e-44:308:84//Hs.136839:H93717
         R-PLACE3000226//ESTs//L3e-49:269:95//Hs.9059:Al359014
45
         R-PLACE3000230//EST//2.3e-34:258:83//Hs.4382:T02878
         R-PLACE3000242//Human trophinin mRNA, complete cds//1.1e-63:546:78//Hs.76313:U04811
         R-PLACE3000244//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [Emericella nidulans]//7.5e-
          110:549:95//Hs.13692:AA632002
          R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:94//Hs.87908:AB002307
50
          R-PLACE3000271//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.3e-62:287:
          82//Hs.97203:U83171
          R-PLACE3000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782
          R-PLACE3000304//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, com-
          plete cds//4.0e-59:456:80//Hs.108966:U48696
55
          R-PLACE3000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45:302:86//Hs.51048:X68830
          R-PLACE3000320//Interleuldn 10//9.6e-42:288:85//Hs.2180:M57627
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R-PLACE3000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [Homo sapiens]//5.8e-34:190:95//Hs.

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114531:N74103
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R-PLACE3000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.7e-32:239:84//Hs.15519: AB018315

R-PLACE3000339//ESTs//1.3e-109:548:96//Hs.7871:AI041837

R-PLACE3000341//EST//1.1e-11:231:68//Hs.131328:AA922688

R-PLACE3000350//Human mRNa for adipogenesis inhibitory factor//8.0e-40:291:76//Hs.1721:X58377

R-PLACE3000352//EST//1.8e-72:343:100//Hs.144871:Al202380

R-PLACE3000353//ESTs//2.0e-75:395:95//Hs.107260:W52683

R-PLACE3000362//EST//2.8e-80:381:99//Hs.136233:AA261888

10 R-PLACE3000363

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R-PLACE3000365//EST//4.8e-50:307:88//Hs.149580:Al281881

R-PLACE3000373//ESTs//5.8e-60:422:83//Hs.142826:W87430

R-PLACE3000388//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-35:427:73//Hs.138795:R98534

15 R-PLACE3000399//ESTs//6.5e-05:162:66//Hs.149440:Al274570

R-PLACE3000400//ESTs//8.3e-05:310:63//Hs.17697:AA287528

R-PLACE3000401//ESTs//4.6e-60:326:80//Hs.139555:N48230

R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227:62//Hs.142570:AF052I60

R-PLACE3000405//Human HsLIM15 mRNA for HsLim15, complete cds//5.3e-43:315:82//Hs.37181:D64108

20 R-PLACE3000406//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.4e-47:302:87// Hs.73614:U83460

R-PLACE3000413//ESTs//1.6e-116:571:97//Hs.10235:H93077

R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300:85//Hs.155464:AF088219

R-PLACE3000425//Homo sapiens 4F5S mRNA, complete cds//1.6e-46:307:85//Hs.32567:AF073519

25 R-PLACE3000455//ESTs//1.0:160:64//Hs.156045:AA884461

R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds//6.1e-84:440:92//Hs. 153487:U43899

R-PLACE3000477//ESTs//2.4e-113:568:96//Hs.24557:AA142980

R-PLACE4000009//ESTs//1.5e-72:361:96//Hs.10119:AA700227

30 R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//8.8e-85:433:95//Hs.105399: AB018352

R-PLACE4000034//ESTs//7.0e-110:550:96//Hs.76607:AA156240

R-PLACE4000049//EST//0.028:87:75//Hs.89303:AA284031

R-PLACE4000052//ESTs//5.6e-116:553:98//Hs.19067:AA521292

R-PLACE4000063//ESTs//5.0e-80:388:98//Hs.135028:AI096444

R-PLACE4000089//ESTs//2.3e-97:479:97//Hs.102425:AA807547

R-PLACE4000093//ESTs//1.5e-82:391:99//Hs.160730:Al142739

R-PLACE4000100

R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.7e-98:419:91//Hs.129937:

40 AB007931

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R-PLACE4000128//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.8e-11:184:71//Hs.154278:N45985

R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//5.2e-21:118:100//Hs. 118164:AB007969

45 R-PLACE4000147//EST//1.6e-23:175:79//Hs.162236:AA551582

R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.0e-47:306:88//Hs.153468: AB011147

R-PLACE4000192//ESTs, Weakly similar to similar to Human zinc finger protein(ZNF142) [H.sapiens]//6.7e-31: 232:82//Hs.16493:T92186

50 R-PLACE4000222//ESTs//2.2e-53:195:85//Hs.141575:AA211734

R-PLACE4000233//ESTs//2.9e-81:456:93//Hs.124964:R81949

R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5e-72:307:85//Hs.113283:AF018080

R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:83//Hs.155464:AF088219

R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216

R-PLACE4000261//EST//0.0063:384:58//Hs.136284:AA400442

R-PLACE4000269//ESTs//7.3e-67:345:97//Hs.5000:R44586

R-PLACE4000270//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-37: 352:77//Hs.77579:AF013263

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R-PLACE4000300//EST//0.26:103:68//Hs.144438:AA780782
        R-PLACE4000320//EST//2.7e-44:298:85//Hs.162404:AA573131
        R-PLACE4000323//ESTs//8.8e-38:178:79//Hs.155475:AA761454
        R-PLACE4000326//ESTs//7.4e-103:516:96//Hs.55042:AA150460
        R-PLACE4000344//ESTs//9.9e-94:463:96//Hs.100057:AA001414
        R-PLACE4000367//ESTs//0.81:102:73//Hs.107692:H38478
        R-PLACE4000369//ESTs//1.5e-69:390:92//Hs.13733:AA418656
        R-PLACE4000379//ESTs//1.3e-67:373:91//Hs.48569:AA905425
        R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.9e-
        44:379:78//Hs.152369:AA504818
10
        R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//2.3e-70:482:83//Hs.140416:
        AA778649
         R-PLACE4000401//ESTs//1.3e-18:151:84//Hs.150355:AI273502
         R-PLACE4000411//ESTs//1.1e-108:543:96//Hs.23901:AA169780
         R-PLACE4000445//ESTs, Weakly similar to C05D9.6 gene product [C.elegans]//2.6e-111:530:98//Hs.12003:
15
         AA643063
         R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//8.5e-58:409:
         72//Hs.1361:M55053
         R-PLACE4000489//ESTs//5.0e-70:342:98//Hs.72865:Al380932
         R-PLACE4000494//EST&//1.4e-109:525:98//Hs.22539:Al334210
20
         R-PLACE4000522//ESTs//6.3e-88:471:93//Hs.8121:AA521290
         R-PLACE4000548//ESTs//3.3e-86:441:96//Hs.5070:AA149527
         R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425:76//
         Hs.23590:U59185
         R-THYRO1000026//ESTs//2.6e-42:331:82//Hs.137875:AA993532
25
         R-THYRO1000034//ESTs//2.1e-43:214:100//Hs.153018:AI243524
         R-THYRO1000035//ESTs//7.6e-52:325:90//Hs.49817:AA001249
         R-THYRO1000040//ESTs//1.7e-94:459:98//Hs.48712:Al027889
         R-THYRO1000070//ESTs//6.7e-43:283:86//Hs.37573:H59651
         R-THYRO1000072//ESTs//1.3e-57:313:96//Hs.127827:H13438
30
         R-THYRO1000085//ESTs//1.1e-90:439:98//Hs.150539:AA908435
         R-THYRO1000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-41:344:79//Hs.153014:AB002353
         R-THYRO1000107//Interieuldn 10//2.8e-43:292:84//Hs.2180:M57627
         R-THYRO1000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//
         1.0e-52:413:80//Hs.140385:AA773359
35
         R-THYRO1000121//EST//0.24:78:74//Hs.156632:Al345108
         R-THYRO1000124//ESTs//2.8e-86:428:96//Hs.141634:AI122764
         R-THYRO1000129//Homo sapiens TED protein (TED) mRNA, complete cds//6.8e-90:449:96//Hs.87619:
         AF087142
         R-THYRO1000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//5.2e-
40
         49:486:77//Hs.24164:N95217
         R-THYRO1000156//ESTs//6.1e-36:344:75//Hs.70279:AA757426
         R-THYRO1000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-38:278:84//Hs.154103:AF061258
         R-THYRO1000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//1.1e-
          111:554:96//Hs.18894:AA910946
45
         R-THYRO1000186//ESTs//1.0e-44:339:83//Hs.155184:AA573189
         R-THYRO1000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305:81//Hs.155464:AF088219
         R-THYRO1000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301:85//Hs.155464:AF088219
          R-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//3.6e-110:535:97//Hs.43445:
50
          AJ005698
          R-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.3e-115:559:97//Hs.79672:
          AB014552
          R-THYRO1000206//ESTs//3.1e-90:507:90//Hs.32456:W29063
          R-THYRO1000221//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING
          ENTRY !!!! [H.sapiens]//1.1e-72:357:98//Hs.140002:AA635349
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R-THYRO1000242//ESTs//4.2e-27:222:85//Hs.77554:W87927

R-THYRO1000241//Homo sapiens mRNA for KIAA0688 protein, complete cds//7.8e-69:524:82//Hs.141874:

AB014588

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R-THYRO1000253//Sialophorin (gpL115, leukosialin, CD43)//7.3e-40:318:80//Hs.80738:X52075
R-THYRO1000270//ESTs//1.9e-99:531:94//Hs.17767:N62925
R-THYRO1000279//EST//2.7e-54:266:99//Hs.149527:AI280674
R-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds//3.5e-100:566:91//Hs.25846:AB016068
R-THYRO1000320//POLYPOSIS LOCUS PROTEIN 1//1.0:321:58//Hs.74648:M73547
R-THYRO1000327//Autocrine motility factor receptor//9.2e-54:289:93//Hs.80731:M63175
R-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//3.4e-113:559:96//Hs.12002:
AB018333
R-THYRO1000358//Human selenium-binding protein (hSBP) mRNA, complete cds//1.5e-48:317:87//Hs.7833:
1129091
R-THYRO1000368//ESTs//4.7e-88:430:98//Hs.146085:AA021064
R-nnnnnnnnn//ESTs//1.0:253:57//Hs.128783:AA436250
R-THYRO1000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds//4.6e-69:
294:84//Hs.151614:AF032456
R-THYRO1000394//Thromboxane A2 receptor//4.1e-40:232:87//Hs.89887:D38081
R-THYRO1000395//ESTs//3.3e-20:160:83//Hs.101570:AA505429
R-THYRO1000401//ESTs//1.3e-109:516:99//Hs.78524:Al140601
R-THYRO1000438//ESTs//2.1e-48:360:83//Hs.141203:H52638
R-THYRO1000452//ESTs, Weakly similar to No definition line found [C.elegans]//8.5e-40:239:90//Hs.84009:
AI309761
R-THYRO1000471//ESTs//3.3e-36:302:80//Hs.70279:AA757426
R-THYRO1000484//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.2e-49:479:75//Hs.17630:
AB018280
R-THYRO1000488//Homa sapiens mRNA for HRIHFB2038, partial cds//4.1e-89:471:94//Hs.28719:AB015333
R-THYRO1000501//ESTs//L5e-46:287:89//Hs.125300:R62360
R-THYRO1000502//ESTs//1.7e-08:63:96//Hs.116319:Al208005
R-THYRO1000505//ESTs, Weakly similar to KIAA0281 [H. sapiens]//3.9e-57:286:96//Hs.105861:AI206965
R-THYRO1000558//ESTs//1.7e-95:454:99//Hs.125063:AA648511
R-THYRO1000569//ESTs//3.2e-89:463:94//Hs.20555:W22193
R-THYRO1000570//ESTs//2.8e-97:471:97//Hs.8245:AA115485
R-nnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds//2.6e-108:533:97//Hs.151411:
R-THYRO1000596//ESTs//3.1e-99:527:94//Hs.6084:AA045247
R-THYRO1000602//EST//6.9e-50:381:83//Hs.161917:AA483223
R-THYRO1000605//ESTs, Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens]//1.2e-96:483:96//
Hs.21907:N24415
R-THYRO1000625//ESTs//5.6e-36:257:84//Hs.139657:AA191742
R-THYRO1000637
R-THYRO1000641//ESTs, Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H.
sapiens]//4.9e-46:245:95//Hs.97398:AA398634
R-THYRO1000658//ESTs//5.8e-48:281:90//Hs.142259:AA828840
R-nnnnnnnnn//ESTs//1.5e-82:389:99//Hs.155573:AA487384
R-THYRO1000666//ESTs//1.4e-26:179:88//Hs.98382:AA779866
R-THYRO1000676//EST//6.4e-05:88:77//Hs.133424:Al061063
R-THYRO1000684//ESTs//1.9e-69:374:94//Hs.144617:R77109
R-THYRO1000699//ESTs//1.7e-58:394:86//Hs.26373:AA700713
R-THYRO1000712
R-THYRO1000734//EST//2.0e-06:95:73//Hs.156201:AA724287
R-THYRO1000748//EST//4.1e-12:155:74//Hs.118694:AA148713
R-THYRO1000756//ESTs, Weakly similar to CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-AL-
PHA-2,3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497:87//Hs.109672:W22624
R-THYRO1000777
R-THYRO1000783//EST//5.6e-100:470:99//Hs.123515:AA812932
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R-THYRO1000815//Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307:87//Hs.22271:D26067

R-THYRO1000787//EST//8.0e-34:175:99//Hs.99607:AA463897 R-THYRO1000793//ESTs//2.2e-106:505:99//Hs.50929:AA443144

R-THYRO1000796//ESTs//4.3e-44:445:75//Hs.55855:AA621381 R-THYRO1000805//EST//2.6e-32:407:67//Hs.123424:AA813594

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R-THYRO1000829
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R-THYRO1000843//Interleukin 10//1.1e-44:285:87//Hs.2180:M57627

R-THYRO1000852//EST//2.3e-20:157:85//Hs.149580:Al281881

R-THYRO1000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011

5 R-THYRO1000865//Protein kinase, interferon-inducible double stranded RNA dependent//2.8e-44:374:79//Hs. 73821:M35663

R-THYRO1000895//ESTs//1.0e-32:196:85//Hs.138630:H97871

R-THYRO1000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234

R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.1e-110: 566:94//Hs.78106:AF079529

R-THYRO1000934//ESTs//7.4e-102:535:95//Hs.58194:W72182

R-THYRO1000951//ESTs//4.2e-11:91:89//Hs.6278:T15859

R-THYRO1000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761

R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.

15 14454:AF047440

10

R-THYRO1000975//EST//9.8e-49:303:89//Hs.149580:Al281881

R-THYRO1000983//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thalianal//1.6e-90:474:93//Hs.106616:Al027524

R-THYRO1000984//ESTs//5.9e-97:481:96//Hs.142457:Al202777

20 R-THYRO1000988//EST//3.5e-42:241:83//Hs.162404:AA573131

R-THYRO1001003//ESTs, Weakly similar to ubiquitin-conjugating enzyme [H.sapiens]//3.0e-57:341:91//Hs. 44049:AA521489

R-THYRO1001031//ESTs//5.5e-47:322:85//Hs.136839:H93717

R-THYRO1001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070

25 R-THYRO1001062//EST//1.5e-46:291:89//Hs.161917:AA483223

R-THYRO1001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497

R-THYRO1001100

R-THYRO1001120//ESTs, Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]// 6.6e-86:491:89//Hs.89135:AI138834

30 R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570: AJ006417

R-THYRO1001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399

R-THYRO1001134//ESTs//1.8e-102:521:95//Hs.108408:N31922

R-THYRO1001142//ESTs//0.26:84:69//Hs.153434:Al287853

35 R-THYRO1001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075

R-THYRO1001177

R-THYRO1001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744

R-THYRO1001204//ESTs, Weakly similar to TH1 protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA709151 R-THYRO1001213//ESTs//1.3e-75:409:92//Hs.140213:AA828932

40 R-THYRO1001262//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.3e-48:349:83//Hs.139107:K00629

R-THYRO1001271//PUTATIVE PROTEIN PHOSPHATASE 2C//1.0:128:64//Hs.118728:D13640

R-THYRO1001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561

R-THYRO1001313//ESTs//3.5e-17:139:87//Hs.15827:H16269

R-THYRO1001320//ESTs//1.4e-61:403:79//Hs.139555:N48230

R-THYRO1001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//8.5e-05:326:60//Hs. 82314:M31642

R-nnnnnnnnnnnn//ESTs//0.16:422:5.9//Hs.23876:AA082935

R-THYRO1001347//ESTs, Weakly similar to C35A5.8 [C.elegans]//1.1e-106:562:94//Hs.15032:AA774250

R-THYRO1001363//ESTs//1.4e-99:508:95//Hs.5028:D51033

50 R-THYRO1001365

R-THYRO1001374

R-THYRO001401//Human HsLIM15 mRNA for HsLiml5, complete cds//2.5e-48:467:75//Hs.37181:D64108

R-THYRO1001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627

R-THYRO1001405//ESTs//4.8e-25:197:84//Hs.6907:W72733

55 R-THYRO1001406//EST//0.0023:117:66//Hs.162931:AA633197

R-THYRO1001411//ESTs//6.1e-77:421:93//Hs.22973:R40979

R-THYRO1001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//9.1e-49:305:86//Hs. 159187:AB007977

R-THYRO1001434//ESTs//0.40:161:61//Hs.161993:AA503172

R-THYRO1001458//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.7e-05:159:66//Hs.104239:AA488082

R-THYRO1001480//Small inducible cytokineA5 (RANTES)//1.3e-40:331:79//Hs.155464:AF088219

5 R-THYRO1001487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.1e-17:134:76//Hs.15731: AB011135

R-THYRO1001534//ESTs//4.6e-96:447:100//Hs.135204:Al093110

R-THYRO1001537//ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-33: 304:80//Hs.108740:W20094

10 R-THYRO1001541//Human peptide transporter (HPEPT1) mRNA, complete cds//9.0e-49:427:76//Hs.2217: U21936

R-THYRO1001559//ESTs//0.99:210:62//Hs.33619:AA021594

R-THYRO1001570//ESTs//4.9e-48:287:91//Hs.27131:AA442413

R-THYRO1001573//ESTs//2.1e-87:446:95//Hs.143669:AA621958

15 R-THYRO1001584//ESTs//1.5e-64:354:95//Hs.146222:AA397741

R-THYRO1001595//ESTs//5.7e-39:366:78//Hs.22562:R54247

R-THYRO1001602//Insulin-like growth factor 1 (somatomedia C)//7.4e-12:288:67//Hs.85112:X57025

R-THYRO1001605//Human GS2 mRNA, complete cds//6.9e-49:359:83//Hs.264:U03886

R-THYRO1001617//Homo sapiens peroxisomal acyl-CoA:dihydroxyacetonephosphate acyltransferase (DHAPAT)

20 mRNA, complete cds//1.3e-82:434:93//Hs.12482:AJ002190

R-THYRO1001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331:83//Hs.127649:AB007874

R-THYRO1001656//ESTs//3.8e-19:209:75//Hs.92186:Al080282

R-THYRO100166I//ESTs//1.4e-56:323:91//Hs.24984:AA534446

R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//-1.6e-111:562:95//

25 Hs.118633:AJ225089

R-THYRO1001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs. 67619:AB007957

R-THYRO1001703//ESTs//1.1e-39:142:97//Hs.110748:AI341726

R-THYRO1001706//ESTs//2.2e-42:214:99//Hs.112536:AI147691

30 R-THYRO1001721

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R-nnnnnnnnnnn//ESTs, Weakly similar to ZK1128.6 [C.elegans]//1.7e-10:147:77//Hs.158196:R53184 R-THYRO1001745//ELK1, member of ETS oncogene family//1.8e-12:282:65//Hs.116549:AL009172

R-THYRO1001746//EST//0.0073:226:61//Hs.146544:AI125323

R-THYRO1001772//ESTs//8.2e-100:495:97//Hs.144993:AA243474

R-THYRO1001793//ESTs//2.5e-89:430:97//Hs.58127:AA534224 R-THYRO1001809//ESTs//1.0e-41:327:80//Hs.146811:AA410788

R-THYRO1001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//5.7e-38:242:83//Hs. 92381:AB007956

R-THYRO1001895//ESTs//1.7e-08:213:64//Hs.156056:Al352123

40 R-THYRO1001907//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.7e-41:362:79//Hs.139007:H74314

R-VESEN1000122

R-Y79AA1000013//ESTs//0.99;233:57//Hs.132216:AA923289

R-Y79AA1000033//EST//1.9e-62:324:95//Hs.157692:Al359321

45 R-Y79AA1000037//ESTs//6.1e-47:234:98//Hs.30773:AA557178

R-Y79AA1000059//Homo sapiens mRNA for KIAA0640 protein, partial cds//2.8e-51:330:89//Hs.153026: AB014540

R-Y79AA1000065//ESTs//2.0e-91:497:94//Hs.37759:H59629

R-Y79AA1000131//EST//2.3e-16:184:75//Hs.141501:N50792

50 R-Y79AA1000181//ESTs, Weakly similar to No definition line found [C.elegans]//2.4e-110:553:95//Hs.23159: AA113849

R-Y79AA1000202//Human mRNA for KIAA0169 gene, partial cds//0.094:185:62//Hs.79414:D79991

R-Y79AA1000214//ESTs//1.7e-93:495:94//Hs.11673:W68103

R-Y79AA1000230//ESTs//3.5e-114:553:98//Hs.47125:Al421812

R-Y79AA1000231//ESTs//1.1e-106:526:97//Hs.82856:Al246624 R-Y79AA1000258//ESTs//1.5e-99:490:97//Hs.6459:Al092936

R-Y79AA1000268//Human mRNA for KIAA0365 gene, partial cds//1.3e-44:320:84//Hs.84123:AB002363

R-Y79AA1000313//ESTs//1.7e-105:558:93//Hs.18851:AA857826

EP 1 074 617 A2 R-Y79AA1000328//ESTs//1.9e-76:448:91//Hs.16470:AA121635 R-Y79AA1000342//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//2.0e-37:239:88//Hs.23476:AA401210 R-Y79AA1000346//ESTs//7.9e-12:139:76//Hs.115987:AA483808 R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]// 4.4e-66:339:97//Hs.8215:AA521150 R-Y79AA1000355//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.2e-44:279:88//Hs.139007:H74314 R-Y79AA1000368//ESTs//3.8e-97:513:94//Hs.68090:AA641018 R-Y79AA1000405//ESTs//4.4e-47:267:94//Hs.125304:R51613 R-Y79AA1000410//ESTs//7.4e-49:359:82//Hs.158107:AA707758 R-Y79AA1000420//EST//0.17:99:69//Hs.160859:Al352292 R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protein AUP46 precursor [M.musculus]//3.1e-60:362:88//Hs.6381:AI188509 R-Y79AA1000480//ESTs//1.0e-75:433:91//Hs.78110:AA741320 R-Y79AA1000538//EST//7.9e-48:307:87//Hs.149580:Al281881 R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.95:172:62//Hs. R-Y79AA1000540//ESTs//1.5e-97:534:93//Hs.67991:AA147848 R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//8.2e-97:482:97//Hs.19121: R-Y79AA1000574//ESTs, Weakly similar to M04B2.4 [C.elegans]//1.3e-107:564:93//Hs.16361:AI147455 R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//3.4e-99:517:94//Hs.60580: AF060503 R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION [Saccharomyces cerevisiae]//8.1e-27:140:100//Hs.129049:H28818 R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//8.7e-114:586: 95//Hs.83023:AF093670 R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III [C.elegans]//9.8e-111:563:95//Hs.19845:Al005330 R-Y79AA1000752//Homo sapiens (huc) mRNA, complete cds//0.97:235:59//Hs.1701:L26405 R-Y79AA1000774//ESTs//5.9e-109:559:95//Hs.17138:N91463 R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds//1.6e-18:107:100//Hs.84753:D87433 R-Y79AA1000784//EST//0.80:87:67//Hs.158558:Al368359 R-Y79AA1000794//ESTs//2.7e-99:498:96//Hs.25441:AA580512 R-Y79AA1000800//ESTs//1.2e-97:532:93//Hs.77822:AA532642 R-nnnnnnnnnn//Carboxypeptidase E//0.018:354:59//Hs.75360:X51405 R-Y79AA1000805 R-Y79AA1000824//ESTs//0.99:276:61//Hs.153992:AA280227 R-Y79AA1000827//ESTs//1.2e-55:326:92//Hs.158127:Al334650 R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds//0.016:386:59//Hs. 55836:U85647 R-Y79AA1000962//EST//0.024:177:63//Hs.25214:R37079 R-Y79AA1000968 R-Y79AA1000969//ESTs//2.9e-70:251:98//Hs.120858:AA417181 R-Y79AA1000976//ESTs//7.8e-56:299:95//Hs.120125:M86049 R-Y79AA1000985 R-Y79AA1001023//ESTs//5.7e-66:379:90//Hs.64616:W22851 R-Y79AA1001041//ESTs//8.6e-06:54:100//Hs.8980:AA629067

R-Y79AA1001048//ESTs//4.4e-97:461:99//Hs.7010:AA837407

R-Y79AA1001061//ESTs//3.8e-105:493:99//Hs.128419:AI271325 50

R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds//4.8e-53:279:83//Hs.15731:

R-Y79AA1001077//ESTs//1.9e-51:339:87//Hs.11197:AA309047

R-Y79AA1001078//ESTs//8.3e-98:528:92//Hs.24608:AA161260

R-Y79AA1001105//ESTs//6.0e-77:393:96//Hs.30837:H08155

R-Y79AA1001145//ESTs//1.7e-13:285:64//Hs.128259:AA343015

R-Y79AA1001167

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R-Y79AA1001177//EST//1.2e-05:92:76//Hs.65277:T15884

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R-Y79AA1001185
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R-Y79AA1001211//ESTs//1.3e-70:344:97//Hs.49760:AA741051

R-Y79AA1001216//ESTs//5.8e-63:416:88//Hs.8595:W60933

R-Y79AA1001228//ESTs//9.3e-101:483:98//Hs.13916:AI025750

5 R-Y79AA1001233//EST//0.00027:232:62//Hs.132431:AA909674

R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))//1.1e-110:549:95//Hs.23170:AJ005892

R-Y79AA1001281//ESTs//3.6e-98:466:99//Hs.104442:AA481271

R-Y79AA1001299//Human Ini1 mRNA, complete cds//9.6e-25:133:100//Hs.155626:U04847

10 R-Y79AA1001312//ESTs//3.4e-92:454:97//Hs.127319:Al191149

R-Y79AA1001323//ESTs//1.6e-67:422:89//Hs.118559:AA887084

R-Y79AA1001384//ESTs//3.1e-104:496:98//Hs.153692:AA604143

R-Y79AA1001391//ESTs//2.2e-77:418:94//Hs.118608:AA101819

R-Y79AA1001394//ESTs//2.1e-78:409:95//Hs.23413:AA579859

15 R-Y79AA1001402//EST//9.3e-08:128:75//Hs.141607:N63891

R-Y79AA1001493//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//4.4e-109:553:95//Hs.106616:AI027524

R-Y79AA1001511//ESTs//4.9e-49:271:92//Hs.109045:AA523704

R-Y79AA1001533//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//6.2e-46:260:

20 94//Hs.24884:AA176812

R-nnnnnnnnnnn//EST//0.62:126:67//Hs.137020:AA868563

R-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//3.5e-95:517:91//Hs.76987:AF012872

R-Y79AA1001555//Collagen, type XI, alpha 1//1.0:157:64//Hs.82772:J04177

R-Y79AA1001585//ESTs//1.9e-90:430:98//Hs.48333:AA704508

25 R-Y79AA1001594//ESTs//9.6e-23:122:100//Hs.63795:Al126237

R-Y79AA1001603//ESTs//1.0e-50:193:100//Hs.25635:Al336204

R-Y79AA1001613//ESTs, Weakly similar to zinc finger protein [H.sapiens]//7.2e-81:400:97//Hs.13323:AA897542 R-Y79AA1001647//ESTs//6.8e-92:479:95//Hs.154270:N26486

R-Y79AA1001665//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//2.5e-19:112:97//Hs.26252:

30 AA643235

R-Y79AA1001679//ESTs, Highly similar to LAMBDA-CRYSTALLIN [Oryctolagus cuniculus]//9.7e-99:553:92//Hs. 108896:R54040

R-nnnnnnnnnnn

R-Y79AA1001696//ESTs//1.4e-84:478:91//Hs.6606:AA211783

35 R-Y79AA1001705//ESTs//6.7e-107:546:95//Hs.106805:AA418490

R-Y79AA1001711//Human DNA sequence from clone 1119D9 on chromosome 20p12. Contains part of a gene for a PAK1 LIKE Serine/Threonine-Protein Kinase and part of the PLCB4 gene for Phopholipase C, beta (1-Phosphatidylinositol -4,5-Bisphosphate Phosphodiesterase Beta 4). Contains ESTs, STSs and GSSs//0.0085:251:63// Hs.21864:AL031652

40 R-Y79AA1001781//ESTs, Weakly similar to partial CDS [C.elegans]//9.4e-87:427:97//Hs.18645:Al023798

R-nnnnnnnnnnn//ESTs//1.1e-112:558:97//Hs.109755:AA180809

R-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//8.1e-95:530: 91//Hs.72444:W23217

R-Y79AA1001846//EST//2.8e-41:312:81//Hs.162236:AA551582

45 R-Y79AA1001848//Human adhalin (DAG2) mRNA, complete cds//0.54:221:58//Hs.99931:L34355

R-Y79AA1001866//ESTs//2.2e-102:498:97//Hs.130683:Al278630

R-Y79AA1001874//ESTs//1.9e-76:377:98//Hs.79707:AA354094

R-Y79AA1001875//ESTs//0.64:152:63//Hs.156159:Al333652

R-Y79AA1001923//EST//0.19:180:58//Hs.148290:AA908404

50 R-Y79AA1002027//ESTs//1.6e-104:497:98//Hs.21275:N73275

R-Y79AA1002083//Homo sapiens mRNA for KIAA0563 protein, complete cds//0.69:93:73//Hs.15731:AB011135 R-Y79AA1002089//Homo sapiens PYRJN (MEFV) mRNA, complete cds//1.1e-46:392:80//Hs.113283:AF018080

R-Y79AA1002093//Homo sapiens GT198 mRNA, complete ORF//1.2e-12:80:100//Hs.78185:L38933

R-Y79AA1002103//ESTs//1.3e-52:535:76//Hs.142167:Al417785

55 R-Y79AA1002115//ESTs//4.2e-101:519:96//Hs.23977:AA115275

R-Y79AA1002125//ESTs//9.8e-68:363:94//Hs.72085:AA193399

R-Y79AA1002139//ESTs//1.2e-100:498:96//Hs.72020:AA149858

R-Y79AA1002204//ESTs//2.1e-83:434:95//Hs.22979:R43725

R-nnnnnnnnnn//ESTs//1.7e-55:478:76//Hs.154554:AA552715

R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]//3.5e-108:553:95//Hs. 50441:AA747428

R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349

5 R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN [H.sapiens]// 6.5e-86:518:90//Hs.25682:AA857843

R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:AI016274

R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:Al039977

R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0e-118:564:98//Hs.100729: AB014592

R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOZYME [D.melanogaster]//9.0e-102: 507:96//Hs.25895:Al341537

R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4e-93:453:97//Hs.96731:AB014555 R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288

15 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1e-110:403:99//Hs.30898: AB014534

R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985

R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371

R-Y79AA1002361

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20 R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908

R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:Al042000

R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753

R-Y79AA100243//EST//6.6e-23:128:98//Hs.128417:AA975026

R-nnnnnnnnnn//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 68 [Saccharomyces cerevisiae]

25 //4.4e-62:390:88//Hs.143930:Al207821

R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870

R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788

R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:N66499

## 30 Homology Search Result Data 6

[0314] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, as and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark.

- C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%//Q61712
- C-HEMBA1000030
- 40 C-HEMBA1000046
  - C-HEMBA1000050
  - C-HEMBA1000076
  - C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).// 1.9E-12//368aa//24%//P08553
- 45 C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3.-GAMMA (HNF-3G).//5E-16//166aa//36%//P35584
  - C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%//P35662
  - C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%//P48555
  - C-HEMBA1000193
  - C-HEMBA1000227
- 50 C-HEMBA1000288
  - C-HEMBA1000302
  - C-HEMBA1000304
  - C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-49//107aa//91 %//035594
- 55 C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%// AL049654
  - C-HEMBA1000387
  - C-HEMBA1000392

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C-HEMBA1000460
        C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%//Q04652
        C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%//P22279
        C-HEMBA1000501
        C-HEMBA1000508
5
        C-HEMBA1000520
        C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAG-
        MENTS).//2.6E-12//73aa//41%//P02826
        C-HEMBA1000534
10
        C-HEMBA1000555
        C-HEMBA1000568
        C-HEMBA1000588
        C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179aa//61%//O43295
        C-HEMBA1000636
        C-HEMBA1000682
15
        C-HEMBA1000686
        C-HEMBA1000719
        C-HEMBA1000727
        C-HEMBA1000752
        C-HEMBA1000817
20
        C-HEMBA1000851
        C-HEMBA1000867
        C-HEMBA1000869
        C-HEMBA1000872
        C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)//
25
        1.6E-30//127aa//40%//P43366
        C-HEMBA1000918
        C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHRO-
        MOSOME X.//1E-10//288aa//23%//Q19124
30
        C-HEMBA1000946
        C-HEMBA1000968
        C-HEMBA1000971
        C-HEMBA1000975
        C-HEMBA1001009
35
        C-HEMBA1001022
        C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//
        1.4E-12//131aa//38%//Q01485
        C-HEMBA1001052
        C-HEMBA1001080
40
        C-HEMBA1001085
        C-HEMBA1001088//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//
        176aa//57%//P48059
        C-HEMBA1001109
        C-HEMBA1001122
45
        C-HEMBA1001133
        C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946)
        (FRAGMENT).//1.5E-116//197aa//58%//Q06730
        C-HEMBA1001140
        C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.8E-79//179aa//80%//P51646
        C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%//
50
        AB020678
        C-HEMBA1001235
        C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733
        C-HEMBA1001281
        C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//
55
        29%//Q60401
        C-HEMBA1001303
        C-HEMBA1001310
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C-HEMBA1001326
        C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.4E-
        133//614bp//99%//AF057358
        C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%//P17081
5
        C-HEMBA1001388
        C-HEMBA1001398
        C-HEMBA1001405
        C-HEMBA1001407
        C-HEMBA1001413
        C-HEMBA1001415
10
        C-HEMBA1001446
        C-HEMBA1001450
        C-HEMBA1001455
        C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//
        63aa//61%//P18850
15
        C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%//P29166
        C-HEMBA1001533
        C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%//AB020657
        C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%//Q14141
20
        C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.6E-10//155aa//28%//
        C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.6E-36//
        365aa//33%//P33450
        C-HEMBA1001702
25
        C-HEMBA1001714//Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//
        99%//AL050386
        C-HEMBA1001731
        C-HEMBA1001744//SCY1PROTEIN.//9.9E-32//481aa//25%//P53009
        C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%//P11675
30
         C-HEMBA1001815
         C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%//Q99676
         C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%//Q07230
         C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%//P20659
35
         C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//
         9.3E-36//395aa//26%//Q63342
         C-HEMBA1001987
         C-HEMBA1002018
40
         C-HEMBA1002049
         C-HEMBA1002084
         C-HEMBA1002125
         C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%//
         P79293
         C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%//
45
         P43694
         C-HEMBA1002191
         C-HEMBA1002199
         C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%//
50
         P18161
         C-HEMBA1002237
         C-HEMBA1002265
         C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%//AF125537
         C-HEMBA1002349
         C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//
 55
         1847bp//99%//AF092563
         C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%//P22793
```

C-HEMBA1002430

- C-HEMBA1002439 C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//109aa//55%//Q00994 C-HEMBA1002460 C-HEMBA1002462 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%//P98175 5 C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.1E-12//285aa// 31%//P17437 C-HEMBA1002477 C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53//257aa//36%//P48732 C-HEMBA1002515 10 C-HEMBA1002542 C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.8E-305//951bp//99%// AF075587 C-HEMBA1002583 C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.4E-253//1149bp//99%//AB011169 15 C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0//1539bp//99%//AB018351 C-HEMBA1002688 C-HEMBA1002696 C-HEMBA1002750 C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4).//1E-80//882bp//61%//AJ000414 20 C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1532bp//99%//AB020636 C-HEMBA1002777 C-HEMBA1002794 C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2e-314//1437bp//99%// 25 C-HEMBA1002818//Homo sapiens, mRNA for fibulin-4.//2E-304//1383bp//99%//AJ132819 C-HEMBA1002850 C-HEMBA1002863 C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.//1.5E-44//188aa// 30 52%//Q09297 C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//1483bp//100%//AB011148 C-HEMBA1002937 C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2E-34//300aa//34%// C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds.//0//1752bp//99%//AB020710 35 C-HEMBA1002954 C-HEMBA1002971 C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).// 1.2E-27//63aa//100%//P14646 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//5 34aa//24%//Q02224 40 C-HEMBA1003033 C-HEMBA1003035 C-HEMBA1003041
- C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%//O75439
  - C-HEMBA1003067
  - C-HEMBA1003096
  - C-HEMBA1003117
  - C-HEMBA1003129
- 50 C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.5E-51//221aa//33%//P41940
  - C-HEMBA1003148//Homo sapiens mRNA full-length insert cDNA clone EUROIMAGE 381801.//0//1583bp//99%// AL079278
- 55 C-HEMBA1003175
  - C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANS-FERASE (EC 2.1.1.61).//5.9E-74//134aa//53%//P44551

- C-HEMBA1003222 C-HEMBA1003235//TROPOMYOSIN.//0.0000023//109aa//33%//Q02088 C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.2E-41//245aa//42%//Q06548 C-HEMBA1003257 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6E-11//239aa//32%//P32506 C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.4E-229// 1043bp//99%//AB024436 C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//0//791bp//99%//AB011109 C-HEMBA1003322 C-HEMBA1003327 10 C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.00000002//248aa//23%//Q02224 C-HEMBA1003370 C-HEMBA1003380 C-HEMBA1003395 15 C-HEMBA1003402 C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//1732bp//98%//AB020712 C-HEMBA1003417//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//1.6e-312// 1414bp//99%//AL050287 C-HEMBA1003418//TRICHOHYALIN.//8.7E-19//281aa//31%//P37709 C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%//AB013139 20 C-HEMBA1003447 C-HEMBA1003461 C-HEMBA1003463 C-HEMBA1003528 C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//8.8E-189//360aa//96%//P50480 25 C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.1E-68//251aa//52%//P53384 C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAM-MA-I).//1.2E-31//71aa//100%//P16874 C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//7.9E-30 49//279aa//32%//P19474 C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.9E-206//445aa//74%//Q13330 C-HEMBA1003581//TALIN.//4.4E-45//52aa//98%//P26039 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.4E-10//118aa// 35%//P19682 35 C-HEMBA1003615 C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//8.2E-178//501bp//97%//AB015344 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.2E-75//151aa//99%//Q13207 C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.1E-59//249aa//47%//P53973 40 C-HEMBA1003711 C-HEMBA1003807 C-HEMBA1003864 C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.8E-16// 89aa//46%//P16372 45 C-HEMBA1003959 C-HEMBA1003989 C-HEMBA1004074 C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.5E-221//1188bp//78%// AF091234 50 C-HEMBA1004146 C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1893bp//98%//AB023145 C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%//U50748 C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//5.7E-217//1217bp//88%//
  - C-HEMBA1004289

99%//AF092094

AF095927 C-HEMBA1004246

55

C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//4.8E-257//738bp//

EP 1 074 617 A2 C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1512bp//96%//AF132955 C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%// AF089841 C-HEMBA1004596 C-HEMBA1004693 C-HEMBA1004736 C-HEMBA1004753 C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.1E-34//515bp//66%//U49082 C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.6E-246//1249bp//94%// L39060 C-HEMBA1004763 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. I/5.4E-111//314aa//58%//P08547 C-HEMBA1004771 C-HEMBA1004776 C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66%//P50851 C-HEMBA1004806 C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.2E-154//317aa//94%// Q00004 C-HEMBA1004850 C-HEMBA1004863//Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022).//0//1443bp// 100%//AL080114 C-HEMBA1004923 C-HEMBA1004929 C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.3E-27//65aa//100%//Q16401 C-HEMBA1004933 C-HEMBA1004954 C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).// 0.00000096//286aa//23%//P12036 C-HEMBA1005475 C-HEMBA1005581//Homo sapiens SLIT2 (SUL2) mRNA, complete cds.//0//1721bp//100%//AF133270 C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23// 151aa//37%//P16372 C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.7E-225//1189bp//88%//AF076183 C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%//P26043 C-HEMBA1006377 C-HEMBA1006467 C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%//Q01552 C-HEMBA1006530 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).// 0.00000043//111aa//40%//Q01485 C-HEMBA1006795 C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa//39%//P16258 C-HEMBA1006936 C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-267//1215bp//99%// AP078849 C-HEMBA1007342 C-HEMBB1000008 C-HEMBB1000018 C-HEMBB1000024

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C-HEMBB1000025

- C-HEMBB1000036

  C-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-187//
  1582bp//80%//AF084928
- 55 C-HEMBB1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%//P11799 C-HEMBB1000103
  - C-HEMBB1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521

```
C-HEMBB1000136
        C-HEMBB1000215
        C-HEMBB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEED8.5.//
        2.7E-12//112aa//47%//Q09530
5
        C-HEMBB1000244
        C-HEMBB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHRO-
        MOSOME V.//6.1E-09//242aa//26%//Q23256
        C-HEMBB1000338
        C-HEMBB1000339
10
        C-HEMBB1000391
        C-HEMBB1000438
        C-HEMBB1000449
        C-HEMBB1000589
        C-HEMBB1000591
15
        C-HEMBB1000623
        C-HEMBB1000630
        C-HEMBB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19//
        232aa//28%//P78970
        C-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%//P27671
20
        C-HEMBB1000671
        C-HEMBB1000673
        C-HEMBB1000705
        C-HEMBB1000706
        C-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-130//692bp//93%//
25
        U53475
        C-HEMBB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847
        C-HEMBB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//
        1.2E-126//613bp//97%//AF111105
        C-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-
30
        54//232aa//43%//P39956
        C-HEMBB1000807
        C-HEMBB1000810
        C-HEMBB1000848
        C-HEMBB1000852
35
        C-HEMBB1000870
        C-HEMBB1000887
        C-HEMBB1000908
        C-HEMBB1000927//Homo sapiens calsenilin mRNA, complete cds.//1.1E-70//595bp//76%//AF120102
        C-HEMBB1000947//Homo sapiens clone HAW 100 putative ribonuclease III mRNA, complete cds.//0//2292bp//
40
        99%//AF116910
        C-HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.4E-120//580bp//67%//AF099974
        C-HEMBB1000975
        C-HEMBB1000985//MEPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-
        18//178aa//30%//P28575
45
        C-HEMBB1000991
        C-HEMBB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%//
        P51523
        C-HEMBB1001014
        C-HEMBB1001024
50
        C-HEMBB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED
        NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%//P46087
        C-HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.6E-52//331bp//
        80%//AF010144
        C-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%//AF034803
55
        C-HEMBB1001096
        C-HEMBB1001105
        C-HEMBB1001117
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C-HEMBB1001126

- C-HEMBB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435 C-HEMBB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.2E-210//1835bp//76%//AF110267
- C-HEMBB1001153
- 5 C-HEMBB1001169
  - C-HEMBB1001175//ANKYRIN.//6.9E-11//169aa//31%//Q02357
  - C-HEMBB1001182
  - C-HEMBB1001199
  - C-HEMBB1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0//1816bp//99%//AB023187
- 10 C-HEMBB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.8E-284//713bp//100%//AF089897
  - C-HEMBB1001288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp//99%//AF132966
  - C-HEMBB1001289
  - C-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%//P17081
- 15 C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//
  724bp//86%//U92703
  - C-HEMBB1001331
  - C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%//P98175
  - C-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1E-58//292bp//99%//AF097441
  - C-HEMBB1001369
  - C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757
  - C-HEMBB1001387
  - C-MAMMA1002317
- 25 C-MAMMA1002319

- C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//0.00000015//206aa//29%//Q02926
- C-NT2RM1000080//UNC-1 PROTEIN.//5.9E-25//211aa//31%//Q21190
- C-NT2RM1000242
- C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143aa//91%//P49028
- 30 C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V- AT-PASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%//P39942
  - C-NT2RM1000669
  - C-NT2RM1000781
  - C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798bp//99%//AF092138
- 35 C-NT2RM1001008
  - C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.000000002//980bp//95%//AF085360 C-NT2RM1001074
  - C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000056//239aa//27%//
  - C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseu-
- dogene similar to MMS2, ESTs and GSSs, complete sequence.//0//1740bp//99%//AL031291
  C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.2E-144//362aa//71%//P25167
  - C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//31%//P54703
- 45 C-NT2RM2000032
  - C-NT2RM2000042
  - C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).// 1.3E-36//160aa//40%//P50102
- 50 C-NT2RM2000093
  - C-NT2RM2000101
  - C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223
  - C-NT2RM2000192
- 55 C-NT2RM2000239
  - C-NT2RM2000250//Homo sapiens mRNA; cDNA DKFZp564L232 (from clone DKFZp564L232).//4.2e-314// 1416bp//100%//AL080069
  - C-NT2RM2000259

- C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.6E-19//181-aa//34%//P14918
- C-NT2RM2000287
  - C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds.//3.4E-294//863bp//99%// AB020666
    - C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//0//1637bp//99%//AB011132
    - C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.8E-14//245aa//29%//P11274
    - C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%// U48251
- 10 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLE-OTIDE//1.7E-68//419aa//36%//P50849
  - C-NT2RM2000374
  - C-NT2RM2000395
  - C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-
- ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//1.6E-54//344aa//33%//P32802
  - C-NT2RM2000407
  - C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1E-222//237aa//89%//
- 20 C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//0.0000001//
  157aa//28%//P36113
  - C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//0.0000089//377aa//24%// P22211
  - C-NT2RM2000490//SYNAPTOTAGMIN(P65).//1.8E-13//166aa//34%//P41823
- 25 C-NT2RM2000502
  - C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243 C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.3E-12//282aa//32%//P17437
  - C-NT2RM2000540
- 30 C-NT2RM2000567
  - C-NT2RM2000569
  - C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).// 1.7E-187//741aa//46%//P73505
  - C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//3001bp//99%//D86987
- 35 C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.8E-60//384aa//40%//P53973
  - C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.// 0//2712bp//99%//AF156487
  - C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.9E-70//838bp//69%//AF179221
- 40 C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.4E-32//319aa//35%//Q08170
  - C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//0//3791bp//99%//AB018272
  - C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//0//2530bp//99%//AB014558 C-NT2RM2000639
- 45 C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1543bp//99%//AB014576 C-NT2RM2000669
  - C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.7E-142//285aa//90%//P32391
  - C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//3.8E-23//184aa//36%//Q15404
- 50 C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//4.4E-231//1065bp//99%//AB015342 C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.7E-53//266aa//43%// P41877
  - C-NT2RM2000795
  - C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETACOP).//9.5E-279//545aa//98%//P23514
  - C-NT2RM2000837

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C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.7E-200//927bp//99%//AB015046

	C-NT2RM2000952
	C-NT2RM2000984
	C-NT2RM2001004
	C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%//Q60809
5	C-NT2RM2001065
	C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.4E-15//266aa//
	26%//P46577
	C-NT2RM2001131
	C-NT2RM2001141
10	C-NT2RM2001152
	C-NT2RM2001177//Homo sapiens mRNA; cDNA DKFZp586G1822 (from clone DKFZp586G1822).//2.1E-293//
	1335bp//99%//AL080109
	C-NT2RM2001194
	C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//35%//P05143
15	C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF5).//0.00000015//95aa//35%//
	P48724
	C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (PCIP10).//3.6E-10//177aa//
	32%//P97924
	C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-
20	DOHYDROLASE).//1.3E-180//328aa//99%//P13264
	C-NT2RM2001243
	C-NT2RM2001247
	C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166//312aa//98%//
	P53995
25	C-NT2RM2001291
	C-NT2RM2001306//Homo sapiens mRNA; cDNA DKFZp564I052 (from clone DKFZp564I052).//0//1694bp//99%//
	AL080063
	C-NT2RM2001312
	C-NT2RM2001319
30	C-NT2RM2001324//ZYXIN.//6.8E-55//200aa//41%//Q04584
	C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000029//334aa//22%//000808
	C-NT2RM2001370
	C-NT2RM2001393
	C-NT2RM2001420
35	C-NT2RM2001424//Homo sapiens mRNA; cDNA DKFZp586D0920 (from clone DKFZp586D0920).//0//1621bp//
	100%//AL050146
	C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.4E-121//
	437aa//57%//P52569
	C-NT2RM2001504
40	C-NT2RM2001524
	C-NT2RM2001544
	C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.9E-27//
	90aa//42%//P38660
	C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SSA)) (RO(SS-A)).//4.3E-
45	61//312aa//44%//P19474
	C-NT2RM2001582
	C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0//1000bp//100%//AB014610
	C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%//P28692
	C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2390bp//99%//AB007931
50	C-NT2RM2001930
	C-NT2RM2001935 C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.7E-27//216aa//34%//P28320
	C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBRT INTERGENIC REGION.//2.7E-27//2 Toaai/3476//P20320 C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001//
55	212aa//23%//P38250
J.J	C-NT2RM2001982

C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.9E-39//253aa//35%//

C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.3E-10//232aa//

P37838

- 28%//Q12730
- C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//3.1E-12//206aa//30%//Q09782
- C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).// 0.000000029//83aa//44%//P40796
  - C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.1E-89// 425aa//41%//P46837
  - C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.// 0//1959bp//99%//AB016789
- 10 C-NT2RM2002049

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- C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa// 24%//Q07878
- C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).// 5E-62//104aa//57%//Q61990
- 15 C-NT2RM2002091
  - C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840 C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0// 1868bp//99%//AF030435
  - C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//
- 20 26%//P49695
  - C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8E-31//105aa//47%//P47805
  - C-NT2RM2002178//Homo sapiens mRNA; cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//99%//AL117402
  - C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA
- 25 POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%//P25167
  - C-NT2RM4000061
    - C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%//P52742
    - C-NT2RM4000139//R.norvegicus trg mRNA.//2.3E-114//1161bp//72%//X68101
    - C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.8E-13//686aa//23%//
  - C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439aa//41%//P16381
    - C-NT2RM4000197
      C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0//1926bp//100%//AB018255
    - C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.1E-27//633bp//64%//L20303
  - C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.2E-276//1124bp//97%//M99438
    - C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%//AJ132637
- 40 C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%//AF083246
  - C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21//208aa//35%//Q24371
  - C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//86%//AB025412 C-NT2RM4000395
  - C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%//AJ133769
- 45 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8E-20//393aa// 24%//Q10297
  - C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%//AF097025 C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.8E-11//242aa//31%//P04280
- 50 C-NT2RM4000496//SAP1 PROTEIN.//8.3E-53//434aa//29%//P39955
  - C-NT2RM4000511
  - C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.1E-11//394aa//24%//P16884
  - C-NT2RM4000520
- 55 C-NT2RM4000585
  - C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.// 1.1E-285//1293bp//99%//AF186273
  - C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0//1940bp//95%//AB014587

- C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%//AB020657 C-NT2RP1000040 C-NT2RP1000063 C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsal2.//0//1162bp//99%//X98834 C-NT2RP1000101 C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%//P93471 C-NT2RP1000112 C-NT2RP1000124 C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//60%//P51859 C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0//1889bp//98%//AB023165 10 C-NT2RP1000170 C-NT2RP1000191 C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%//Q02357 C-NT2RP1000243 C-NT2RP1000259 15 C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp// 93%//AF067730 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%//AF053551 C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%//P32447 20 C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%//P25343 C-NT2RP1000357 C-NT2RP1000376//Homo sapiens mRNA; cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp// 95%//AL080187 C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%//AB011159 25 C-NT2RP1000416 C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.8E-94// 1019bp//63%//AF111423 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%//Q08257 30 C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.6E-94// 254aa//47%//P34580 C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%//P09653 C-NT2RP1000481 C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//2728bp//99%//D87686 35 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%//P49020 C-NT2RP1000574//HOMEOBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%// P97367 40 C-NT2RP1000581 C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%//P25233 C-NT2RP1000688 C-NT2RP1000695 C-NT2RP1000733//Human mRNA for GSPT1-TK protein,complete cds.//0//2057bp//99%//E14379 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete 45 cds.//0//2186bp//99%//AF101434 C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-OPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//O35566 C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%//Q07960 50 C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp// 99%//AF067223 C-NT2RP1000846 C-NT2RP1000851
- C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-55 OPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%//035566 C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%//Q13823 C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds.//4.6E-

- 105//504bp//99<%//U39317 C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%//Q04652 C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa//25%//Q13823 C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//966bp//99%// C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%//P19338 C-NT2RP1000980 C-NT2RP1000988 C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.2E-78// 1529bp//61%//L01790 10 C-NT2RP1001014 C-NT2RP1001395 C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//67%//P91917 C-NT2RP1001424 C-NT2RP1001449 15 C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp// 100%//AJ005257 C-NT2RP1001466 C-NT2RP1001475 C-NT2RP1001482 20 C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%//Q08891 C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%// P42803 C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-OPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%//035566 25 C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.8E-121// 271aa//89%//P47758 C-NT2RP1001616 C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%//P02594 C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa// 30 55%//O34136 C-NT2RP2000007 C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%// C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP1).//1.8E-22//184aa// 35 C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.// 0//1390bp//98%//AF061749 C-NT2RP2000054 C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-40 SILON).//9.4E-16//45aa//100%//P49446 C-NT2RP2000067 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.4E-51// 383aa//32%//P33450 45 C-NT2RP2000079 C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0//2286bp//100%//AB018338 C-NT2RP2000091
  - C-NT2RP2000097 C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356 C-NT2RP2000120 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.5E-117//541aa//42%//

  - C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2286bp//99%//AB023206 C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN
- AP47) (GOLGI ADAPTOR AP-1-47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.4E-226//423aa//99%//P35585 C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%//P41891
  - C-NT2RP2000157//MLO2 PROTEIN.//2.6E-11//62aa//40%//Q09329

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C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds.//3.4e-315//1430bp//99%//
        AB023225
        C-NT2RP2000173
        C-NT2RP2000175
5
        C-NT2RP2000195
        C-NT2RP2000205
        C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds.//0//2898bp//99%//AB020699
        C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS1).//0.000043//103aa//28%//P35568
        C-NT2RP2000232
10
        C-NT2RP2000233
        C-NT2RP2000239
        C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE
        110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.4E-21//210aa//33%//P56558
        C-NT2RP2000270
15
        C-NT2RP2000274
        C-NT2RP2000283
        C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.6E-27//576aa//
        25%//Q10297
        C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%//Q99676
        C-NT2RP2000298
20
        C-NT2RP2000310//Human proline-dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.3E-279//
        1193bp//99%//U82381
        C-NT2RP2000328
        C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//
25
        226aa//92%//P08760
        C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//6.3E-115//
        674aa//46%//P17564
        C-NT2RP2000369
        C-NT2RP2000412
        C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.3E-228//415aa//
30
        100%//P52597
        C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//
        99%//AF102265
        C-NT2RP2000438
        C-NT2RP2000448//KES1 PROTEIN.//8.7E-54//392aa//38%//P35844
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        C-NT2RP2000503
        C-NT2RP2000510
        C-NT2RP2000516
        C-NT2RP2000603
40
        C-NT2RP2000617
        C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//0//2482bp//99%//AB014514
        C-NT2RP2000656
        C-NT2RP2000658
        C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577
45
        C-NT2RP2000704
        C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-TRNA LIGASE)//2.7E-100//
        488aa//44%//O32038
        C-NT2RP2000764//NIFS PROTEIN.//6.6E-36//252aa//42%//P12623
         C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds.//0//3347bp//99%//AB020680
         C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.000000056//179aa//
50
        29%//Q99104
         C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//0.00000011//96aa//29%//
         C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.000000079//172aa//28%//P26174
55
         C-NT2RP2000819
        C-NT2RP2000841
        C-NT2RP2000845
        C-NT2RP2000863
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EP 1 074 617 A2 C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%//060841 C-NT2RP2000892 C-NT2RP2000931//MATRIN 3.//2.4E-289//467aa//95%//P43244 C-NT2RP2000932//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//2487bp//99%// AL050390 C-NT2RP2000938 C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//0//3458bp//99%//AB018298 C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%//AB024704 C-NT2RP2000985 C-NT2RP2001036 C-NT2RP2001044 C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//0//2749bp//99%// AB007957 C-NT2RP2001065 C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).// 5.8E-46//222aa//45%//Q20939 C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.2E-118//430aa//54%//P50232 C-NT2RP2001094 C-NT2RP2001119 C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%//AJ132440 C-NT2RP2001218 C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).// 2.2E-10//366aa//28%//P14105 C-NT2RP2001381 C-NT2RP2001397//Homo sapiens mRNA; cDNA DKFZp434B174 (from clone DKFZp434B174).//0//1495bp// 100%//AL080146 C-NT2RP2001427 C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//0//1748bp//99%//AB018340 C-NT2RP2001675 C-NT2RP2001721 C-NT2RP2001907 C-NT2RP2001969 C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.7E-177// 1538bp//74%//AF062378 C-NT2RP2002046 C-NT2RP2002154 C-NT2RP2002208 C-NT2RP2002270//AF-9 PROTEIN.//0.00000012//74aa//36%//P42568 C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%//Y16521 C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.4E-254//1158bp//99%//AB015594 C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.3E-240// 1105bp//99%//AF038958 C-NT2RP2002426 C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%// C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.2E-19//288aa//26%// Q11073 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa// 42%//P12815 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%//

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P55345

C-NT2RP2002621 C-NT2RP2002672

30%//014345

C-NT2RP2002769
C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10// 203aa//27%//P29764

C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.9E-14//210aa//

C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp// 100%//AF038392

C-NT2RP2002954

C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2),//4.6E-80//147aa//100%//P51669

C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.00000001//98aa//36%//P10129

C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%// AB026190

C-NT2RP2003108

10 C-NT2RP2003117

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C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete eds.//2.3E-82//642bp//68%//

C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%//004652 C-NT2RP2003177

15 C-NT2RP2003194

C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811 C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%// AB006572

C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14//332aa//32%//

P26337 20

C-NT2RP2003367

C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//269aa//91%//P38378 C-NT2RP2003446

C-NT2RP2003533

25 C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.7E-17// 148aa//34%//P74261

C-NT2RP2003596

C-NT2RP2003629

C-NT2RP2003687

30 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.4E-29//85aa//72%// Q05481

C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%//P51669 C-NT2RP2003793

35 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMI-NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%//O09175 C-NT2RP2003986

C-NT2RP2004042

C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered pieces.//8.2E-202//926bp//100%//AL096820

C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15// 126aa//39%//P38120

C-NT2RP2004392//MNN4 PROTEIN.//1.4E-11//143aa//27%//P36044

C-NT2RP2004463

45 C-NT2RP2004602

40

C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%//AB023139 C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%//AJ006291 C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I.//5.6E-64//616aa// 33%//Q92355

C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-TRNA 50 LIGASE) (LEURS).//9.5E-73//153aa//59%//Q10490

C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%//P53588 C-NT2RP2004802

55 C-NT2RP2004841

C-NT2RP2004936

C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%//P13692

C-NT2RP2004999

- C-NT2RP2005000
- C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0//l694bp//99%//AB014515
- C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779
- C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%//P32447
- 5 C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%// X98743
  - C-NT2RP2005140
  - C-NT2RP2005147
  - C-NT2RP2005159
- 10 C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025 C-NT2RP2005270
  - C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%//D89053 C-NT2RP2005293
  - C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1515bp//99%//AB014576
- 15 C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%//AF072247
  - C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%//Q13823
  - C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.2E-13//185aa//38%//Q08170
- 20 C-NT2RP2005441
  - C-NT2RP2005453
  - C-NT2RP2005464
  - C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%//P38127
  - C-NT2RP2005472
- 25 C-NT2RP2005495

- C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.2E-81//166aa//88%//P36876 C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803
- C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%//AF092563
  - C-NT2RP2005525//Mus musculus kanadaptin mRNA, complete cds.//2.4E-304//1687bp//85%//AF035526
  - C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0//2856bp//99%//AB007963
  - C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE
- 35 METHYLGLYOXAL LYASE).//2E-20//181aa//36%//Q39366
  - C-NT2RP2005555
  - C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%//AF062529
  - C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//1455bp//98%//AF062085
- 40 C-NT2RP2005622
  - C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(\*) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//P47623
  - C-NT2RP2005637
  - C-NT2RP2005640
- 45 C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%//P56I01
  - C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%//AJ010973
  - C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.4E-200//908bp//99%//AF089814
  - C-NT2RP2005683
- 50 C-NT2RP2005690
  - C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%//AB018342 C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//
  - 0.00000003//169aa//28%//P38074
  - C-NT2RP2005748
- 55 C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%//
  - C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%// AF082516

C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374aa//38%//P47943

C-NT2RP2005767//G.gallus PB1 gene.//5E-163//1158bp//81%//X90849

C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.// 2.7E-180//656bp//99%//AF151351

5 C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITO-CHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%//Q02038

C-NT2RP2005781

C-NT2RP2005804

10 C-NT2RP2005835//SHP1 PROTEIN.//1.8E-28//208aa//32%//P34223

C-NT2RP2005853

C-NT2RP2005868

C-NT2RP2005886

C-NT2RP2005890

15 C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0//1977bp//99%//AB023188 C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//155aa//34%//P48837

C-NT2RP2006038

C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75),//1.5E-13//185aa//38%//Q08170

20 C-NT2RP2006052

C-NT2RP2006069

C-NT2RP2006071

C-NT2RP2006100//Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102).//0//1759bp//99%//AL049970

25 C-NT2RP2006106

C-NT2RP2006141

C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.3E-189//899bp//97%//AB014554 C-NT2RP2006196

C-NT2RP2006200

30 C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.1E-214//1026bp//97%//X96484

C-NT2RP2006237

C-NT2RP2006238

C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2E-59//388aa//32%//P46821

35 C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274//1236bp//99%//AF035262 C-NT2RP2006333

C-NT2RP2006365

C-NT2RP2006393

C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEOBOX PROTEIN (RATHKE POUCH HOMEO BOX).//

40 0.00000034//50aa//50%//Q61658

C-NT2RP2006456

C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266

C-NT2RP2006467

C-NT2RP2006472

45 C-NT2RP2006565//Sus scrofa mRNA for SCAMPI protein.//0//1276bp//84%//Y15710

C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYPIIG1) (P450-NMB) (OLFACTIVE).//4.2E-134//486aa//50%//P24461

C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%//P09543

50 C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%//AB020708 C-NT2RP3000072

C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%//AB011164 C-NT2RP3000220

C-NT2RP3000251

55 C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334 C-NT2RP3000312

C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%//AJ242978

```
C-NT2RP3000333
        C-NT2RP3000348
        C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN
        HP0303.//0.000000028//185aa//31%//O25074
        C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//
5
        226aa//92%//P08760
        C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1
        and Prp6.//0//2072bp//98%//AB019219
        C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1E-107//206aa//99%//P35293
        C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//
10
        1.7E-139//679aa//41%//O43143
        C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185
        C-NT2RP3000484
        C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.8E-28//536aa//27%//P28160
        C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.9E-12//192aa//30%//
15
        C-NT2RP3000596/TRICHOHYALIN.//2.5E-17//304aa//28%//Q07283
         C-NT2RP3000599
        C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3E-140//499aa//46%//P51523
20
         C-NT2RP3000644
         C-NT2RP3000661
         C-NT2RP3000665
         C-NT2RP3000690
         C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7E-28//176aa//34%//Q94650
         C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.5E-36//417aa//31%//Q61982
25
         C-NT2RP3000836
         C-NT2RP3000841
         C-NT2RP3000850
         C-NT2RP3000852
         C-NT2RP3000859
30
         C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete
         cds.//6.9E-69//1611bp//61%//U53445
         C-NT2RP3000869
         C-NT2RP3000901
         C-NT2RP3000917//Homo sapiens Dhm1-like protein mRNA, complete cds.//0//3199bp//99%//AF064257
35
         C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//
         2.7E-185//585bp//88%//AF015264
         C-NT2RP3000980
         C-NT2RP3000994//MATERNAL EFFECT PROTEIN
         STAUFEN.//0.00000006//78aa//48%//P25159
40
         C-NT2RP3001004
         C-NT2RP3001081
         C-NT2RP3001084
         C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds.//1.7E-94//787bp//66%//AF087433
         C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3E-44//260aa//40%//P55201
45
         C-NT2RP3001109
         C-NT2RP3001116
         C-NT2RP3001119
         C-NT2RP3001133
         C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//0//2802bp//99%//AB018305
 50
         C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%//AJ006266
         C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION.//1.7E-10//
         196aa//27%//P53154
         C-NT2RP3001214
         C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa//33%//
 55
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C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-

BUTYROBETAINE HYDROXYLASE).//1.9E-31//353aa//30%//P80193

	C-NT2RP3001236
	C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT
	CHAIN LC1].//1.2E-166//395aa//51%//P14873 C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0//2497bp//99%//AB020718
_	C-NT2RP3001307
5	C-NT2RP3001325
	C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//
	0//1213bp//99%//AB025905
	C-NT2RP3001392
10	C-NT2RP3001396
	C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.3E-61//374aa//36%//P49711
	C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009
	C-NT2RP3001420
	C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1E-16//77aa//46%//O33529 C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa//33%//O09053
15	
	C-NT2RP3001457 C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.1E-13//87aa//43%//P11632
	C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%//U13395
	C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//
20	0//2295bp//99%//AF064801
	C-NT2RP3001529//SPO0B-ASSOCIATED GTP-BINDING PROTEIN.//1E-61//345aa//42%//P20964
	C-NT2RP3001621
	C-NT2RP3001629
	C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.8E-18//91aa//38%//Q92609
25	C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.8E-09//132aa//31%//O22468
	C-NT2RP3001676 C-NT2RP3001679
	C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.6E-11//348aa//27%//P24733
	C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.4E-18//249aa//30%//Q04652
30	C-NT2RP3001896
	C-NT2RP3001915
	C-NT2RP3001929
	C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.3E-98//269aa//62%//P52742
35	C-NT2RP3004466 C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.3E-113//466aa//42%//
33	P34110
	C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//0//1520bp//99%//AB014532
	C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//0//974bp//95%//AB011126
	C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//0.000000038//
40	150aa//28%//Q01484
	C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//0//1770bp//99%//
	AF026445 C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//0//1639bp//99%//AB007946
	C-NT2RP3004578//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ006266
45	C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.2E-75//464aa//35%//Q02084
	C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%//
	AF093097
	C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.7E-72//254aa//
	45%//P54352
50	C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.6E-98//239aa//64%//P35526
	C-NT2RP4000051//SYNAPTONEMAL COMPLEX-PROTEIN SC65.//4.9E-51//335aa//37%//Q64375 C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//3013bp//99%//AB020657
	C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%//AB011538
	C-NT2RP4000109//Homo sapiens finited for MEGF 5, partial cass/one to represent the Control of th
55	KD SUBUNIT).//0//728aa//99%//Q10568
	C-NT2RP4000129
	C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating protein (ARF1-GAP) mRNA, com-
	plete cds.//3.8E-28//528bp//67%//AF011427

C-NT2RP4000150
C-NT2RP4000151
C-NT2RP4000159
C-NT2RP4000185
C-NT2RP4000210
C-NT2RP4000212
P15287
C-NT2RP4000243
C-NT2RP4000259

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- C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//0//4149bp//99%//AB014600 C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.9E-15//104aa//40%// P15287
  - C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470 C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.7E-84//208aa//76%//Q03173
- 10 C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//153aa//43%//O23968 C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.5E-297//1024aa//55%//P87115
  - C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//1.5E-26//237aa//28%//Q01631
- 15 C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.0000003//101aa// 32%//P26372
  - C-NT2RP4000355
  - C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//0//4074bp//99%//AB018281
  - C-NT2RP4000367//Homo sapiens lkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//4782bp//99%//AF044195
  - C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.6E-77//262aa//54%//O75570
  - C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243 C-NT2RP4000381
- 25 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%//P52738 C-NT2RP4000415
  - C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-AL-PHA-MANNOSIDASE) (FRAGMENT).//2.6E-51//438aa//33%//P45701
  - C-NT2RP4000448//Homo sapiens mRNA; cDNA DKFZp566G0746 (from clone DKFZp566G0746).//0//3991bp//99%//AL050078
  - C-NT2RP4000449
  - C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO.//0.0000003//175aa//27%//P09309 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15)(DEUBIQUITINATING ENZYME 15).// 2.5E-37//291aa//38%//P50101
  - C-NT2RP4000480
    - C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).// 1.9E-67//721aa//29%//Q09475
    - C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%//P40484
- 40 C-NT2RP4000500
  - C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//45%//P45818
  - C-NT2RP4000524
  - C-NT2RP4000541
  - C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%//P40319
- 45 C-NT2RP4000560
  - C-NT2RP4000588
  - C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.9E-188//863bp//99%//AF067730
  - C-NT2RP4000638
- 50 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//0.00000037//175aa//27%//P09309 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.1E-32//350aa//30%//P39625
  - C-NT2RP4000704
  - C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.1E-13//295aa//27%//
  - C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.2E-191//199aa//78%//P10267 C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds.//0//3392bp//95%//AB023148 C-NT2RP4000737

- C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds.//0//3574bp//99%//AB023229 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.// 0.000000032//67aa//31%//P53915
- C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//0//1927bp//99%//AB007939
- 5 C-NT2RP4000833
  - C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.3E-94//810bp//65%//Y18265
    C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.5E-21//271 aa//28%//Q00808
    C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV)(AP-B).//5.7E-82//324aa//48%//009175
- 10 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa//55%//P16415 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%//O35682 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.6E-96//513aa//42%//P22314 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.6E-26//227aa//36%//Q06828
- 15 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-ZYME 1).//1.5E-76//346aa//43%//Q61068
  - C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521
  - C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.00000014//185aa//25%//Q58900
- 20 C-NT2RP4000955
  - C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//90aa//42%//P38660
  - C-NT2RP4000975
  - C-NT2RP4000979
- 25 C-NT2RP4000984
  - C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%//P34579
  - C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700
  - C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%//P39968
- 30 C-NT2RP4001006
  - C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete cds.//0//2482bp//99%//AB023181 C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE)//1.5E-92//443aa//44%//Q09996
  - C-NT2RP4001057
- 35 C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%//Q64375 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.3E-123//563aa//46%//P13586
  - C-NT2RP4001080//Homo sapiens mRNA for Rodi, complete cds.//0//1439bp//99%//AB023967 C-NT2RP4001086
- 40 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAM-INASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa//36%//P51400
  C-NT2RP4001100
  - C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115//224aa//100%//
- 45 C-NT2RP4001122//TIPD PROTEIN.//1.4E-65//253aa//41%//O15736
  - C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%//Q07283
  - C-NT2RP4001138
  - C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18) (SDAP).//0.00000021//93aa//33%//P44514
- 50 C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%//P33750
  - C-NT2RP4001149
  - C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).// 3.4E-29//385aa//29%//P35331
  - C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//
- 4.7E-29//227aa//35%//P52178
   C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.4E-104//1460bp//
  - C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mkNA, complete cds.//4.4E-104//1460bp//65 %//U95760
  - C-NT2RP4001207

- C-NT2RP4001210
- C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.2E-27//90aa//42%//P38660
- C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43%//Q04652
- 5 C-NT2RP4001235
  - C-NT2RP4001256
  - C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2876bp//99%//AB020682
  - C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.4E-58//1196bp//61%//U49082 C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32-%//Q07283
  - C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLO-CASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%//P24391
    - C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.5E-213//1129bp//92%// AJ001119
    - C-NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.//9.2E-160//736bp//99%//AJ007014
- 15 C-NT2RP4001343

10

40

- C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7e-310// 1400bp//100%//AB017494
- C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.4E-58//2425bp//59%//U53445
- 20 C-NT2RP4001353
  - C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.6E-19//222aa//30%//Q08180
  - C-NT2RP4001373
  - C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
- 25 TEIN KINASE 1).//9.2E-17//146aa//35%//P18160
  - C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I.//2E-53//436aa//30%// Q10085
    - C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2716bp//99%//AB023140 C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82%//Q14141
- 30 C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54%//Q99676 C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%//AF129131
  - C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%//Q02218
- 35 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//29%//P39010
  - C-NT2RP4001502
  - C-NT2RP4001507
  - C-NT2RP4001524
  - C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.7E-54//242aa//3 8%//P25656
  - C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mR-NA, complete cds.//0//3202bp//99%//AF152961
    - C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa//24%//P96902
    - C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.00000054//213aa//26,%//Q02453
- 45 C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%//P35197
  - C-NT2RP400157
  - C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0//3046bp//99%//AF100756
  - C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087bp//87%//AJ223830
  - C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).// 1.7E-141//373aa//47%//P73505
    - C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0//1897bp//99%//AB020676 C-NT2RP4001614
      - C-NT2RP4001634
      - C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//234aa//32%//P40469
- 55 C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-19//111aa//45%//P25323
  - C-NT2RP4001677 C-NT2RP4001679
  - C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF

- 100 KD SUBUNIT).//4E-10//243aa//25%//Q10568
- C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10//128aa//32%//Q10282
- C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)
- 5 (DUGT).//6.4E-170//1168aa//33%//Q09332
  - C-NT2RP4001739
  - C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E-236//665aa//58%//P51523
  - C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
- 10 CIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%//P98174 C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete cds.//0//3144bp//99%//AB023232 C-NT2RP4001803
  - C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-OPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%//O35566
- 15 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//54%//P55083 C-NT2RP4001828
  - C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.3E-99//555.bp//73%//AF155595
  - C-NT2RP4001861//TRICHOHYALEN.//1E-35//307aa//34%//P37709
- 20 C-NT2RP4001893//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//1306bp//98%// AL050390
  - C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E1.//0.000000014//345aai/25%//Q00808 C-NT2RP4001901
  - C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258aa//32%//Q12024
- 25 C-NT2RP400193 8//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//38%//P49711
  C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.5E-13//211aa//28%//Q43209
  C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//356aa//27%//P13816
- 30 C-NT2RP4001953
  - C-NT2RP4001966
  - C-NT2RP4001975
  - C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370aa//27%//Q04652 C-NT2RP4002052
- 35 C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//1E-137//679aa//40%//O43143
  - C-NT2RP4002071
  - C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3E-150//722aa// 39%//Q05481
- 40 C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIAL).//0.0000067//250aa//31%//P52655
  C-NT2RP4002298
  - C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//53%//P38938 C-NT2RP4002791
- 45 C-NT2RP4002888//Homo sapiens mRNA; cDNA DKFZp434Fl 72 (from clone DKFZp434F172).//0//2557bp//99%//
  - C-NT2RP4002905
  - C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%//P53552
  - C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.5E-15//280aa//27%//Q00808
- 50 C-NT2RP5003492
  - C-NT2RP5003500
  - C-NT2RP5003506
  - C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.3E-23//219aa//40%//P37116
- 55 C-NT2RP5003524
  - C-NT2RP5003534
  - C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%//P02262
  - C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//0.0000042//102aai/32%//

- 014727 C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//1393bp//97%//AF058922 C-OVARC1000035
- C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).// 0.00000032//60aa//45 %//P80022 5
  - C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%//Q02874
  - C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).// 8 4E-14//259aa//30%//P51610
  - C-OVARC1000113
- C-OVARC1000139//Homo sapiens CGi-21 protein mRNA, complete cds.//0//1562bp//99%//AF132955 10 C-OVARC1000148
  - C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Sp1.// 2.5E-95//461bp//98%//AJ242975
  - C-OVARC1000168
- C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.8E-32//511bp//65%// 15 AF068332
  - C-OVARC1000212
  - C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.2E-120//351aa//54%//Q16665
- C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEU-20 CINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.4E-53//384aa// 30%//P14904
  - C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%//P23249
  - C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//38%//P29363
- C-OVARC1000321 25
  - C-OVARC1000326
  - C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.9E-14// 200aa//27%//P40004
  - C-OVARC1000347
- C-OVARC1000384 30

- C-OVARC1000411
- C-OVARC1000420
- C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%//Q04205
- C-OVARC1000443//Homo sapiens mRNA; cDNA DKFZp434A073 (from clone DKFZp434A073).//0//1216bp// 99%//AL080126
- C-OVARC1000461
  - C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//25%//P11075
  - C-OVARC1000466
  - C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPE-
- CIFICITY PROTEIN PHOSPHATASE VHR).//3.1E-10//125aa//35%//P51452 40
  - C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1919bp//99%//AB020636
  - C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2E-157//892bp//91 %//AF051850
  - C-OVARC1000564
  - C-OVARC1000576
- 45 C-OVARC1000588
  - C-OVARC1000605
  - C-OVARC1000640
  - C-OVARC1000649//Human squamous cell carcinama of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//0//1812bp//98%//D43772
- C-OVARC1000661
  - C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%//P08886
  - C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%//Q58343
  - C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//1113bp//86%//AF001533
  - C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//01/1172bp//97%//AJ130978
- C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1E-215//1027bp//98%//AF132946 55
  - C-OVARC1001162
  - C-OVARC1001243
  - C-OVARC1001296

	C-OVARC1001360
	C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//6E-148//683bp//
	99%//AJ224819
	C-OVARC1001425
5	C-PLACE1000005
	C-PLACE1000066//SSU72 PROTEIN.//1.1E-39//206aa//43%//P53538
	C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.8E-29//
	134aa//43%//P52046
10	C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete cds.//5.5e-312//1411bp//99%// AB020639
10	· · · · · · · · · · · · · · · · · · ·
	C-PLACE1000185
	C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1904bp//99%//AB023194
	C-PLACE1000347
	C-PLACE1000374
15	C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//2208bp//99%//AB020660
	C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ224979
	C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.7E-30//352aa//31%//
	P15151
	C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2E-132//334aa//72%//P23246
20	C-PLACE1000420//7.8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6) (8-OXO-DGTPASE).//
	0.0000028//134aa//29%//P53368
	C-PLACE1000435
	C-PLACE1000444
	C-PLACE1000562
25	C-PLACE1000564
	C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-
	BINDING PROTEIN 1).//1.6E-270//437aa//86%//P32455
	C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//2393bp//99%//AB020657
	C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2E-55//779bp//67%//
30	AF044201
	C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.2E-39//261aa//27%//Q08891
	C-PLACE1000716
	C-PLACE1000748
	C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete-cds.//4.6E-250//1189bp//97%//AB028449
35	C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2002bp//99%//AB014548
	C-PLACE1000798
	C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN
	YHR148W.//2.5E-49//181aa//54%//P32899
	C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.6E-19//404aa//26%//P39010
40	C-PLACE1000948
	C-PLACE1000972
	C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.4E-22//129aa//35%//Q03070
	C-PLACE1001000
	C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%//AF065485
45	C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.3E-54//257aa//46%//Q04652
	C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQ-
	UIEM).//3E-33//138aa//42%//Q61103
	C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.3E-61//
	132aa//46%//Q12929
50	C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, complete sequence.//0//2118bp//
	99%//AC005412
	C-PLACE1001412
	C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22, WORKING DRAFT SEQUENCE, in unordered
	pieces.//0//1440bp//99%//AL031660
55	C-PLACE1001503
	C-PLACE1001570
	C-PLACE1001610
	C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)

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(THIOESTERASE n).//4E-81//263aa//56%//P08635
        C-PLACE1001729
        C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.5E-75//439aa//41%//P16381
        C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.4E-63//427aa//35%//
5
        C-PLACE1001810
        C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//
        0//1995bp//99%//AF058953
        C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%//P94524
        C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0//1196bp//99%//AF131737
10
        C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935
        C-PLACE1001928
        C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091
        C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%//Q61211
        C-PLACE1002072
15
        C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLA-
        SE).//0.00000053//188aa//29%//P49606
         C-PLACE1002140
         C-PLACE1002163
20
         C-PLACE1002170
         C-PLACE1002433
         C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133aa//29%//Q13105
         C-PLACE1002465
        C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.7E-214//956bp//94%//AB018256
         C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//
25
         1750bp//99%//AF068180
         C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//305aai/33%//Q15391
         C-PLACE1002794
         C-PLACE1002815
30
         C-PLACE1002839
         C-PLACE1002851
         C-PLACE1002941
         C-PLACE1002996
         C-PLACE1003045
         C-PLACE1003092
35
         C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%//Q13268
         C-PLACE1003108
         C-PLACE1003145
         C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
         LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.8E-37//143aa//51%//P42743
40
         C-PLACE1003190//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750
         C-PLACE1003200
         C-PLACE1003296//Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173).//0//1706bp//
         C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.9E-206//396aa//86%//
 45
         P51522
         C-PLACE1003334
         C-PLACE1003342
         C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete
         cds.//0//2435bp//99%//U92715
 50
         C-PLACE1003369
         C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%//D83200
         C-PLACE1003611
          C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.2E-10//380aa//25%//P18824
          C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR
 55
          SRP75).//8E-19//209aa//34%//Q08170
          C-PLACE1003711
          C-PLACE1003723
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C-PLACE1003762

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C-PLACE1003771
        C-PLACE1003784
        C-PLACE1003923
5
        C-PLACE1003936
        C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//
        2.4E-124//326aa//73%//P80385
        C-PLACE1004104
        C-PLACE1004114
        C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA
10
        CHAIN 4).//6.1E-181//340aa//96%//P29387
        C-PLACE1004149
        C-PLACE1004156
        C-PLACE1004161
        C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%//AJ010071
15
        C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.5E-10//208aa//27%//Q62556
        C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//
        0//1882bp//99%//AF069493
        C-PLACE1004258
        C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36//389aa//31%//O15393
20
        C-PLACE1004277//Homo sapiens two pore domain K<sup>+</sup> channel (TASK-2) mRNA, complete cds.//0//1498bp//99%//
        AF084830
        C-PLACE1004289
         C-PLACE1004302//SOF1 PROTEIN.//1.9E-110//325aa//48%//P33750
25
        C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767bp//99%//Y11588
         C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//
        2512bp//99%//AF100153
        C-PLACE1004376
        C-PLACE1004388
30
        C-PLACE1004405
        C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa//33%//Q63448
        C-PLACE1004437//Human NAD*-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene
         encoding mitochondrial protein, complete cds.//0//985bp//99%//U49283
        C-PLACE1004451
35
         C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%//P25823
         C-PLACE1004473
        C-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete//1.3E-209//954bp//
        99%//AF026445
        C-PLACE1004516
40
        C-PLACE1004548
        C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100
        KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%//Q10568
        C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//264aa//32%//Q13438
        C-PLACE1004645
45
        C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.4E-42//985bp//59%//
        X66277
        C-PLACE1004664
        C-PLACE1004672
        C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.6E-95//191aa//
50
        96%//P12815
        C-PLACE1004691
        C-PLACE1004722
        C-PLACE1004736
        C-PLACE1004740
        C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPO-
55
        NENT) (N- RECOGNIN).//4.4E-35//578aa//27%//O60152
        C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyttransferase ST3Gal VI, complete cds.//7.1E-224//
        790bp//98%//AB022918
```

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C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.9E-32//259aa//
        32%//P30337
        C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLA-
        SE).//4.7E-65//695aa//29%//Q01631
        C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR
5
        SRP75).//5.9E-19//196aa//36%//Q08170
        C-PLACE1004824
        C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%//Q08891
        C-PLACE1004885
        C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE
10
        SPAC10F6.02C.//9.3E-11//94aa//47%//O42643
        C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDHA).//4.9E-48//198aa//44%//
        C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds//0//1853bp//98%//AF099936
15
        C-PLACE1004934
        C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%//Q93794
        C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2E-14//205aa//26%//
        Q11073
        C-PLACE1004982
        C-PLACE1005026
20
        C-PLACE1005027
        C-PLACE1005046
        C-PLACE1005077
        C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//1E-209//1031bp//96%//L40401
        C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%//Q04652
25
        C-PLACE1005111
        C-PLACE1005181
        C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%//P05636
        C-PLACE1005206
         C-PLACE1005232
30
        C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577
         C-PLACE1005261
         C-PLACE1005266
         C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//3.2E-297//1341bp//100%//AB011182
         C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%//P53352
35
         C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//
         226aa//92%//P08760
         C-PLACE1005308
         C-PLACE1005313
40
         C-PLACE1005327
         C-PLACE1005335
         C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYN-
         THASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.6E-09//194aa//
         27%//O33335
         C-PLACE1005374
 45
         C-PLACE1005480
         C-PLACE1005481
         C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//
         C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.6E-52//173aa//
 50
         57%//Q09251
         C-PLACE1005550
         C-PLACE1005554
         C-PLACE1005623
         C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//
 55
         C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLE-
         OTIDE REDUCTASE).//2.1E-148//321aa//83%//P31350
```

C-PLACE1005730

```
C-PLACE1005755
        C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)
        (THIOESTERASE II).//2.5E-79//209aa//53%//P08635
5
        C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.1E-217//994bp//99%//
        AF027156
        C-PLACE1005851
        C-PLACE1005921//AIG1 PROTEIN.//3E-31//284aa//31%//P54120
        C-PLACE1005923
10
        C-PLACE1005925
        C-PLACE1005934
        C-PLACE1005936
        C-PLACE1005951
        C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.7E-30//198aa//37%//P43636
15
        C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)//5.4E-
        54//455aa//32%//P14904
        C-PLACE1005966/TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90).//0.00000014//
        254aa//25%//P38129
        C-PLACE1005990
20
        C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%//AJ236876
        C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.7E-161//744bp//99%//X99906
        C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.5E-148//681bp//99%//
        AF039023
        C-PLACE1006139
25
        C-PLACE1006159
        C-PLACE1006167
        C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cds.//4.5E-293//953bp//99%//AB020706
        C-PLACE1006195
        C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.7E-116//496aa//48%//Q09747
30
        C-PLACE1006225
        C-PLACE1006236
        C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2E-16//244aa//31%//
        P28675
35
        C-PLACE1006246
        C-PLACE1006325//Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142).//3.8E-278//
        1271-bp//99%//AL080066
        C-PLACE1006335
        C-PLACE1006357
        C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%//AF062085
40
        C-PLACE1006412
        C-PLACE1006414
        C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45//122aa//43%//P49910
        C-PLACE1006445
45
        C-PLACE1006470
        C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-55//142aa//85%//Q90595
        C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.1E-229//367aa//96%//
        Q00004
        C-PLACE1006492
50
        C-PLACE1006531
        C-PLACE1006552
        C-PLACE1006598//Homo sapiens clone NH0310K15, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//
        2182bp//99%//AC007383
        C-PLACE1006615
55
        C-PLACE1006626//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1760bp//99%//AB023145
        C-PLACE1006673
        C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.8E-24//
        734bp//62%//AB015630
```

	C-PLACE1006704
	C-PLACE 1000704  C-PLACE 1000704  C-PLACE 10007031//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.9E-13//177aa//33%//Q59263
	C-PLACE1006782
_	C PLACE1006819/J. INE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8E-213//232aa//80%//P0854/
5	O DI ACE 1006930//URIQUITIN CARROYYI - TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-
	RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-
	TOUS NUCLEAR PROTEIN).//2E-15//188aa//29%//P35123
	C-PLACE1006883
10	C-PLACE1006901
	C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%//Q99181
	C-PLACE1006932
	C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.7E-48//278aa//41%//
	Q10000
15	C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E-86//522aa//36%//P97998
	C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%//
	AB023421
	C-PLACE1006961
	C-PLACE1006962
20	C-PLACE1006966 C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12)
	(DER12).//3.2E-35//180aa//33%//Q14542
	C-PLACE1007021
	C-PLACE1007105
25	O DI A 054007479
	C-PLACE1007176  C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1)
	(COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1E-42//3/0aa//31%//F34304
	C B! ACE1007238
	C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.5E-
30	216//1068bp//96%//D50495
	C-PLACE1007242 C-PLACE1007243//UNC-47 PROTEIN.//0.00000017//211aa//27%//P34579
	C-PLACE1007243/JONC-47 PROTEIN://0.000000 17/12 11dat/21 John Color Colo
	C-PLACE 1007274
35	C-PLACE 1007274  C-PLACE 1007282
55	O DI A 0E 1007201
	C-PLACE1007301  C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.1E-17//1037bp//56%//
	AF117649
	C-PLACE1007342
40	C-PLACE 1007342  C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//
	99%//AF096870
	C-PLACE1007367
	C-PLACE 1007367  C-PLACE 1007367  C-PLACE 1007367  C-PLACE 1007367
	30%//P27715
45	C-PLACE1007386 C-PLACE1007402
	O DI A CEACOZAGO/ANULTE PROTEIN //1 1F-64//42822//32%//Q17320
	C. DI ACE1007416//DIPERTIDY: PEPTIDASE IV (EC.3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD20)
	(TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.8E-25//140aa//35%//P27487
50	C-PLACE1007450
	C-PLACE1007452
	C-PLACE1007460
	C-PLACE1007484
	C-PLACE 1007464  C-PLACE 1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
55	CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.4E-53//426aa//33%//P52734

C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.4E-85//385aa//

C-PLACE1007507

45%//P08728

- C-PLACE1007524
- C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316// 1485bp//98%//AF159164
- C-PLACE1007544
- 5 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1E-49//361aa//36%// P34537
  - C-PLACE1007583
  - C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.6E-143//666aa//44%//Q99676
  - C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//713bp//99%//AB023194
- 10 C-PLACE1007621
  - C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//0.0000001//228aa//31%//P32506
  - C-PLACE1007645
  - C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1952-bp//99%//AB023194
  - C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//
- 15 8.7E-09//279aa//28%//Q26457
  - C-PLACE1007690
  - C-PLACE1007697//GCN20 PROTEIN.//7.6E-119//717aa//38%//P43535
  - C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%//AF061243
- 20 C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.5E-44//231aa//42%//P10265 C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//9.2E-294//1504bp//94%// AB014585
  - C-PLACE1007746
  - C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%//AB019602
- 25 C-PLACE1007810
  - C-PLACE1007843
  - C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 3/13.//0//1751bp//99%//AP000010
  - C-PLACE1007858/Homo sapiens mRNA for KIAA0766 protein, complete cds.//0//3112bp//99%//AB018309
- 30 C-PLACE1007897
  - C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.6E-14//370aa//25%//Q99323
  - C-PLACE1007954
  - C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//
- 35 AF084530
  - C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2300bp//99%//AF079529
  - C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.1E-36//202aa//48%//P52272
- 40 C-PLACE1007990
  - C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//6.1E-14//128aa//39%//Q63622
  - C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0// 1833bp//99%//AC005628
- 45 C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NU-CLEOPORIN) (P105).//4.6e-318//613aa//94%//P52590
  - C-PLACE1008095
  - C-PLACE1008122
  - C-PLACE1008129
- 50 C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.3E-24//395aa// 31%//Q09531
  - C-PLACE1008177/TRICHOHYALIN.//2.3E-29//487aa//26%//P37709
  - C-PLACE1008209
  - C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.3E-283//
- 55 671aa//77%//P53620
  - C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.3E-18//162aa//37%//P12689
  - C-PLACE1008280
  - C-PLACE1008309

	C-PLACE1008329
	C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//0//1853bp//100%//AB014579
	C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.3E-114//243aa//87%//P05432
	C DI ACE1008401
5	C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED
	PROTFIN) (TAP).//0//698aa//95%//P41541
	C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.1E-11//189aa//32%//Q06527
	C-PLACE1008457
	C-PLACE1008465
10	C DI ACE1008488
70	C DI ACE 1009534//Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a
	gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs,
	the gene for a novel BZRP (peripheral benzodiazapine recepto//0//1980bp//99%//AL031778
	C-PLACE1008531
45	C-PLACE1008532
15	C-PLACE1008532//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.1E-09//62aa//
	48%//P22620
	C-PLACE1008568 C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NU-
	CLEOPORIN) (P140).//7.8E-236//453aa//96%//P37199
20	
	C-PLACE1008621
	C-PLACE1008626 C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591
	C-PLACE1008629 C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//0//1548bp//100%//
25	
	AF044333
	C-PLACE1008693 C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8)
	gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF038406
	C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA
30	C-PLACE 1008/30//IMPORTIN ALFTIA-0 3000//IT (10///10/11/10///10///
	S2).//3.1E-280//533aa//98%//O35345 C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.3E-269//1225bp//99%//
	AJ004974
	C-PLACE1008813
35	C-PLACE1008854
	C-PLACE1008867
	C-PLACE1008887
	C-PLACE1008902
	C-PLACE1008925 C-PLACE1009020//NIFS PROTEIN.//3.9E-55//279aa//41%//P12623
40	C-PLACE1009020//NIFS PROTEIN.//3.9E-33//27-9aa//47////1919bp//99%//AJ003112
	C-PLACE1009045 C-PLACE1009060//BRO1 PROTEIN.//6.7E-19//567aa//24%//P48582
	C-PLACE1009090
45	C-PLACE1009091 C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.9E-44//480aa//30%//
	P30432 C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452aa//67%//P51814
	C-PLACE1009110
50	C-PLACE1009111  C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2) (ONCOGENIC PROTEIN-ASSOCIATED
	C-PLACE1009130//UBIQUITIN-PROTEIN LIGAGE ESA (EG 0.0.2.7) (6100001101)
	PROTEIN E6-AP).//2E-68//181aa//43%//Q05086
	C-PLACE1009158
	C-PLACE1009166
55	C-PLACE1009174
	C-PLACE1009186
	C-PLACE1009190
	C-PLACE1009230

EP 1 074 617 A2 C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.1E-132//1229bp//75%//AF107295 C-PLACE1009328 C-PLACE1009335 C-PLACE1009338 C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.5E-10//151aa//29%//Q12067 C-PLACE1009375 C-PLACE1009388 C-PLACE1009404/HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME 1.//0.000000047// 165aa7/33%//Q09820 C-PLACE1009434 C-PLACE1009443 C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KI-NASE) (PI4K-ALPHA).//7.8E-71//82aa//89%//P42356 C-PLACE1009459 C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1E-289//550aa//93%//P54319 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//3.9E-40// 179aa//37%//P34580 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FAC-TOR).//8.1E-99//228aa//75%//Q99418 C-PLACE1009542 C-PLACE1009571 C-PLACE1009581 C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.1E-54//291aa//40%//Q00808 C-PLACE1009607 C-PLACE1009621 C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3E-60//209aa//41%//P25159 C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAPI PROTEIN).//1.5E-285//538aa//99%// P55161 C-PLACE1009665 C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp//100%//AF062534 C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//7E-33//166aa//43%//Q09876 C-PLACE1009721//MSF1 PROTEIN.//1.7E-22//176aa//33%//P35200 C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%//P54120 C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds.//4.3E-294//1329bp// 100%//AB012190 C-PLACE1009794 C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//2685bp//99%//AB020712 C-PLACE1009886 C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION.//1.9E-108//277aa//43%//P53145 C-PLACE1009971 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.6E-59//450aa//34%// C-PLACE1009995//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1962bp//99%// C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.2E-70// 736bp//73%//U48288 C-PLACE1010023 C-PLACE1010031 C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//6E-279//1402bp//94%//X84692

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- C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%//AF065482
- C-PLACE1010076 C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.4E-268//506aa//98%//Q62671
  - C-PLACE1010102
  - C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537aa//44%//004652
  - C-PLACE1010106//Homo sapiens mRNA; cDNA DKFZp586M1418 (from clone DKFZp586M1418).//0//1974bp//

99%//AL049385

C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.7E-20//156aa//42%//P22082

C-PLACE1010148//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.00000046//431aa//23%//P35662 5 C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.8E-11//95aa//49%//Q01130 C-PLACE1010202

C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62%//P25722

C-PLACE1010274//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123).//0//1964bp//99%// 10 AI 080122

C-PLACE1010293

C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).// 1.1E-09//350aa//22%//P52178

C-PLACE1010324 15

C-PLACE1010329

C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//0.0000000002//126aa//29%//P34024 C-PLACE1010364

C-PLACE1010383 20

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C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cds.//0//2121bp//99%//AB020643 C-PLACE1010491

C-PLACE1010492

C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//

0//1981bp//99%//AB022718 25

C-PLACE1010529 C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000012//616aa//24%//

C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0// 1904bp//99%//AB017546

C-PLACE1010616

C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%//P02642 C-PLACE1010629

C-PLACE1010630

C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39%//Q01755 35 C-PLACE1010714

C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4E-299// 1091bp//99%//AB019987

C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.9E-91//668bp//82%//

C-PLACE1010771//M.musculus HCNGP mRNA.//7.4E-168//966bp//89%//X68061

C-PLACE1010786

C-PLACE1010800

C-PLACE1010811

C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.3E-143//407aa// 45

C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//0//1885bp//99%//AB011182

C-PLACE1010900

C-PLACE2000050

C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN)-// 50 2.4E-191//828aa//48%//P21783

C-PLACE4000590

C-PLACE4000638

C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.9E-17//201aal/34%//

P49816 55

C-Y79AA1001647

Homology Search Result Data 7.

[0315] The result of the homology search of the SwissProt using the 5'-end sequence (54 clones selected in EXAM-PLE 16).

5 [0316] Data include

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the name of clone,

definition of the top hit data,

the P-value: the length of the compared sequence: identity (%), and

the organism and the Accession No. of the top hit data, as in the order separated by //.

[0317] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497//METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G).//0.13//52//38//P25860

F-HEMBA1001750//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME
64E).//2.2e-28//104//59//Q24574

F-HEMBA1003854//VERPROLIN.//0.012//138//31//P37370

F-HEMBA1004193//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) (FRAGMENT).//0.93//39//33//Q37131

F-HEMBA1004860//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2).//0.90//20//50//P38524 F-HEMBA1005572//ZINC FINGER PROTEIN 124 (HZF-16).//7.6e-46//141//58//Q15973

F-HEMBA1006038//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENT).//0.0033//32//46//P70560

F-HEMBA1006092//VERPROLIN.//1.0//62//35//P37370

F-HEMBA1006406//MATING PHEROMONE ER-10 PRECURSOR (EUPLOMONE R10).//0.30//41//36//P12350 F-HEMBA1006650//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.089//21//52//Q02593 F-HEMBA1006812//HEAT SHOCK PROTEIN HTGA (HEAT SHOCK PROTEIN HTPY).//0.38//156//30//P28697 F-HEMBB1000672

F-HEMBB1001197//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0//30//36//P16012

30 F-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//3.7e-54// 241//47//P47853

F-MAMMA1001252//HYPOTHETICAL 9.1 KD PROTEIN IN NIRQ 3'REGION (ORF3).J/0.59//48//39//Q51483 F-MAMMA1002094

F-NT2RM4000634//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.26//58//27//P06333

F-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//8.9e-20//83//48//P10895 F-NT2RM4000783//ZINC FINGER PROTEIN (FRAGMENT).//1.0//42//40//P19326

F-NT2RM4000857//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR (ALS).//6.0e-23//207//32//002833

40 F-NT2RM4001178//HOMEOBOX PROTEIN OTX3 (ZOTX3).//0.012//156//28//Q90267

F-NT2RM4002420//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//0.0012//81//37//P13816

F-NT2RP2000198//CREB-BINDING PROTEIN.//0.29//98//37//Q92793

F-NT2RP2000551//PROTEIN Q300.//0.00017//23//60//Q02722

F-NT2RP2000660//HYPOTHETICAL PROTEIN MJ0401.//1.0//41//29//Q57844

45 F-NT2RP2001214//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.27//13//61//Q01644

F-NT2RP2001460//PROTEIN KINASE C-LIKE (EC 2.7.1.-).//0.089//99//29//Q99014

F-NT2RP2001756//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT)-//4.0e-13//177// 28//P16372

F-NT2RP2002056//HYPOTHETICAL 6.0 KD PROTEIN IN THI12 5'REGION.//0.37//12//75//P53820

50 F-NT2RP2002677//NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3).//0.99//61//32//Q42616 F-NT2RP2002755//OCTAPEPTIDE-REPEAT PROTEIN T2.//3.3e-10//90//35//Q06666

F-NT2RP2002843//CYTOCHROME B.//0.78//103//26//P48884

F-NT2RP2003101//ATPASE INHIBITOR, MITOCHONDRIAL HOMOLOG.//0.40//28//46//P37209

F-NT2RP2003799//HYPOTHETICAL PROTEIN MJ0116.1.//0.80//55//32//P81303

55 F-NT2RP2004095

F-NT2RP2004732

F-NT2RP2004920//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.18//18//55//Q48251

F-NT2RP2005454

F-NT2RP2005776//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-FERASE) (FRAGMENT).//7.4e-38//136//41//P51003

F-NT2RP2005806//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.0e-08//180//28//P32323 F-NT2RP2005882

- F-NT2RP3001282//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.0022//69//39//P39217 5 F-NT2RP3001723//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).//0.00035//127//31//P15276
  - F-NT2RP3002099//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.97//71//28//P05204

F-NT2RP3003155//CCAAT DISPLACEMENT PROTEIN (HOMEOBOX PROTEIN CLOX) (CLOX-1) (FRAG-MENT).//0.064//110//34//P39881

F-NT2RP3004028//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.020//95// 29//P15583

F-OVARC1000008//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.8e-05//165//29// P17437

F-OVARC1000724//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAG-15 MENT).//0.035//152//30//P10162

F-OVARC1000751//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VMW118 PROTEIN).//0.38//124// 31//P28284

F-OVARC1001029

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F-PLACE1000814//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.45//61//24//Q42377 20 F-PLACE1003030//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PRO-TEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.70//121//32//P47845

F-PLACE1005549//RHO1 GDP-GTP EXCHANGE PROTEIN 1 (PROTEIN KINASE C SUPPRESSOR SKC1).// 3.2e-08//205//24//P53046

F-PLACE1007218//IG KAPPA CHAIN V-III REGION (PC 7210).//0.99//52//38//P01668

Homology Search Result Data 8.

[0318] The result of the homology search of the GenBank using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) except EST and STS. [0319] Data include

the name of clone,

definition of the top hit data,

the P-value: the length of the compared sequence: identity (%), and

the Accession No. of the top hit data, as in the order separated by //.

[0320] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497

F-HEMBA1001750//Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs.//6.6e-101//473//99//V00710

F-HEMBA1003854//Homo sapiens clone RG270D13, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 18 unordered pieces.//1.7e-05//412//61//AC005081

F-HEMBA1004193//Human BAC clone RG343H22 from 7q31, complete sequence.//0.77//466//59//AC002386 F-HEMBA1004860//Human pigment epithelium-derived factor gene, complete cds.//6.7e-07//492//57//U29953 F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt].//2.9e-47//341//77//S54641

F-HEMBA1006038//Human DNA sequence from clone 989H11 on chromosome 22q13.1-13.2, complete sequence.//0.28//436//59//Z83851

F-HEMBA1006092//Human chromosome 16pl3.11 BAC clone CIT987SK-29B12 complete sequence.//0.28//309// 60//U95738

F-HEMBA1006406//HS\_2268\_B2\_C07\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=14 Row=F, genomic survey sequence.//3.7e-69//340//99//AQ070566 F-HEMBA1006650//H.sapiens CpG island DNA genomic Mse1 fragment, clone 5h5, forward read cpg5h5.f1a.//

9.4e-24//143//96//Z55730 F-HEMBA1006812//X.laevis xUBFalphal mRNA for upstream binding factor 2.//0.96//234//64//X59863

- F-HEMBB1000672//CIT-HSP-2350H6.TF CIT-HSP Homo sapiens genomic clone 2350H6, genomic survey sequence.//1.1e-68//375//94//AQ059158
- F-HEMBB1001197//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//2.8e-10//229//66//
- 5 F-HEMBB1001871//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//1.2e-27//619//62// AF038127
  - F-MAMMA1001252
  - F-MAMMA1002094//H.sapiens CpG island DNA genomic Mse1 fragment, clone 184g7, forward read cpg184g7.ft1a.//3.4e-29//167//97//Z59993
- F-NT2RM4000634//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//1.4e-21//230//73//
  - F-NT2RM4000657//Human mRNA for phospholipase C, complete cds.//0.029//245//61//D42108
  - F-NT2RM4000783//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//3.7e-36// 324//70//AC005199
- 15 F-NT2RM4000857//RPCI11-49P19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-49P19, genomic survey sequence.//1.5e-62//322//97//AQ051961
  - F-NT2RM4001178//Streptomyces coelicolor cosmid 7H1.//0.0025//296//62//AL021411
  - F-NT2RM4002420//Homo sapiens chromosome 17, clone hRPK.63\_A\_1, complete sequence.//0.00013//121//76//AC005670
- 20 F-NT2RP2000198//Human platelet glycoprotein IX mRNA, 3' end.//0.016//246//62//M25827
  - F-NT2RP2000551//Rattus norvegicus microsatellite sequence clone 82G9.//2.0e-08//223//69//AJ233812
  - F-NT2RP2000660//Homo sapiens chromosome 19, cosmid R30953, complete sequence.//0.0073//209//66// AC005622
  - F-NT2RP2001214

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- 25 F-NT2RP2001460//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.0//80//76// AC005189
  - F-NT2RP2001756//CIT-HSP-2373P1.TR CIT-HSP Homo sapiens genomic clone 2373P1, genomic survey sequence.//3.0e-38//220//94//AQ110589
  - F-NT2RP2002056//Genomic sequence from Human 17, complete sequence.//1.2e-80//317//91//AC002094
- 30 F-NT2RP2002677//Homo sapiens chromosome 10 clone CIT987SK-1031G15 map 10q25, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 1 ordered pieces.//0.032//141//70//AC006097
  - F-NT2RP2002755//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 9/13.7/1.8e-22// 377//69//AP000018
  - F-NT2RP2002843//Homo sapiens BAC clone RG030L05 from 7q22, complete sequence.//6.5e-16//311//63//
  - F-NT2RP2003101//Human FMR1 gene, 5' end.//0.32//105//67//L19476
  - F-NT2RP2003799//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//1.6e-33// 119//96//X52233
  - F-NT2RP2004095//HS\_3083\_A1\_A02\_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3083 Col=3 Row=A, genomic survey sequence.//1.0e-14//154//79//AQ106698
  - F-NT2RP2004732//CIT-HSP-631P16.TP CIT-HSP Homo sapiens genomic clone 631P16, genomic survey sequence.//2.3e-20//120//99//B79035
  - F-NT2RP2004920//Plasmodium falciparum MAL3P4, complete sequence.//0.030//397//59//AL008970
  - F-NT2RP2005454//Plasmodium falciparum chromosome 2, section 47 of 73 of the complete sequence.//0.97// 455//56//AE001410
    - F-NT2RP2005776//H.sapiens PAP mRNA.//1.0e-33//451//68//X76770
    - F-NT2RP2005806//Mus musculus musculus sex determining protein (Sry) gene, complete cds.//0.029//412//60//
    - F-NT2RP2005882//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//9.4e-25//155//90//Z93242
    - F-NT2RP3001282//RPCI11-52L16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-52L16, genomic survey sequence //3.2e-21//122//100//AQ052775
    - F-NT2RP3001723//H.sapiens CpG island DNA genomic Mse1 fragment, clone 13g5, reverse read cpg13g5.rt1a.// 2.2e-18//163//85//Z56771
- 55 F-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296\_K\_1, complete sequence.//1.3e-76//351//86// AC005180
  - F-NT2RP3003155
  - F-NT2RP3004028//Sequence 1 from patent US 5618695.//3.3e-13//217//70//140055

F-OVARC1000008///0.0040//674//57//M82836

F-OVARC1000724//Herpes simplex virus type I immediate early (IE) gene 3 for transcriptional activator IE175 (= ICP 4).//1.1e-07//519//59//X06461

F-OVARC1000751//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//7.2e-11//509//62//AC004221

F-OVARC1001029//Human DNA sequence from clone 19408 on chromosome 6q24.1-25.3 Contains STS and GSSs, complete sequence.//1.1e-05//388//61//AL031769

F-PLACE1000814//Homo sapiens BAC clone GS011E15 from 5q31, complete sequence.//1.4e-84//717//78//AC002427

F-PLACE1003030

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F-PLACE1005549//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//4.9e-56//709//68//U02081

F-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//3.1e-39//214//98//AL031660

Homology Search Result Data 9.

[0321] The result of the homology search of the GenBank using the clone sequence of 3'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

20 [0322] Data include

the name of clone,

definition of the top hit data,

the P-value: the length of the compared sequence: identity (%), and

the Accession No. of the top hit data, as in the order separated by //.

[0323] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0324] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000497//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.4e-38//185//84//U14567
R-HEMBA1001750//Hansenula wingei mitochondrial DNA, complete sequence.//1.7e-07//399//59//D31785
R-HEMBA1003854//Human DNA sequence from clone 224A6 on chromosome 1p35.1-36.23 Contains part of a gene similar to Mouse Wnt-4 protein, the gene for CDC42 (cell division cycle 42 (GTP-binding protein, 25kD)), ESTs, STSs, GSSs and a CpG Island, complete sequence.//1.4e-75//309//85//AL031281

R-HEMBA1004193//\*\*\*ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-34//188//81//U14567
R-HEMBA1004860//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-06//239//66//AC004241

R-HEMBA1005572//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2, complete sequence.//3.1e-21//341//67//AJ010598

40 R-HEMBA1006038//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//1.7e-24//307//71//
AC004678

R-HEMBA1006092//H.Sapiens mRNA for alpha2-subunit of soluble guanylyl cyclase.//0.76//246//62//X63282 R-HEMBA1006406//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4 Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.3e-31//297//77//AL023574

R-HEMBA1006650//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.8e-15//350//65//AC003071

R-HEMBA1006812//Homo sapiens chromosome X clone RP3-424J12, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//1.8e-55//430//81//Z82207

R-HEMBB1000672//Homo sapiens clone UWGC:y54c283 from 6p21, complete sequence.//9.1e-39//437//71// AC006166

R-HEMBB1001197//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.5e-37//275//85//AC004593

R-HEMBB1001871//Plasmodium falciparum chromosome 12 clone 3D7, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 5 unordered pieces.//0.00097//410//59//AC004688

R-MAMMA1001252//Homo sapiens clone 201104, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 4 unordered pieces.// 2.9e-13//364//64//AC004529

R-MAMMA1002094//HS\_3163\_A1\_A09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=17 Row=A, genomic survey sequence.//5.9e-41//256//91//AQ141441

- R-NT2RM4000634//Homo sapiens chromosome 19, cosmid R30783, complete sequence.//1-6e-21//283//73//AC005258
- R-NT2RM4000657
- R-NT2RM4000783
- 5 R-NT2RM4000857//RPCI11-63K2.TK RPCI-11 Homo sapiens genomic clone RPCI-11-63K2, genomic survey sequence.//4.0e-07//62//98//AQ203073
  - R-NT2RM4001178
  - R-NT2RM4002420

- R-NT2RP2000198//Homo sapiens Chromosome 16 BAC clone CIT987-SK37914 -complete genomic sequence, complete sequence.//0.58//108//67//AC002307
  - R-NT2RP2000551//Homo sapiens DNA, pseudoautosomal boundary-like sequence PABL2.//6.2e-72//391//87//
  - R-NT2RP2000660//Homo sapiens chromosome 17, clone hRPK.640\_I\_15, complete sequence.//0.0058//166//69//AC005324
- R-NT2RF2001214//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//0.93//117//65//U49822 R-NT2RP2001460
  - R-NT2RP2001756//CIT-HSP-2382021.TR CIT-HSP Homo sapiens genomic clone 2382021, genomic survey sequence.//3.4e-91//507//92//AQ114228
- 20 R-NT2RP2002056//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//0.00022//225//69//Z97181 R-NT2RP2002677//CIT-HSP-2349K20.TF CIT-HSP Homo sapiens genomic clone 2349K20, genomic survey sequence.//3.1e-29//178//94//AQ062168
  - R-NT2RP2002755//Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X \*.//5.3e-39//449//72//Z81014
    - R-NT2RP2002843//Homo sapiens chromosome 17, clone hRPK.22\_N\_12, complete sequence.//0.0097//498//59//AC005412
    - R-NT2RP2003101//CIT-HSP-238301.TR CIT-HSP Homo sapiens genomic clone 238301, genomic survey sequence.//1.2e-32//344//75//AQ196754
- 30 R-NT2RP2003799////3.6e-05//408//60//AL010237
  - R-NT2RP2004095//Plasmodium falciparum chromosome 4 strain 3D7, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//2.1e-10//455//61//AL034557
  - R-NT2RP2004732//Human DNA sequence from clone 703H14 on chromosome 1q23.2-24.3 Contains 3' end of a novel gene, ESTs, CA repeat(D1S445), STS, GSSs, complete sequence.//5.1e-51//383//74//AL031287
- 35 R-NT2RP2004920//Homo sapiens chromosome 5, P1 clone 878H11 (LBNL H45), complete sequence.//0.062// 315//61//AC005219
  - R-NT2RP2005454//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindDIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//0.75//246//63// Z86062
- 40 R-NT2RP2005776//Homo sapiens PAC clone DJ1189D06 from 7p15.3-p14, complete sequence.//0.91//232//61// AC005232
  - R-NT2RP2005806//Human neurofibromatosis type 1 (NF1) gene, intron 19a, complete sequence.//1.3e-19//405//66//U37368
  - R-NT2RP2005882//Plasmodium falciparum MAL3P1, complete sequence.//1.1e-09//533//60//Z97348
- 45 R-NT2RP3001282//Plasmodium falciparum MAL3P8, complete sequence.//0.00026//499//58//AL034560 R-NT2RP3001723//Human BAC clone RG354L07 from 7q31, complete sequence.//0.00035//337//61//AC002466 R-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296\_K\_1, complete sequence.//1.8e-44//307//86// AC005180
  - R-NT2RP3003155
- 50 R-NT2RP3004028//F14A6-Sp6 IGF Arabidopsis thaliana genomic clone F14A6, genomic survey sequence.//0.95//95//65//B21351
  - R-OVARC1000008
  - R-OVARC1000724//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.91//83//71//AC005161
- R-OVARC1000751//HS\_2222\_A2\_C09\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=18 Row=E, genomic survey sequence.//2.8e-12//176//72//AQ033143
  R-OVARC1001029//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence.//1.2e-09//165//75//AC002357

R-PLACE1000814//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence.//6.2e-52//514//75// AC004744

R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//9.6e-33//225//90//AF032387

R-PLACE10e5549//Arabidopsis thaliana genomic DNA, chromosome 5, TAC cione: K19P17, complete sequence.//0.097//323//61//AB007644

R-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, \*\*\* SEQUENCING IN PROGRESS \*\*\*, in unordered pieces.//1.1e-88//497//91//AL031660

Homology Search Result Data 10. 10

> [0325] The result of the homology search of the Human Unigene using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) .

[0326] Data include

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the name of clone,

title of the top hit data,

the P-value: the length of the compared sequence: identity (%), and

the Accession No. of the top hit data, as in the order separated by //.

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[0327] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497//ou15a11.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1626332 3', mRNA sequence.//1.0//186//65//AI018130

F-HEMBA1001750//Human mRNA for TI-227H.//2.5e-101//473//99//D50525

F-HEMBA1003854//Homo sapiens mRNA for KIAA1031 protein, partial cds.//7.2e-06//103//80//AB028954

F-HEMBA1004193//Homo sapiens mRNA for TL132.//0.75//334//59//AJ012755

F-HEMBA1004860//ny07e01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1271064 3' similar to contains Alu repetitive element;, mRNA sequence.//3.7e-06//140//70//AA749151

F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatob-30 lastoma cell line, HEP-G2, mRNA, 2080 nt].//1.1e-48//341//77//S54641

F-HEMBA1006038//Homo sapiens gene for insulin receptor substrate-2, complete cds.//0.036//297//60// AB000732

F-HEMBA1006092//ab80f12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853295 3' similar to contains Alu repetitive element;, mRNA sequence.//0.65//150//63//AA663266

F-HEMBA1006406//ws26e11.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2498348 3' similar to TR: 002710 002710 GAG POLYPROTEIN; mRNA sequence.//1.4e-32//518//67//AI989639

F-HEMBA1006650//Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds.//1.3e-19//136//90//AF006087

F-HEMBA1006812//zh49f01.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE: 40 415417 3', mRNA sequence.//1.3e-120//579//98//W80404

F-HEMBB1000672//Homo sapiens mRNA for KIAA1040 protein, partial cds.//0.00047//706//57//AB028963

F-HEMBB1001197//tq45e03.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2211772 3' similar to TR: 001940 001940 STRAWBERRY NOTCH ;, mRNA sequence.//1.2e-16//117//92//AI580023

F-HEMBB1001871//Human chondroitin/dermatan sulfate proteoglycan (PG40) core protein mRNA, complete 45 cds.//4.6e-26//527//62//M14219

F-MAMMA1001252

F-MAMMA1002094

F-NT2RM4000634//DKFZp434D1813\_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1813 5', mRNA sequence.//9.7e-16//226//69//AL040136

F-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//7.6e-179//817//99//AB028992

F-NT2RM4000783//wd82f06.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2338115 3', mRNA sequence.//1.8e-20//470//65//AI703299

F-NT2RM4000857//Homo sapiens KIAA0416 mRNA, partial cds.//1.9e-46//749//65//AB007876

F-NT2RM4001178//Homo sapiens protein tyrosine phosphatase (PAC-1) mRNA, complete cds.//0.0024//254//63//

F-NT2RM4002420//wg39f11.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE: 2367501 3' similar to contains element L1 L1 repetitive element; mRNA sequence.//1.4e-13//127//84//AI742251

F-NT2RP2000198//Human mRNA for platelet glycoprotein IX.//0.0033//241//62//X52997

F-NT2RP2000551//ze37d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361175 3', mRNA sequence.//5.0e-07//116//71//AA017066

F-NT2RP2000660//qx01g11.x1 NGI\_CGAP\_Br14 Homo sapiens cDNA clone IMAGE:1999364 3', mRNA sequence.//0.027//120//65//AI225283

F-NT2RP2001214

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F-NT2RP2001460//wb50h10.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2309155 3', mRNA sequence.//0.0013//89//78//AI651878

F-NT2RP2001756//zw54e12.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:773902 3' similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1; mRNA sequence.//2.3e-18//120//93//AA427992 F-NT2RP2002056//tw44g09.x1 NCI\_CGAP\_Ut1 Homo sapiens cDNA clone IMAGE:2262592 3' similar to contains Alu repetitive element; mRNA sequence.//2.4e-07//99//79//AI811687 F-NT2RP2002677

F-NT2RP2002755//zj83d10.s1 Soares\_fetal\_liver\_spleen\_1NFLS\_S1 Homo sapiens cDNA clone IMAGE:461491 3' similar to contains element TAR1 repetitive element; mRNA sequence.//1.9e-19//229//76//AA705059 F-NT2RP2002843//wt88dl2.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:2514551 3' similar to TR: P79522 P79522 MHC CLASS I REGION PROLINE RICH PROTEIN.; mRNA sequence.//8.2e-15//314//67// AI964055

F-NT2RP2003101//wi65a03.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2398156 3', mRNA sequence.//0.38//106//68//AI763133

F-NT2RP2003799//Homo sapiens mRNA; cDNA DKFZp564C142 (from clone DKFZp564C142).//2.5e-29//124//91//AL049979

F-NT2RP2004095

F-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//2.6e-109//533//96//AB020691 F-NT2RP2004920//wz68d10.x1 NCI\_CGAP\_Mel15 Homo sapiens cDNA clone IMAGE:2563219 3' similar to TR: 000172 000172 LINE-1 REVERSE TRANSCRIPTASE;, mRNA sequence.//0.0020//220//61//AI969546

F-NT2RP2005454//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0.058//143//69//AB023194 F-NT2RP2005776//H.sapiens PAP mRNA.//4.3e-35//451//68//X76770

F-NT2RP2005806//HSZ78328 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone 2.48 (CEPH) 3', mR-NA sequence.//2.0e-05//385//62//Z78328

F-NT2RP2005882//Human mRNA for KIAA0364 gene, complete cds.//7.3e-23//141//94//AB002362 F-NT2RP3001282

F-NT2RP3001723//ws73d05.x1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:2503593 3' similar to contains MSR1.t1 TAR1 TAR1 repetitive element; mRNA sequence.//2.6e-07//245//66//AW008782

35 F-NT2RP3002099//yg49d01.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:36239 3', mRNA sequence.//0.58//164//R46086

F-NT2RP3003155

F-NT2RP3004028//Homo sapiens mRNA for KIAA1074 protein, complete cds.//1.3e-29//488//66//AB028997 F-OVARC1000008//Homo sapiens mRNA for KIAA0665 protein, complete cds.//0.00032//430//59//AB014565

F-OVARC1000724//Homo sapiens mRNA for KIAA0641 protein, complete cds.//0.0054//426//58//AB014541 F-OVARC1000751//Human Tis11d gene, complete cds.//4.6e-12//527//62//U07802

F-OVARC1001029//qv29c05.x1 NCI\_CGAP\_Ov31 Homo sapiens cDNA clone IMAGE:1982984 3' similar to contains element L1 repetitive element; mRNA sequence.//0.0012//145//68//AI252422

F-PLACE1000814//ak42f05.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1408641 3', mRNA sequence.//7.1e-31//275//76//AA868469

F-PLACE1003030

F-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.// 1.2e-57//737//67//AJ010046

F-PLACE1007218//yo34a08.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:179798 3', mRNA sequence.//2.2e-21//216//76//H52716

Homology Search Result Data 11.

[0328] The result of the homology search of the Human Unigene using the clone sequence of 3'-end (54 clones selected in EXAMPLE 16.).

[0329] Data include

the name of clone,

title of the top hit data,

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- the P-value: the length of the compared sequence: identity (%), and
- the Accession No. of the top hit data, as in the order separated by //.
- [0330] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.
  - [0331] Data are not shown for the clones in which the P-value was higher than 1.
    - R-HEMBA1000497//np09h02.s1 NCI\_CGAP\_Pr3 Homo sapiens cDNA clone IMAGE:1115859 similar to contains Alu repetitive element; contains element MER22 repetitive element; mRNA sequence.//6.2e-38//185//83// AA614254
      - R-HEMBA1001750//yy71b10.s1 Soares\_multiple\_sclerosis\_2NbHMSP Homo sapiens cDNA clone IMAGE: 278971 3', mRNA sequence.//0.004511193//63//N63303
      - R-HEMBA1003854//Homo sapiens mRNA; cDNA DKFZp564F133 (from clone DKFZp564F133).//3.4e-72//310// 80//AL049263
- R-HEMBA1004193//tr01e08.x1 NCI\_CGAP\_Ov23 Homo sapiens cDNA clone IMAGE:2217062 3' similar to con-15 tains Alu repetitive element; contains element MER4 repetitive element; mRNA sequence. I/1.5e-33//186//81// AI914747
  - R-HEMBA1004860//qh16b06.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1844819 3', mRNA sequence.//0.017//118//69//AI218308
- R-HEMBA1005572//wj16h05.x1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2403033 3', mRNA se-20 quence.//4.6e-111//522//99//AI861830
  - R-HEMBA1006038//DKFZp434E1117\_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E1117 5', mRNA sequence.//1.2e-22//295//72//AL041450
  - R-HEMBA1006092//qt30d09.x1 Soares\_pregnant\_uterus\_NbHPU Homo sapiens cDNA clone IMAGE: 1949489
  - 3' similar to contains element PTR5 repetitive element; mRNA sequence.//1.4e-87//422//98//Al337963
    - R-HEMBA1006406//Homo sapiens mRNA for KIAA0752 protein, partial cds.//4.1e-30//291-//76//AB018295 R-HEMBA1006650//H.sapiens mRNA for serine/threonine protein kinase EMK.//3.6e-09//319//62//X97630
    - R-HEMBA1006812//Human mRNA for KIAA0118 gene, partial cds.//3.1e-52//337//87//D42087
    - R-HEMBB1000672//Homo sapiens mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011).//3.2e-48//276//
    - R-HEMBB1001197//zt35b11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724317 5' similar to contains Alu repetitive element; mRNA sequence.//9.9e-44//275//88//AA410788
    - R-HEMBB1001871//wg20c02.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE: 2365634 3', mRNA sequence.//6.3e-104//501//98//AI741321
- R-MAMMA1001252//aa61h04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:825463 3' similar to con-35 tains Alu repetitive element; contains element XTR repetitive element; mRNA sequence.//9.0e-19//127//91// AA504355
  - R-MAMMA1002094//wd28h12.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2329511 3', mR-NA sequence.//2.5e-68//328//99//AI936520
- R-NT2RM4000634//DKFZp434F20I6\_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434F2016 3', 40 mRNA sequence.//8.2e-20//185//81//AL041146
  - R-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//5.7e-62//335//94//AB028992 R-NT2RM4000783
  - R-NT2RM4000857//Human megakaryocyte stimulating factor mRNA, complete cds.//0.00074//360//61//U70136 R-NT2RM4001178//tk08e03.x1 NCI\_CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2150428 3', mRNA sequence.//0.77//96//62//AI457506
  - R-NT2RM4002420//wl58b04.x1 NCI\_CGAP\_Bm25 Homo sapiens cDNA clone IMAGE:2429071 3', mRNA sequence.//2.4e-85//438//94//AI857508
  - R-NT2RP2000198//nx19b11.s1 NCI\_CGAP\_GC3 Homo sapiens cDNA clone IMAGE:1256541 3', mRNA sequence.//1.9e-45//270//91//AA738352
  - R-NT2RP2000551//tg80h11.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:2115141 3', mRNA sequence.//3.3e-53//311//85//AI417680
  - R-NT2RP2000660//ns42a06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1186258 3', mRNA sequence.//4.3e-26//142//97//AA805691
- R-NT2RP2001214//tw65g08.x1 NCI\_CGAP\_Ut3 Homo sapiens cDNA clone IMAGE:2264606 3' similar to contains 55 element MSR1 repetitive element; mRNA sequence.//1.5e-57//289//97//AI680174 R-NT2RP2001460
  - R-NT2RP2001756//zw54e12.s1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:773902 3'

- similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1; mRNA sequence.//6.0e-13//85//96//AA427992 R-NT2RP2002056//yh26a12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130846 3', mRNA sequence.//0.0016//208//65//R22302
- R-NT2RP2002677//Homo sapiens mRNA for KIAA0524 protein, partial cds.//3.4e-26//339//71//AB011096
- 5 R-NT2RP2002755//qd50d10.x1 Soares\_fetal\_heart\_NbHH19W Homo sapiens cDNA clone IMAGE:1732915 3', mRNA sequence.//1.5e-26//419//66//Al190698
  - R-NT2RP2002843//at31f08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373639 3' similar to contains L1.t1 L1 repetitive element;, mRNA sequence.//1.8e-45//463//74//AI749673
  - R-NT2RP2003101//ty24h05.x1 NCI\_CGAP\_Ut3 Homo sapiens cDNA clone IMAGE:2280057 3', mRNA sequence.//7.5e-73//347//99//AI758824
  - R-NT2RP2003799//Homo sapiens mRNA for KIAA0751 protein, complete cds.//0.0026//247//65//AB018294 R-NT2RP2004095//zv08c02.s1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE:753026 3' similar to contains element MER32 repetitive element; mRNA sequence.//9.6e-07//188//66//AA436455
  - R-NT2RP2004732//tu60a07.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2255412 3' similar to contains Alu repetitive element;contains element L1 repetitive element; mRNA sequence.//4.3e-25//414//68//AI678956
    - R-NT2RP2004920//wd13h02.x1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:2328051 3', mRNA sequence.//6.8e-91//483//93//Al694022
    - R-NT2RP2005454//yy77g09.s1 Soares\_multiple\_sclerosis\_2NbHMSP Homo sapiens cDNA clone IMAGE: 279616 3', mRNA sequence.//0.0070//325//59//N48302
    - R-NT2RP2005776//qq97d06.x1 Soares\_total\_fetus\_Nb2HF8\_9w Homo sapiens cDNA clone IMAGE:1939307 3', mRNA sequence.//7.5e-08//89//82//AI338419
    - R-NT2RP2005806//wc29h01.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:2316625 3' similar to contains MER2.b3 MER2 repetitive element; mRNA sequence.//3.2e-16//235//71//Al671398
- 25 R-NT2RP2005882//wo31f09.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2456969 3', mRNA sequence.//0.00095//352//59//AI925528
  - R-NT2RP3001282//wg35b03.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone IMAGE: 2367053 3', mRNA sequence.//1.7e-113//555//97//AI769199
  - R-NT2RP3001723//wo48e06.x1 NCI\_CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2458594 3', mRNA sequence.//4.2e-98//471//98//AI926617
  - R-NT2RP3002099//DKFZp564L227\_s1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564L227 3', mR-NA sequence.//9.2e-50//329//87//AL037910
  - R-NT2RP3003155//zp07a07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595668 3', mRNA sequence.//1.4e-30//159//99//AA173172
- 35 R-NT2RP3004028//Homo sapiens protein kinase C-alpha mRNA, partial 3' UTR.//0.43//66//75//AF035594 R-OVARC1000008//wa69e12.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2301454 3', mRNA sequence.//1.0e-77//376//98//AI699393
  - R-OVARC1000724//tf94b10.x1 NCI\_CGAP\_CLL1 Homo sapiens cDNA clone IMAGE:2106907 3', mRNA sequence.//0.71//27//100//AI380236
- R-OVARC1000751//og93d04.s1 NCI\_CGAP\_Kid5 Homo sapiens cDNA clone IMAGE:1455847 3', mRNA sequence.//3.5e-13//274//63//AA863306
  - R-OVARC1001029//yz96e02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:290906 5' similar to contains Alu repetitive element; contains element PTR5 repetitive element; mRNA sequence//3.5e-13//175//74// N99464
- 45 R-PLACE1000814//tg49a08.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2112086 3' similar to contains Ll.t2 L1 L1 repetitive element; mRNA sequence.//2.2e-18//285//69//Al424789
  - R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//4.0e-34//225//90//AF032387
  - R-PLACE1005549//tm26b11.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:2157693 3', mRNA sequence.//0.91//127//66//AI480253
  - R-PLACE1007218//yq06e01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196152 5' similar to contains Alu repetitive element; contains LTR4 repetitive element; mRNA sequence.//2.4e-36//245//87// R92256
- 55 Homology Search Result Data 12.

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[0332] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology,

and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//6.4E-99//457aa//45%//Q09996

- 5 C-HEMBA1000020//Homo sapiens beta 2 gene.//7.5E-264//1194bp//95%//X02344
  - C-HEMBA1000129//HYTOTHETICAL HELICASE C8A4.08C IN CHROMOSOME I.//3.8E-25//166aa//36%//
  - C-HEMBA1000201//Homo sapiensimRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-
- 10 TEIN).//1E-86//146aa//56%//Q61221
  - C-HEMBA1000231
  - C-HEMBA1000264
  - C-HEMBA1000280
  - C-HEMBA1000282
- 15 C-HEMBA1000303//" Mus musculus Plenty of SH3s (POSH) mRNA, complete cds. " //7.1E-254// 1440bp//87%//AF030131
  - C-HEMBA1000333//"Homo sapiens mRNA for KIAA0874 protein, partial cds."//4.8E-253//1148bp//99%//AB020681
  - C-HEMBA1000351
- 20 C-HEMBA1000356//Homo sapiens mRNA; cDNA DKFZp566C243 (from clone DKFZp566C243).//3.3E-287// 815bp//98%//AL050274
  - C-HEMBA1000396
  - C-HEMBA1000411//ANKYRIN.//5.7E-12//127aa//38%//Q02357
  - C-HEMBA1000442
- 25 C-HEMBA1000456
  - C-HEMBA1000504
  - C-HEMBA1000518//PECANEX PROTEIN.//2.1E-19//227aa//38%//P18490
  - C-HEMBA1000519
  - C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.4E-44//292aa//36%//Q01755
- 30 C-HEMBA1000542//"Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds."//2.2E-194// 663bp//83%//D89340
  - C-HEMBA1000545
  - C-HEMBA1000557
  - C-HEMBA1000592//"Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds."//0//1465bp//99%//
- 35 AF121856
  - C-HEMBA1000594
  - C-HEMBA1000604
  - C-HEMBA1000622
  - C-HEMBA1000637
- 40 C-HEMBA1000655
  - C-HEMBA1000657//"Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds."//7.2E-156//1366bp//76%//U35776
  - C-HEMBA1000749
  - C-HEMBA1000769
- 45 C-HEMBA1000773
  - C-HEMBA1000774
  - C-HEMBA1000822
  - C-HEMBA1000843
  - C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1E-78//119aa//87%//P51689
- 50 C-HEMBA1000870

- C-HEMBA1000908
- C-HEMBA1000934
- C-HEMBA1000972
- C-HEMBA1000986 C-HEMBA1000991
- C-HEMBA1001008
  - C-HEMBA1001059//"Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14."//4.8E-169//786bp//99%//U06088

C-HEMBA1001094

C-HEMBA1001302//"Homo sapiens calcium binding protein precursor, mRNA, complete cds."//9.6E-258//682bp//94%//AF153686

C-HEMBA1001330

5 C-HEMBA1001497

C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.3E-53//110aa//100%//P19065

C-HEMBA1001570

C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%//

10 P42803

C-HEMBA1001640

C-HEMBA1001655

C-HEMBA1001672//"Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds."//0//1707bp//98%//AF072247

15 C-HEMBA1001711

C-HEMBA1001723//"Rattus norvegicus G beta-like protein GBL mRNA, complete cds."//4.7E-172// 1240bp//81%//AF051155

C-HEMBA1001746//"Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds."//7.6E-59//998bp//64%//AF098066

20 C-HEMBA1001781

C-HEMBA1001804//"Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds. "//0//1637bp//99%//AF125158

C-HEMBA1001822//"Mus musculus Ese2L protein mRNA, complete cds."//1.9E-235//1329bp//89%// AF132479

25 C-HEMBA1001824

C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//5.7E-51//234aa//41%//Q09332

C-HEMBA1001910

C-HEMBA1001913//GCN20 PROTEIN.//2.3E-81//158aa//50%//P43535

30 C-HEMBA1001921//"Homo sapiens germinal center kinase related protein kinase mRNA, complete cds. 
"//0//1850bp//99%//AF000145

C-HEMBA1001939

C-HEMBA1001950//"Homo sapiens mRNA for KIAA0971 protein, complete cds."//0//1974bp//99%//AB023188

35 C-HEMBA1001967//"Homo sapiens NY-REN-57 antigen mRNA, partial cds."//0//1721bp//99%// AF155114

C-HEMBA1002035//Homo sapiens mRNA; cDNA DKFZp586E0518 (from clone DKFZp586E0518).//0//2149bp// 99%//AL050089

C-HEMBA1002092//"Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds. "//1.3E-271//1583bp//88%//U92703

C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357

C-HEMBA1002150

C-HEMBA1002151//"Rattus norvegicus p34 mRNA, complete cds."//1.1E-153//1059bp//82%// AF178669

45 C-HEMBA1002189

40

C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.2E-199//392aa//89%//P47226

C-HEMBA1002229

C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087

50 C-HEMBA1002341//"Homo sapiens mRNA for KIAA0771 protein, partial cds."//0//1514bp//99%// AB018314

C-HEMBA1002417//"Homo sapiens chromosome 19, cosmid R28784, complete sequence."//1.4E-299//294bp//100%//AC005954

C-HEMBA1002547//" Homo sapiens agrin precursor mRNA, partial cds."//0//1605bp//97%//AF016903

55 C-HEMBA1002703

C-HEMBA1002779

C-HEMBA1002816

C-HEMBA1002970

```
C-HEMBA1002999//"Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.
       "//1.4E-171//1552bp//75%//U20286
       C-HEMBA1003021
       C-HEMBA1003077//SLIT PROTEIN PRECURSOR.//2.6E-15//199aa//31%//P24014
5
        C-HEMBA1003079
        C-HEMBA1003273
        C-HEMBA1003304
        C-HEMBA1003309
        C-HEMBA1003376
        C-HEMBA1003384
10
        C-HEMBA1003531
        C-HEMBA1003548
        C-HEMBA1003556
        C-HEMBA1003571
        C-HEMBA1003579
15
        C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2E-73//526aa//32%//Q13105
        C-HEMBA1003692
        C-HEMBA1003720
        C-HEMBA1003725
20
        C-HEMBA1003729
        C-HEMBA1003758
        C-HEMBA1003773//"Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.
        "//5.8E-81//511bp//86%//U17343
        C-HEMBA1003783//"Mus musculus bromodomain-containing protein BP75 mRNA, complete cds."//
25
        1.1E-190//1204bp//84%//AF084259
        C-HEMBA1003799
        C-HEMBA1003804
        C-HEMBA1003805//"Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds."//
        0//988bp//95%//AF090402
        C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%//P40484
30
        C-HEMBA1003856
        C-HEMBA1003866//"Mus musculus semaphorin VIa mRNA, complete cds."//1.2E-105//1192bp//70%//
        AF030430
         C-HEMBA1003879
         C-HEMBA1003880
35
         C-HEMBA1003893
         C-HEMBA1003908
         C-HEMBA1003937
         C-HEMBA1003942
40
         C-HEMBA1003958
         C-HEMBA1003976
         C-HEMBA1003978//"Homo sapiens mRNA for KIAA0840 protein, partial cds."//0//1530bp//100%//
         AB020647
         C-HEMBA1003985
 45
         C-HEMBA1004011
         C-HEMBA1004024
         C-HEMBA1004038
         C-HEMBA1004045
         C-HEMBA1004048
         C-HEMBA1004111//"Homo sapiens mRNA for KIAA1276 protein, partial cds."//1.00E-163//751bp//
 50
         99%//AB033102
         C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.6E-166//416aa//72%//Q14141
         C-HEMBA1004138
         C-HEMBA1004143
         C-HEMBA1004150
 55
         C-HEMBA1004168//"Homo sapiens geminin mRNA, complete cds."//3.9E-208//951 bp//99%//
         AF067855
         C-HEMBA1004200
```

```
C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.2E-30//208aa//37%//P51153
        C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.5E-12//258aa//29%//P40991
        C-HEMBA1004238
        C-HEMBA1004248//"Homo sapiens insulin induced protein 2 mRNA, complete cds."//8.20E-175//
        552bp//97%//AF125392
5
        C-HEMBA1004272
        C-HEMBA1004274
        C-HEMBA1004275//"Homo sapiens mRNA for KIAA1111 protein, partial cds."//0//1341bp//99%//
        C-HEMBA1004286//"Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds."//
10
        0//1982bp//99%//AF022795
        C-HEMBA1004312
        C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.3E-93//357aa//42%//Q99676
        C-HEMBA1004323
15
        C-HEMBA1004327
        C-HEMBA1004330
        C-HEMBA1004341
        C-HEMBA1004366
        C-HEMBA1004372
        C-HEMBA1004389//" Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.
20
        "//0//1437bp//99%//AF125158
        C-HEMBA1004394
        C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CY-
        CLOPHILIN-10).//3.2E-32//148aa//52%//P52017
25
        C-HEMBA1004429
        C-HEMBA1004460
        C-HEMBA1004461
        C-HEMBA1004502
        C-HEMBA1004554
30
        C-HEMBA1004560
        C-HEMBA1004610
        C-HEMBA1004629
        C-HEMBA1004632
        C-HEMBA1004637
35
        C-HEMBA1004670
        C-HEMBA1004672
        C-HEMBA1004697
        C-HEMBA1004711
        C-HEMBA1004725
40
        C-HEMBA1004730
        C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
        LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%//P42743
        C-HEMBA1004751
        C-HEMBA1004752
        C-HEMBA1004889//"Human C3f mRNA, complete cds."//6.70E-24//341aa//26%//U72515
45
        C-HEMBA1004934
        C-HEMBA1004944
        C-HEMBA1004973
        C-HEMBA1004977
        C-HEMBA1005009//"Homo sapiens BAF53a (BAF53a) mRNA, complete cds."//0//1813bp//99%//
50
        AF041474
        C-HEMBA1005083
        C-HEMBA1005113
        C-HEMBA1005133
55
        C-HEMBA1005185
        C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.3E-10//189aa//25%//P39929
        C-HEMBA1005252//"Homo sapiens mRNA for KIAA0585 protein, partial cds."//1.2E-268//1215bp//
```

99%//AB011157

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C-HEMBA1005296
        C-HEMBA1005314
        C-HEMBA1005331
        C-HEMBA1005394
        C-HEMBA1005403
5
        C-HEMBA1005423//"Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.
        "//2E-213//537bp//99%//AF041248
        C-HEMBA1005468
        C-HEMBA1005469
        C-HEMBA1005474
10
        C-HEMBA1005517
        C-HEMBA1005518
        C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.1E-154//285aa//99%//Q60809
        C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929
        C-HEMBA1005576//"Homo sapiens mRNA for KIAA0463 protein, partial cds."//1.1E-181//835bp//
15
        99%//AB007932
        C-HEMBA1005582//"TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL
        TROPOMYOSIN)."//0.00000009//213aa//27%//P09492
        C-HEMBA1005583
        C-HEMBA1005595//"DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC)."//2.3E-54//562aa//29%//P34036
20
        C-HEMBA1005609//Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKFZp564K133).//2.2e-315//
        1448bp//99%//AL050012
        C-HEMBA1005621//"Homo sapiens Mad2B protein (MAD2B) mRNA, complete cds."//2.9E-224//
        1031bp//99%//AF139365
        C-HEMBA1005666
25
        C-HEMBA1005680
        C-HEMBA1005685
        C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//
        4.4E-17//167aa//34%//P25296
30
        C-HEMBA1005746
        C-HEMBA1005755
        C-HEMBA1005813
        C-HEMBA1005822
        C-HEMBA1005834
35
        C-HEMBA1005884
        C-HEMBA1005891
        C-HEMBA1005909
        C-HEMBA1005911
         C-HEMBA1005931
         C-HEMBA1005963
40
         C-HEMBA1005991
         C-HEMBA1006005
         C-HEMBA1006031//"Homo sapiens mRNA for putative phospholipase, complete cds."//0//1413bp//
         99%//AB019435
         C-HEMBA1006067
45
         C-HEMBA1006081
         C-HEMBA1006091
         C-HEMBA1006100
         C-HEMBA1006108//"Homo sapiens mRNA for KIAA0943 protein, partial cds."//4.8E-245//764bp//
50
         99%//AB023160
         C-HEMBA1006121
         C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25%//Q93794
         C-HEMBA1006155
         C-HEMBA1006158//" Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds."
         //0//1551bp//99%//AF048693
 55
         C-HEMBA1006182
         C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.9E-19//215aa//39%//P05142
```

C-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//0//1615bp//99%//AF070557

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C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR.//0.00000002//
        62aa//53%//P42698
        C-HEMBA1006259
        C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.3E-123//200aa//73%//P10265
        C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-
5
        FERASE).//1E-210//490aa//77%//P25500
        C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2.//0.000000012//176aa//
        30%//P32505
        C-HEMBA1006284
10
        C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5 .-.-.).//4.2E-12//215aa//23%//P70473
        C-HFMBA1006293
        C-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//1.4E-48//
        248aa//43%//P38821
        C-HEMBA1006349
        C-HEMBA1006364
15
        C-HEMBA1006381
        C-HEMBA1006398//"Human L1 element L1.6 putative p150 gene, complete cds."//2E-277//1729bp//
        85%//U93563
        C-HEMBA1006445//&guot;Homo sapiens putative tumor supressor NOEY2 mRNA, complete cds."//1.4E-
        270//1224bp//100%//U96750
20
        C-HEMBA1006483
        C-HEMBA1006492
        C-HEMBA1006497
        C-HEMBA1006502
        C-HEMBA1006507//"Homo sapiens mRNA for KIAA0666 protein, partial cds."//0//2334bp//99%//
25
        AB014566
        C-HEMBA1006535
        C-HEMBA1006559//"Mus musculus PRAJA1 (Praja1) mRNA, complete cds."//2.8E-206//1107bp//83
        %//U06944
30
        C-HEMBA1006566
        C-HEMBA1006579
        C-HEMBA1006583
        C-HEMBA1006612
        C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.0000069//109aa//
35
        38%//Q58323
        C-HEMBA1006643
        C-HEMBA1006674
        C-HEMBA1006682
        C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2
        INTERGENIC REGION.//3.3E-22//241aa//31%//P53196
4n
        C-HEMBA1006717
        C-HEMBA1006744
        C-HEMBA1006754
        C-HEMBA1006767
45
        C-HEMBA1006789
        C-HEMBA1006832
        C-HEMBA1006885//"Homo sapiens gene for Proline synthetase associated, complete cds."//0//
        1467bp//96%//AB018566
        C-HEMBA1006900
50
        C-HEMBA1006926
        C-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.8E-226//1039bp//99%//
        C-HEMBA1006973//"Horno sapiens rab3-GAP regulatory domain mRNA, complete cds."//5.6E-143//
        740bp//94%//AF004828
55
        C-HEMBA1006993
        C-HEMBA1007002
        C-HEMBA1007062
```

C-HEMBA1007080

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C-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//2E-45//304aa//32%//Q57626
        C-HEMBA1007112//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//1619bp//
        99%//AL117450
        C-HEMBA1007194//" Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.
        "//0//1588bp//99%//AF139658
5
        C-HEMBA1007206
        C-HEMBA1007256
        C-HEMBA1007267
        C-HEMBA1007281
        C-HEMBA1007300//"Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA,
10
        splice variant 1, complete cds."//0//1519bp//99%//AF127479
        C-HEMBA1007301
        C-HEMBA1007319
        C-HEMBA1007320
15
        C-HEMBA1007327
        C-HEMBA1007347
        C-HEMBB1000005
        C-HEMBB1000030
        C-HEMBB1000048
        C-HEMBB1000099
20
        C-HEMBB1000141
        C-HEMBB1000198
        C-HEMBB1000217//" Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.
        &quot://0//1038bp//99%//AF090385
        C-HEMBB1000218
25
        C-HEMBB1000274
         C-HEMBB1000312
         C-HEMBB1000402
         C-HEMBB1000420
         C-HEMBB1000480
30
         C-HEMBB1000530
         C-HEMBB1000550
        C-HEMBB10000556//"Homo sapiens mRNA for KIAA0750 protein, complete cds."//6.3E-74//1213bp//
         64%//AB018293
35
         C-HEMBB1000586
         C-HEMBB1000592
         C-HEMBB1000593//"Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA, complete cds."//1.3E-
         107//503bp//99%//AF067864
         C-HEMBB1000649
         C-HEMBB1000693//"Homo sapiens neuroan1 mRNA, complete cds."//0//2952bp//94%//AF040723
         C-HEMBB1000822
         C-HEMBB1000826
         C-HEMBB1000890
         C-HEMBB1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//
 45
         31%//P29122
         C-HEMBB1001008
         C-HEMBB1001020//"Homo sapiens mRNA for KIAA0889 protein, complete cds."//0//1812bp//98%//
         AB020696
         C-HEMBB1001051
         C-HEMBB1001112//"Homo sapiens sec61 homolog mRNA, complete cds."//6E-145//961bp//83%//
 50
         AF077032
         C-HEMBB1001221
         C-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.4E-93//196aa//54%//P46938
         C-HEMBB1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7E-43//394aa//34%//
 55
         P16157
         C-HEMBB1001302
         C-HEMBB1001335
         C-HEMBB1001337
```

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C-HEMBB1001356
        C-HEMBB1001364
        C-HEMBB1001366
        C-HEMBB1001367
5
        C-HEMBB1001527
        C-HEMBB1001537
        C-HEMBB1002359
        C-HEMBB1002415
        C-HEMBB1002457
10
        C-HEMBB1002492
        C-HEMBB1002495
        C-HEMBB1002502
        C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5E-28//266aa//33%//P27544
        C-HEMBB1002600//"Homo sapiens tetraspan NET-5 mRNA, complete cds."//0//1417bp//99%//
15
        C-HEMBB1002607//" Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.
        "//2E-136//660bp//98%//AF105421
        C-HEMBB1002684
        C-HEMBB1002692
        C-HEMBB1002697
20
        C-HEMBB1002705//"Homo sapiens CGI-27 protein mRNA, complete cds."//7.80E-285//841bp//96%//
        AF132961
        C-MAMMA1000019
        C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FM05).//8.2E-198//868bp//99%//
25
        Z47553
        C-MAMMA1000025
        C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.5E-90//323aa//48%//P47226
        C-MAMMA1000069
        C-MAMMA1000084
30
        C-MAMMA1000139
        C-MAMMA1000163
        C-MAMMA1000171
        C-MAMMA1000173//"Homo sapiens src homology 3 domain-containing protein H1P-55 mRNA, complete
        cds.&quot://2.6E-164//1044bp//87%//AF197060
35
        C-MAMMA1000277
        C-MAMMA1000278
        C-MAMMA1000284//P.walti mRNA for mp associated protein 55.//2.2E-109//864bp//76%//X99836
        C-MAMMA1000309
        C-MAMMA1000312
40
        C-MAMMA1000313
        C-MAMMA1000361
        C-MAMMA1000388//"Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds."//
        0//1466bp//99%//AB015132
        C-MAMMA1000395
        C-MAMMA1000410
45
        C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//2.00E-30//119aa//
        53%//Q09232
        C-MAMMA1000421
         C-MAMMA1000422
50
         C-MAMMA1000468
         C-MAMMA1000472
         C-MAMMA1000490
         C-MAMMA1000524
         C-MAMMA1000567
         C-MAMMA1000612//"Rattus norvegicus G beta-like protein GBL mRNA, complete cds."//1E-95//
55
         1115bp//72%//AF051155
         C-MAMMA1000623
```

C-MAMMA1000625//GYP7 PROTEIN.//2.1E-41//198aa//40%//P48365

	C-MAMMA1000664
	C-MAMMA1000670
	C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16).//4.4E-33//250aa//
	33%//P42660
5	C-MAMMA1000713//L-RIBULOKINASE (EC 2.7.1.16).//7.70E-17//246aa//29%//P94524
	C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1E-77//395aa//45%//
	014646
	C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779
	C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//9E-299//1033aa//
10	55%//P87115
	C-MAMMA1000746
	C-MAMMA1000775
	C-MAMMA1000824//ACTIN.//6.2E-20//284aa//28%//P53500
	C-MAMMA1000831
45	C-MAMMA1000831 C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.8E-40//101aa//54%//027540
15	
	C-MAMMA1000842
	C-MAMMA1000843
	C-MAMMA1000856
	C-MAMMA1000865
20	C-MAMMA1000875
	C-MAMMA1000906
	C-MAMMA1000908
	C-MAMMA1000914
	C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%//AJ250711
25	C-MAMMA1000968
	C-MAMMA1000979
	C-MAMMA1001008//"Homo sapiens aspartic-like protease mRNA, complete cds."//2.50E-276//
	1263bp//99%//AF117892
	C-MAMMA1001021
30	C-MAMMA1001041//"SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN)
	(FODRIN BETA CHAIN) (SPTBN1)."//1.6E-16//113aa//41%//Q01082
	C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99%//AJ237946
	C-MAMMA1001075//"Homo sapiens CGI-72 protein mRNA, complete cds."//1.3E-181//397bp//98%//
	AF151830
35	C-MAMMA1001078
	C-MAMMA1001091
	C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4E-49//125aa//68%//P51521
	C-MAMMA1001110
	C-MAMMA1001126
40	C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%//Q09273
	C-MAMMA1001143
	C-MAMMA1001154
	C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q92338
	C-MAMMA1001215
45	C-MAMMA1001244
70	C-MAMMA1001259//"Mus musculus F-box protein FBX18 mRNA, partial cds."//2.3E-271//1414bp//
	89%//AF184275
	C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.1E-52//630aa//
	30%//P34537
50	C-MAMMA1001343 C-MAMMA1001411//Homo sapiens mRNA; cDNA DKFZp56400823 (from clone DKFZp56400823).//0//2131bp//
	99%//AL080121
	C-MAMMA1001419
	C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//
55	6.5E-129//260aa//92%//P52623
	C-MAMMA1001510
	C-MAMMA1001522  C-MAMMA1001576//&guot:Human gamma-tubulin mRNA, complete cds."//7.5E-276//1561bp//90%/.
	C_MAMMA1001576//":Human gamma-tubulin mRNA, complete cqs."///.bc-2/6///15610p//90/6//

M61764

	M0 1704
	C-MAMMA1001604
	C-MAMMA1001620
	C-MAMMA1001635
5	C-MAMMA1001649
	C-MAMMA1001686
	C-MAMMA1001692
•	C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8.5E-32//171aa//36%//
	P21572
10	C-MAMMA1001754//"Homo sapiens CGI-11 protein mRNA, complete cds."//0//1837bp//98%//
,,	AF132945
	C-MAMMA1001757
	C-MAMMA1001764
	C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.8E-45//351aa//38%//Q58556
	C-MAMMA1001776//CEEE DIVISION C10EE1110 12
15	
	C-MAMMA1001790 C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.6E-77//507aa//38%//Q07230
	C-MAMMA1001858
	C-MAMMA1001868//TRICHOHYALIN.//2.7E-19//359aa//25%//P22793
20	C-MAMMA1001970
	C-MAMMA1002042
	C-MAMMA1002068
	C-MAMMA1002153
	C-MAMMA1002156
25	C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6E-66//157aa//70%//P15880
	C-MAMMA1002174
	C-MAMMA1002209
	C-MAMMA1002219//"Homo sapiens mRNA for KIAA1067 protein, partial cds."//1.1E-181//861bp//
	98%//AB028990
30	C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EX-
	CHANGE FACTOR).//8.8E-217//310aa//86%//P70541
	C MAMMA 1002243
	C-MAMMA1002268//"Mus musculus sphingosine kinase (SPHKIa) mRNA, partial cds."//1E-190//
	1624bp//76%//AF068748
35	C-MAMMA1002269
	C-MAMMA1002292
	C MANMA 1002294
	C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.1E-214//881bp//97%//
	AJ011679
40	C-MAMMA1002312
	C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%//X85991
	C-MAMMA1002333
	C-MAMMA1002351//FERRIPYOCHELIN BINDING PROTEIN.//0.000078//127aa//26%//P40882
	C-MAMMA1002353
45	C-MAMMA1002355
45	C-MAMMA1002356
	C-MAMMA1002362
	C-MAMMA1002380
	•
	C-MAMMA1002384
50	C-MAMMA1002427  C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(*) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%//
	P47623 C-MAMMA1002485//"Homo sapiens stanniocalcin-related protein mRNA, complete cds."//0//1822bp//
	99%//AF098462
55	C-MAMMA1002494
	C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.2E-34//
	337aa//31%//P43571
	C-MAMMA1002530//"Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete

	cds."//0//1910bp//99%//AF065214
	C-MAMMA1002554
	C-MAMMA1002585//"Homo sapiens mRNA for KIAA0860 protein, complete cds."//0//1405bp//99%//
	AB020667
5	C-MAMMA1002598
	C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15)
	(UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-
	ZYME).//9.5E-16//159aa//37%//Q09931
	C-MAMMA1002655//"Homo sapiens mRNA for ganglioside sialidase, complete cds."//0//1515bp//
10	99%//AB008185
	C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL-AC-
	TIVATING ENZYME).//1.1E-45//618aa//26%//P27550
	C-MAMMA1002673 C-MAMMA1002684//"Homo sapiens mRNA for KIAA0214 protein, complete cds."//0//3174bp//99%//
15	D86987
	C-MAMMA1002711  C-MAMMA1002769//"Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete
	cds."//2.2E-25//330bp//77%//AF011794
	C-MAMMA1002775
20	C-MAMMA1002782
20	C-MAMMA1002796
	C-MAMMA1002807
	C MANMA 1002838
	C-MAMMA1002842//"Mus musculus c-Cb1 associated protein CAP mRNA, complete cds."//2.6E-58//
25	272ha//019/ // I59993
	C-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//1.4E-160//
	20522/J85%/JP48059
	C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.7E-30//214aa//
	35%//P48060
30	C-MAMMA1002886
	C-MAMMA1002890 C-MAMMA1002938//"Homo sapiens mRNA for KIAA0698 protein, complete cds."//8.4E-252//1139bp//
	100%//AB014598
	C-MAMMA1002964 C-MAMMA1003011//HESTONE MACRO-H2A.1.//2.7E-123//370aa//66%//Q02874
35	C-MAMMA1003011//HESTONE MACRO-112A: 13/21 E-125/3701010101010101010101010101010101010101
	C-MAMMA1003015
	C MANNA 1003019
	C-MAMMA1003019  C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEU-
40	DOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.9E-13//108aa//33%//P23851
40	C-MAMMA1003039
	C-MAMMA1003044
	C-MAMMA1003049
	C-MAMMA1003056
45	C-MAMMA1003057//MD6 PROTEIN.//3.1E-225//419aa//97%//Q60584
	C-MAMMA1003066
	C-MAMMA1003099
	C-MAMMA1003104
	C-MAMMA1003113//" Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds."//
50	1.1E-234//1178bp//86%//AF071316
	C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.2E-105//217aa//89%//P46735
	C-MAMMA1003135
	C-MAMMA1003146//Homo sapiens mRNA for GaIT3 protein.//4.3E-218//996bp//99%//Y15062 C-MAMMA1003150//"Homo sapiens mRNA for KIAA1096 protein, partial cds."/0//1342bp//99%//
55	AB029019  C-MAMMA1003166//"Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds."//
	C-MAMMA1003100//addoctroing sapiets with separative region from (mer.)

3.10E-158//592bp//97%//AF123052

C-NT2RM1000032

- C-NT2RM1000035//"Human mRNA for KIAA0199 gene, partial cds."//0//2948bp//99%//D83782 C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-) (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596
- C-NT2RM1000055//"Homo sapiens mRNA for KIAA0829 protein, partial cds."//0//3111bp//99%//
- 5 AB020636

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- C-NT2RM1000059
- C-NT2RM1000062
- C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072
- 10 C-NT2RM1000119
  - C-NT2RM1000127
  - C-NT2RM1000131//"Homo sapiens mRNA for KIAA0792 protein, complete cds."//0//2980bp//99%//
  - C-NT2RM1000132//" Homo sapiens NADH: ubiquinone oxidoreductas NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds. " //7.8E-110//516bp//99%//AF044959
  - C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.3E-3 8//469aa//27%//P49902 C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.2E-10//150aa//28%//P87072
  - C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.1E-10//94aa//47%//042643
  - C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%// AJ245820
  - C-NT2RM1000244//"Homo sapiens TRAF4 associated factor 1 mRNA, partial cds."//2E-126//592bp// 99%//U81002
- 25 C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.7E-35//569bp//64%//X73882
  - C-NT2RM1000256//"Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.&quot://0//3012bp//99%//AB016789
  - C-NT2RM1000260//"Human mRNA for KIAA0130 gene, complete cds."//0//3139bp//98%//D50920 C-NT2RM1000271
- 30 C-NT2RM1000300
  - C-NT2RM1000314//"Human mRNA for KIAA0159 gene, complete cds."//0//4349bp//99%//D63880 C-NT2RM1000354//"Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds. "//7.4E-245//2101bp//68%//AF111423
  - C-NT2RM1000355//"Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds."//0// 1599bp//99%//AF152462
    - C-NT2RM1000365
    - C-NT2RM1000377//" Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds. " //3.2E-196//1016bp//94%//AF179212
    - C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.// 0.000000019//67aa//31%//P53915
    - C-NT2RM1000399
    - C-NT2RM1000430//"Homo sapiens erythrobiast macrophage protein EMP mRNA, complete cds."// 1.4E-185//1486bp//81%//AF084928
- C-NT2RM1000555//"Homo sapiens mRNA for KIAA0885 protein, complete cds."//0//2885bp//99%//
  AB020692
  - C-NT2RM1000563//TRANSMISSION-BLOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//30%//Q08372
  - C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.5E-75//301aa//39%//P43636
  - C-NT2RM1000661//"Homo sapiens translation initiation factor 4e mRNA, complete cds."//4.3E-210//960bp//99%//AF038957
  - C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.2E-09//165aa//34%//P16989
  - C-NT2RM1000672
  - C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440
  - C-NT2RM1000699
- 55 C-NT2RM1000741//"Homo sapiens mRNA for KIAA0567 protein, partial cds."//1.1E-295//1338bp// 99%//AB011139
  - C-NT2RM1000742//"Homo sapiens AC133 antigen mRNA, complete cds."//0//3524bp//99%//AF027208

- C-NT2RM1000746//"Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds."// 6.70E-227//1043bp//99%//AF141310
- C-NT2RM1000770//DXS6673E PROTEIN.//1.4E-39//194aa//48%//Q14202
- C-NT2RM1000772//VEGETATTOLE INCOMPATIBILITY PROTEIN HET-E-1.//7.3E-15//280aa//27%//Q00808
- 5 C-NT2RM1000780

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- C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indl gene).//1.1E-98//571bp//89%//Z97207 C-NT2RM1000802
- C-NT2RM1000811//"Homo sapiens AC133 antigen mRNA, complete cds."//0//3524bp//99%// AF027208
- C-NT2RM1000826//"Homo sapiens mRNA for KIAA0885 protein, complete cds."//0//2885bp//99%// 10 AB020692
  - C-NT2RM1000829
  - C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.7E-42//333aa//36%//
- C-NT2RM1000852//"Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds. 15 "//0//2206bp//99%//AF077033
  - C-NT2RM1000857//"Homo sapiens mRNA for KIAA0962 protein, partial cds."//0//3716bp//99%// AB023179
  - C-NT2RM1000874//"Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds."//1.4E-244//1113bp//99%//AF043733
  - C-NT2RM1000882//"Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds."//4.30E-122// 1394bp//69%//AF126799
  - C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.8E-56//630aa// 30%//P34537
- C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA 25 POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700
  - C-NT2RM1000898//"ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR)."//8.9E-26//229aa//29%//
  - C-NT2RM1000905//"Homo sapiens HSPC021 mRNA, complete cds."//0//1480bp//99%//AF077207
- C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1E-15//266aa//26%// 30 P46577
  - C-NT2RM1000927
  - C-NT2RM1000962
  - C-NT2RM1000978
- C-NT2RM1001003//"Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds."//0// 35 2230bp//99%//AF030233
  - C-NT2RM1001043
  - C-NT2RM1001066
  - C-NT2RM1001072//"1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAM-MA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148)."//8.3E-47//
  - 259aa//35%//P08487
    - C-NT2RM1001085//"Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds. "//3.7E-32//460bp//64%//AF053768
    - C-NT2RM1001102//"Human HEM45 mRNA, complete cds."//2.3E-27//482bp//63%//U88964
- 45 C-NT2RM1001105
  - C-NT2RM1001139//Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522).//0//1756bp// 99%//AL049943
  - C-NT2RM2000420
  - C-NT2RM2000566//"Homo sapiens integrin alpha-7 mRNA, complete cds."//0//2519bp//96%// AF032108
  - C-NT2RM2000609
  - C-NT2RM2000612//"Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds."//2.6E-106//1069bp//74%//U35776
  - C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-103//249aa//73%//P28160
- C-NT2RM2001588 55
  - C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ132440
  - C-NT2RM2001613//"Homo sapiens sec61 homolog mRNA, complete cds."//0//2601bp//99%// AF084458

- C-NT2RM2001632//KES 1 PROTEIN.//1.40E-31//342aa//34%//P35844
- C-NT2RM2001648//"Homo sapiens sec61 homolog mRNA, complete cds."//0//2421bp//99%//
- C-NT2RM2001652//"Homo sapiens guanine nucleotide exchange factor mRNA, complete cds."//0// 2608bp//99%//AF111162
  - C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.4E-39//161aa//34%//P20107
  - C-NT2RM2001664//"Homo sapiens lkappaB kinase complex associated protein (IKAP) mRNA, complete cds."//0//2471bp//99%//AF044195
- C-NT2RM2001668//"Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending in intron 11, complete cds."//6.2E-16//464bp//62%//AF083391
  - C-NT2RM2001671//"Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds. "//0//1843bp//94%//U21155
  - C-NT2RM2001675

10

- C-NT2RM2001681
- 15 C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//4.60E-20//253aa// 30%//Q09674
  - C-NT2RM2001695//Homo sapiens clone H63 unknown mRNA.//0//2016bp//99%//AF103804
  - C-NT2RM2001696
  - C-NT2RM2001698//"Homo sapiens XGalT-1 mRNA for galactosyltransferase i, complete cds."//6.2E-253//1170bp//99%//AB028600
  - C-NT2RM2001700//"ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VL-CAD) (FRAGMENT)."//5.7E-130//536aa//49%//P50544
  - C-NT2RM2001716
  - C-NT2RM2001723
- 25 C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//7.2E-16//381aa//27%//Q09931
  - C-NT2RM2001743//"Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds."// 0//1498bp//99%//AF011792
- 30 C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.8E-11//119aa//36%//Q92609
  - C-NT2RM2001760//"Homo sapiens sec61 homolog mRNA, complete cds."//0//2379bp//99%// AF084458
  - C-NT2RM2001768
  - C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.4E-154//394aa//64%//P52742
- 35 C-NT2RM2001782//"Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds. 
  "//0//1470bp//99%//AF135422
  - C-NT2RM2001784
  - C-NT2RM2001785//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2146bp// 99%//AL050118
- 40 C-NT2RM2001813
  - C-NT2RM2001823//CHD1 PROTEIN.//1.8E-106//631aa//39%//P32657
  - C-NT2RM2001839//"Homo sapiens calumein (Calu) mRNA, complete cds."//0//2415bp//97%// AF013759
  - C-NT2RM2001840
- 45 C-NT2RM2001855
  - C-NT2RM2001867//"Homo sapiens mRNA for KIAA0943 protein, partial cds."//0//967bp//99%//AB023160
  - C-NT2RM2001879
  - C-NT2RM2001983//"Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds."//0// 1658bp//98%//AF089816
  - C-NT2RM2002145//"Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds."// 8.5E-191//1524bp//81%//AF084928
  - C-NT2RM4000027
  - C-NT2RM4000030//LAS1 PROTEIN.//5.6E-12//184aa//32%//P36146
- 55 C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003
  - C-NT2RM4000155//"THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE-TRNA LIGASE) (THRRS)."//1.2E-157//321aa//6l%//P26639
  - C-NT2RM4000156//H.sapiens HPBRII-7 gene.//3.6E-21//785bp//60%//X67336

```
C-NT2RM4000167//"Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds."//0//
        1946bp//99%//AF071592
        C-NT2RM4000199
        C-NT2RM4000200
        C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.9E-32//170aa//41%//Q16600
5
        C-NT2RM4000233//"Mus musculus semaphorin VIa mRNA, complete cds."//3.4E-231//1395bp//86%//
        AF030430
        C-NT2RM4000244
        C-NT2RM4000251
10
        C-NT2RM4000265
        C-NT2RM4000324
        C-NT2RM4000327
        C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.9E-80//213aa//75%//P35292
        C-NT2RM4000425
        C-NT2RM4000433//"Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds."//
15
        4.1E-271//2085bp//77%//AF062476
        C-NT2RM4000514
        C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.4E-89//389aa//43%//007230
        C-NT2RM4000532
        C-NT2RM4000534
20
        C-NT2RM4000603
        C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.9E-09//108aa//31%//Q00808
        C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- AC-
        TIVATING ENZYME).//2.7E-146//420aa//60%//P27550
        C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//1.2E-28//180aai/30%//P74168
25
         C-NT2RM4000689
         C-NT2RM4000698
         C-NT2RM4000700
        C-NT2RM4000712//"Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds."//1E-
         136//1104bp//77%//AF022789
30
         C-NT2RM4000717
        C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%//P52154
         C-NT2RM4000734//"Homo sapiens mRNA for KIAA0760 protein, partial cds."//0//2273bp//99%//
         C-NT2RM4000741//"Homo sapiens hSGT1 mRNA for hSgt1p, complete cds."//0//2184bp//99%//
35
         D88208
         C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.9E-125//301aa//53%//Q99676
         C-NT2RM4000764
         C-NT2RM4000778
         C-NT2RM4000787
 40
         C-NT2RM4000790
         C-NT2RM4000795//"Homo sapiens mRNA for KIAA0951 protein, complete cds."//0//1847bp//96%//
         AB023168
         C-NT2RM4000796
         C-NT2RM4000798//" Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA,
 45
         complete cds."//0//2603bp//99%//AF084521
         C-NT2RM4000813
         C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE
         AC45 SUBUNIT).//1.10E-24//138aa//44%//P40682
         C-NT2RM4000833
 50
         C-NT2RM4000848
         C-NT2RM4000852
         C-NT2RM4000855
         C-NT2RM4000887
         C-NT2RM4000895
 55
         C-NT2RM4000950
         C-NT2RM4000979
         C-NT2RM4001002//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2259bp//
```

- 100%//AL050092
- C-NT2RM4001032
- C-NT2RM4001047//M025 PROTEIN.//8E-140//333aa//80%//Q06138
- C-NT2RM4001054//"Homo sapiens sec61 homolog mRNA, complete cds."//3.1E-190//1315bp//81%//
- 5 AF077032
  - C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000032// 165aa//33%//Q09820
  - C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II.//5.9E-86//292aa//48%//Q09417
- 10 C-NT2RM4001140//HOMEOBOX PROTEIN MSH-D.//1E-11//103aa//38%//Q01704
  - C-NT2RM4001151
  - C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//4.1E-197//445aa//78%//Q27969
  - C-NT2RM4001160
  - C-NT2RM4001187
- 15 C-NT2RM4001191//"Homo sapiens clone 24963 mRNA sequence, complete cds."//0//1950bp//99%// AF131737
  - C-NT2RM4001200//ZINC FINGER PROTEIN 135.//9.5E-135//375aa//60%//P52742
  - C-NT2RM4001203//"Homo sapiens mRNA for KIAA0839 protein, partial cds."//0//3047bp//99%// AB020646
- 20 C-NT2RM4001204//"Homo sapiens mRNA for KIAA1089 protein, partial cds."//0//2349bp//99%// AB029012
  - C-NT2RM4001217//"Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds."// 7.3E-148//1409bp//72%//AF059611
  - C-NT2RM4001256//"Xenopus laevis putative Zic3 binding protein mRNA, complete cds."//4.30E-55//
- 25 289bp//77%//AF129131
  - C-NT2RM4001258
  - C-NT2RM4001309
  - C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K).//3.50E-35//124aa//65%//P54676
- 30 C-NT2RM4001316//"ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD)."//2.3E-31//334aa//30%//P08503
  - C-NT2RM4001320//"Homo sapiens mRNA for Neuroblastoma, complete cds."//1.8E-39//728bp//64%// D89016
  - C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1E-28//171aa//37%//P32626
- 35 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//8.1E-30//265aa//33%//P53742
  - C-NT2RM4001347//"Homo sapiens NY-REN-25 antigen mRNA, partial cds."//0//2300bp//99%// AF155103
  - C-NT2RM4001371//"Homo sapiens IDN3 mRNA, partial cds."//0//2524bp//99%//AB019494
- 40 C-NT2RM4001382//"Homo sapiens RanBP7/importin 7 mRNA, complete cds."//2.2E-237//1079bp//99%//AF098799
  - C-NT2RM4001384
  - C-NT2RM4001410
  - C-NT2RM4001411//" Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds." //0//1962bp//87%//AF020526
  - C-NT2RM4001412//"Homo sapiens nGAP mRNA, complete cds."//0//1918bp//99%//AF047711
  - C-NT2RM4001414

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- C-NT2RM4001437
- C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//
- 50 1.4E-118//444aa//46%//P73505
  - C-NT2RM4001454
  - C-NT2RM4001455
  - C-NT2RM4001483//ZINC FINGER PROTEIN 136.//5.1E-106//357aa//55%//P52737
  - C-NT2RM4001489//"Homo sapiens mRNA for KIAA0685 protein, complete cds."//0//1810bp//99%//AB014585
    - C-NT2RM4001522
    - C-NT2RM4001557//"Homo sapiens mRNA for KIAA1040 protein, partial cds."//0//1547bp//97%// AB028963

C-NT2RM4001565

C-NT2RM4001566//"Homo sapiens mRNA for KIAA1114 protein, complete cds."//0//1900bp//99%// AB029037

C-NT2RM4001582//"Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds."// 1.5E-284//1082bp//90%//AF071317

C-NT2RM4001592//"Homo sapiens mRNA for KIAA1122 protein, partial cds."//0//2170bp//99%// AB032948

C-NT2RM4001594

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C-NT2RM4001597//M.musculus red-1 gene.//2.1E-171//1414bp//78%//X92750

C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.6E-32//203aa//39%//Q12600 10 C-NT2RM4001629//"MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3)."//1.5E-93//278aa//38%//Q13368

C-NT2RM4001650

C-NT2RM4001662

C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//2.7E-84// 15 410aa//42%//P37339

C-NT2RM4001682

C-NT2RM4001710

C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.9E-141//354aa//72%//Q14141

C-NT2RM4001715 20

C-NT2RM4001731//"Homo sapiens mRNA for KIAA1004 protein, partial cds."//0//1922bp//100%// AB023221

C-NT2RM4001746

C-NT2RM4001754

C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-).//4.1E-186//639aa// 25 58%//Q05512

C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.9E-66//311aa//35%//Q03164

C-NT2RM4001810//"Homo sapiens mRNA for KIAA0863 protein, complete cds."//0//2377bp//99%// AB020670

C-NT2RM4001813//LECTIN BRA-2.//0.00000048//114aa//30%//P17346 30

C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).///2.9E-55//325aa//37%//P28160 C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.9E-161//481aa//56%// P51523

C-NT2RM4001836

C-NT2RM4001841//"Homo sapiens mRNA for KIAA0920 protein, complete cds."//0//1861bp//98%// 35 AB023137

C-NT2RM4001842

C-NT2RM4001856

C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.5E-22//126aa//46%//P79779

C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.3E-244//1248bp//94%//Y17711 40 C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.5E-23//184aa//

C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.9E-09//268aa//26%//P47486 C-NT2RM4001922//"Homo-sapiens mRNA for KIAA0957 protein, complete cds."//0//2165bp//99%//

AB023174 45

C-NT2RM4001930//"Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds."//0//1930bp//99%//AF102851

C-NT2RM4001940//"Homo sapiens timeless homolog mRNA, complete cds."//0//2087bp//99%// AF098162

C-NT2RM4001953 50

C-NT2RM4001965

C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.6E-261//1563bp//84%//X99330

C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.8E-112//457aa//47%// P51523

C-NT2RM4001984 55

C-NT2RM4001987//"NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140]."//3.2E-17//281aa//30%//P16170

C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1

INTERGENIC REGION.//6.9E-94//589aa//35%//P42935

C-NT2RM4002018

C-NT2RM4002034//"Homo sapiens hiwi mRNA, partial cds."//1.9E-53//1585bp//60%//AF104260 C-NT2RM4002044

5 C-NT2RM4002054

15

30

C-NT2RM4002063//"Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds."//0// 1865bp//99%//U82267

C-NT2RM4002066//"Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds."//1.50E-211//1123bp//71%//AF117755

10 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.8E-105//556aa//41%//Q04652

C-NT2RM4002128

C-NT2RM4002140

C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%//P24014

C-NT2RM4002161//"Homo sapiens laforin (EPM2A) mRNA, complete cds."//0//2671bp//99%// AF084535

C-NT2RM4002174//MRP PROTEIN.//9.1E-68//264aa//51%//P21590

C-NT2RM4002189//"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."//6.2E-33//688aa//27%//P08640

C-NT2RM4002205//"ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)."//3E-

20 37//122aa//72%//Q07803

C-NT2RM4002213//"Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds. "//0//2452bp//100%//AF157028

C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.7E-19//147aa//41%//P40809

C-NT2RM4002251//"ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYL-

TRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLU-COSAMINYLTRANSFERASE I) (GNT-I) (GLCNAC-TI)."//2.2E-36//320aa//38%//P27808

C-NT2RM4002256

C-NT2RM4002266

C-NT2RM4002281

C-NT2RM4002287

C-NT2RM4002294

C-NT2RM4002301

C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33 %//P48778

C-NT2RM4002339

35 C-NT2RM4002344

C-NT2RM4002373//"Homo sapiens mRNA for KIAA0649 protein, complete cds."//0//2666bp//99%//AB014549

C-NT2RM4002374

C-NT2RM4002383

40 C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-TIVATING ENZYME).//1.3E-29//275aa//30%//P27095

C-NT2RM4002438//"Xenopus laevis putative Zic3 binding protein mRNA, complete cds."//1.1E-49//611bp//70%//AF129131

C-NT2RM4002446

45 C-NT2RM4002452

C-NT2RM4002457

C-NT2RM4002460//"ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20]."//0.0000016//226aa//24%//P51515

C-NT2RM4002493

50 C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.9E-15//366aa//27%//Q00808

C-NT2RM4002532//PROTEIN HOM1.//2E-16//276aa//28%//P55137

C-NT2RM4002558//"Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds."//0// 1797bp//99%//AF055899

C-NT2RM4002567

55 C-NT2RM4002593

C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.7E-68//236aa//58%//P54815

C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-TRNA LIGASE) (ASPRS).// 2.3E-101//488aa//45%//032038

C-NT2RP1000324

C-NT2RP1000363//"Homo sapiens mRNA for KIAA0638 protein, partial cds."//0//1345bp//99%//AB014538

C-NT2RP1000418

5 C-NT2RP1000513//"Human NifU-like protein (hNifU) mRNA, partial cds."//6.50E-171//516bp//99%//

C-NT2RP1000721

C-NT2RP1000730

C-NT2RP1000767

10 C-NT2RP1000836

C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.2E-20//306aa//33%//Q09531

C-NT2RP1000943

C-NT2RP1001033//"Homo sapiens delta-tubulin mRNA, complete cds."//2.10E-285//1290bp//100%//

15 AF201333

25

C-NT2RP1001073//"Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds. "//8.1E-107//504bp//99%//AF182291

C-NT2RP1001199

C-NT2RP1001248

20 C-NT2RP1001253//"Homo sapiens oscillin (hLn) mRNA, complete cds."//0//2020bp//99%//AF029914 C-NT2RP1001286

C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024

C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024

C-NT2RP1001310//"Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear gene for mitochondrial product."//0//1732bp//99%//AF176006

C-NT2RP1001361//"Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds."//6.5E-116//541bp//100%//AF070652

C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.7E-22// 284aa//25%//P40074

30 C-NT2RP1001432

C-NT2RP2000040//"Homo sapiens mRNA for KIAA0747 protein, partial cds."//0//2648bp//99%//AR013290

C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene).//7.9E-20//265bp//73%//AJ242730

35 C-NT2RP2000098

C-NT2RP2000108

C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.7E-41//278aa//36%//P40556

C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (A1 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//

40 7.1E-12//213aa//23%//P35251

C-NT2RP2000289

C-NT2RP2000327

C-NT2RP2000337

C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.5E-33//155aa//52%//P49910

45 C-NT2RP2000459

C-NT2RP2000498

C-NT2RP2000758

C-NT2RP2001137

C-NT2RP2001149

50 C-NT2RP2001168//VERPROLIN.//1.5E-09//143aa//33%//P37370

C-NT2RP2001173//"Homo sapiens mRNA for KIAA0480 protein, complete cds."//0//1780bp//99%// AB007949

C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT).//6E-10//88aa//38%//P18722

55 C-NT2RP2001196

C-NT2RP2001226

C-NT2RP2001268//"Homo sapiens mRNA for KIAA0810 protein, partial cds."//0//3301bp//98%//AB018353

- C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT).//4.4E-91//179aa//99%//P28663
- C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.3E-39//161aa//34%//P20107 C-NT2RP2001312
- 5 C-NT2RP2001327//"TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN)."//5.5E-116//311aa//71%//Q13829
  - C-NT2RP2001328
  - C-NT2RP2001366
  - C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2E-11//403aa//25%//Q02817
- 10 C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//8.4E-192//
  581aa//54%//P93647
  - C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%//Y18004
  - C-NT2RP2001420//"Mus musculus nuclear protein NIP45 mRNA, complete cds."//9E-112//742bp//82%//U76759
- 15 C-NT2RP2001450
  - C-NT2RP2001467
  - C-NT2RP2001506
  - C-NT2RP2001511//"Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds."//3.2E-297//2206bp//75 %//AF093097
- 20 C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//0//2502bp//99%//Y14494 C-NT2RP2001536//"Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds."//0//2326bp//99%//AF035586
  - C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//27%//Q60992
  - C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME I.//8.2E-29//294aa//
- 25 31%//Q09837
  - C-NT2RP2001581
  - C-NT2RP2001597//"RYANODINE RECEPTOR, CARDIAC MUSCLE."//0.000000036//127aa//36%// P30957
  - C-NT2RP2001628
- C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.1E-47//126aa//53%//P42897
  C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DI-PHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSTRANSFERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa//97%//P14324
- 35 C-NT2RP2001813
  - C-NT2RP2001883//"Homo sapiens CGI-01 protein mRNA, complete cds."//0//2306bp//99%//AF132936
  - C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.3E-38//395aa//30%//P53946
  - C-NT2RP2001947
- 40 C-NT2RP2001985//"Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds."//2.00E-38//435bp//67%//AF090989 C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.5E-129//279aa//85%//
  - C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.5E-129//279aa//85%//Q08469
  - C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).// 1.7E-47//247aa//52%//P35331
    - C-NT2RP2002058//"Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds."//0//2510bp//99%//AF083217
    - C-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.7/1.5E-294//1334bp//99%//AF052183 C-NT2RP2002078//PECANEX PROTEIN.//1.8E-09//195aa//32%//P18490
- 50 C-NT2RP2002079//"HISTONE H1, GONADAL."//4.4E-11//214aa//34%//P02256
  - C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//3389bp//99%//AJ007509
  - C-NT2RP2002185//"Homo sapiens ubiquilin mRNA, complete cds."//0//1789bp//99%//AF176069
  - C-NT2RP2002193//"Homo sapiens PIAS3 mRNA for protein inhibitor of activatied STAT3, complete cds. "//0//2809bp//99%//AB021868
- 55 C-NT2RP2002231

- C-NT2RP2002235
- C-NT2RP2002252//"Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds."//0//3118bp//91%//L38621

- C-NT2RP2002292
- C-NT2RP2002408
- C-NT2RP2002442//HESA PROTEIN.//2.8E-14//163aa//30%//P46037
- C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PS02/SNM1.//6.50E-07//171aa//27%//P30620
- C-NT2RP2002498 5
  - C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.6E-144//537aa//49%//Q02386
  - C-NT2RP2002520//"Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds."//3.70E-34//668bp//61%//AF105427
  - C-NT2RP2002549
- C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08// 10 109aa//37%//P19076
  - C-NT2RP2002706
  - C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.9E-85//489aa//43%//P55194
  - C-NT2RP2002800
- C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%//P14922 15 C-NT2RP2002891
  - C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHRO-MOSOME II.//4.1E-87//395aa//40%//Q18964
  - C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.4E-70//282aa//42%//P52737
- C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA 20 POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%//P70700
  - C-NT2RP2003034
  - C-NT2RP2003099
  - C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%//P13117
- C-NT2RP2003157//"Homo sapiens CGI-74 protein mRNA, complete cds."//0//2037bp//99%// 25
  - C-NT2RP2003158//"Homo sapiens mRNA for proteasome subunit p58, complete cds."//0//2091bp// 99%//D67025
  - C-NT2RP2003165
- C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor 30 Sp1.//0//1544bp//99%//AJ242978
  - C-NT2RP2003277//"Homo sapiens mRNA for KIAA0625 protein, partial cds."//0//3788bp//99%//
  - C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'- PHOSPHATE CYCLASE) (RNA CYCLASE).//4.1E-88//374aa//47%//Q23400
- 35 C-NT2RP2003297

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- C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.2E-199//550aa//70%//Q07866
- C-NT2RP2003308//CROOKED NECK PROTEIN.//5.4E-244//622aa//67%//P17886
- C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG.//0.000022//261aa// 24%//P48754
- C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor.//0//1509bp//99%//AJ133769
- C-NT2RP2003393
- C-NT2RP2003445
  - C-NT2RP2003466//"Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds."7/0//2194bp// 99%//AF126799
  - C-NT2RP2003480//"Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds. "//0//3012bp//99%//AF125158
  - C-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.4E-14//106aa//46%// P04175
- 50 C-NT2RP2003511
  - C-NT2RP2003513//"Human mRNA for KIAA0270 gene, partial cds."//0//2137bp//97%//D87460
  - C-NT2RP2003567//"Homo sapiens mRNA for KIAA0462 protein, partial cds."//0//2343bp//99%// AB007931
  - C-NT2RP2003604//"Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds."//0// 2442bp//99%//AF030233
    - C-NT2RP2003691
    - C-NT2RP2003713//"Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds."//0// 2018bp//99%//AF073344

C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//869aa//

80%//P53620 C-NT2RP2003764 C-NT2RP2003769 5 C-NT2RP2003777 C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3.7E-21//137aa//43%// Q11076 C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).// 0.00000016//117aa//29%//Q91955 C-NT2RP2003981//"Homo sapiens mRNA for KIAA0804 protein, partial cds."//0//3046bp//99%// 10 AB018347 C-NT2RP2003984//Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026).//0//2514bp// 99%//AL050367 C-NT2RP2004041//SYNAPSINS IA AND IB.//0.00000074//159aa//32%//P17599 C-NT2RP2004066//"Human DNA sequence from clone 134019 on chromosome 1p36.11-36.33, complete 15 sequence."//0//2410bp//99%//AL034555 C-NT2RP2004081 C-NT2RP2004124 C-NT2RP2004152 C-NT2RP2004165 20 C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//5.6E-31//424aa//28%//007231 C-NT2RP2004239//"Homo sapiens lok mRNA for protein kinase, complete cds."//0//3044bp//99%// AB015718 C-NT2RP2004245 25 C-NT2RP2004364 C-NT2RP2004365 C-NT2RP2004366//"Homo sapiens mRNA for KIAA0986 protein, partial cds."//0//2790bp//97%// AB023203 30 C-NT2RP2004373 C-NT2RP2004476//"Homo sapiens cyclin L ania-6a mRNA, complete cds."//0//2075bp//99%// AF180920 C-NT2RP2004551 C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3E-117//625aa//40%//Q09903 35 C-NT2RP2004600 C-NT2RP2004664//"Homo sapiens mRNA for KIAA0460 protein, partial cds."//0//2368bp//99%// AB007929 C-NT2RP2004743 C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.3E-26// 40 190aa//41-%//P38692 C-NT2RP2004816//"Homo sapiens H beta 58 homolog mRNA, complete cds."//0//2144bp//96%// AF054179 C-NT2RP2004861 C-NT2RP2004897 C-NT2RP2004933//"Homo sapiens mRNA for ZIP-kinase, complete cds."//0//2103bp//99%//AB007144 45 C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.3E-47//353aa//30%//Q12386 C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//4E-91//218aa//44%// Q92089 C-NT2RP2005162//"Homo sapiens aspartyl aminopeptidase mRNA, complete cds."//0//1615bp//99%// 50 C-NT2RP2005204//" Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds. "//0//1262bp//99%//AF090385 C-NT2RP2005227 C-NT2RP2005287 55 C-NT2RP2005288//"Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds."//0// 2992bp//99%//AF060219 C-NT2RP2005490//"Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds."//1.8E-175//1102bp//

83%//AF053628

C-NT2RP2005539//"Homo sapiens mRNA for KIAA0850 protein, complete cds."//0//1560bp//99%// AB020657

C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYC-OSYLASE) (GUANINE INSERTION ENZYME).//8.2E-23//164aa//28%//032053

C-NT2RP2005722//"Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds."// 0//2545bp//99%//AB011414

C-NT2RP2005732

C-NT2RP2005784//"Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds."//0//2191bp//92%//AF155120

C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.3E-39// 318aa//31%//P40004

C-NT2RP2005859//"Homo sapiens mRNA for KIAA0863 protein, complete cds."//0//1649bp//99%// AB020670

C-NT2RP2006023 15

10

C-NT2RP2006334//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154).//0//2318bp//99%// AL080155

C-NT2RP2006441

C-NT2RP3000002

C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.2E-150//490aa// 20 53%//Q05481

C-NT2RP3000055

C-NT2RP3000068

C-NT2RP3000080

C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN 25 CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.9E-123//436aa//50%// P46401

C-NT2RP3000092

C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692

30 C-NT2RP3000134

C-NT2RP3000149

C-NT2RP3000197

C-NT2RP3000207//"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLU-COSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."//2.9E-11//721aa//23%//P08640

C-NT2RP3000233//"Human DNA sequence from clone 22D12 on chromosome Xq21.1-21.33. Contains a 35 novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins. Contains ESTs and GSSs, complete sequence."//0//1462bp//99%//AL035424

C-NT2RP3000235

C-NT2RP3000247

C-NT2RP3000267 40

45

C-NT2RP3000299//"Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds."//0// 2730bp//82%//D29766

C-NT2RP3000324

C-NT2RP3000341//"Homo sapiens mitochondrial inner membrane preprotein translocase Timl7a mRNA, nuclear gene encoding mitochondrial protein, complete cds."//1.5E-246//1124bp//99%//AF106622

C-NT2RP3000393//"Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds."// 5.8E-266//1373bp//86%//AF061817

C-NT2RP3000441//"Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds."//3.40E-42//645bp//67%//AF098066

50 C-NT2RP3000449

C-NT2RP3000451

C-NT2RP3000456

C-NT2RP3000542

C-NT2RP3000561

C-NT2RP3000562//"Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds."//0// 55 2165bp//99%//AF093097

C-NT2RP3000578//HES1 PROTEIN.//1-3E-22//229aa//27%//P35843

C-NT2RP3000590//UVS-2 PROTEIN.//1.3E-22//458aa//24%//P33288

C-NT2RP3000592 C-NT2RP3000622

C-NT2RP3000624

C-NT2RP3000685

5 C-NT2RP3000736//HYPOTHETICAL PROTEIN KIAA0140.//1.2E-166//305aa//99%//014153
C-NT2RP3000742//"1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA
1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT)."//4.1E-165//
371aa//49%//P10895
C-NT2RP3000753

10 C-NT2RP3000826

C-NT2RP3000865

C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.7E-87//175aa//98%//Q03426

C-NT2RP3001007

C-NT2RP3001055

15 C-NT2RP300111//"Homo sapiens TRF-proximal protein mRNA, complete cds."//1.50E-149//731bp//97%//AF097725

C-NT2RP3001120//ZINC FINGER PROTEIN 136.//7.8E-170//512aa//58%//P52737

C-NT2RP3001126

C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%//P52154

20 C-NT2RP3001232

C-NT2RP3001268//"Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds."//0// 3606bp//99%//AF198358

C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.// 1.3E-99//669bp//83%//Y18101

25 C-NT2RP3001274//"Homo sapiens mRNA for KIAA1037 protein, partial cds."//0//2254bp//99%// AB028960

C-NT2RP3001281

C-NT2RP3001297

C-NT2RP3001318

C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.4E-16//175aa//28%//P51508
C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.6E-25//129aa//34%//P32089
C-NT2RP3001374

C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.4E-128//152aa//99%//P12270

35 C-NT2RP3001432

C-NT2RP3001447

C-NT2RP3001449//"Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1 beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal

Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence."//0//1827bp//99%//AL031282

45 C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFI-ER 2).//3.2E-90//157aa//59%//P36371

C-NT2RP3001459

C-NT2RP3001527//"Human Spl40 protein (Spl40) mRNA, complete cds."//4.3E-290//793bp//93%//

50 C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T2.8D9.3 IN CHROMOSOME II.//9.10E-10//158aa// 31%//Q10022

C-NT2RP3001580//"Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds." //0//1730bp//85%//AF163665

C-NT2RP3001587//"Human anthracycline-associated resistance ARX mRNA, complete cds."//0//2617bp//99%//U35832

C-NT2RP3001589

55

C-NT2RP3001607

C-NT2RP3001608

C-NT2RP3001671//"Homo sapiens mRNA for KIAA0850 protein, complete cds."//0//2310bp//99%// AB020657

C-NT2RP3001672//"Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete cds."//0//2836bp//99%//AF149046

C-NT2RP3001678

C-NT2RP3001688//"Homo sapiens glucocorticoid modulatory element binding protein-1 (GMEB1) mRNA, complete cds."//0//1695bp//99%//AF099013

C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000024//481aa//21%// P25386

C-NT2RP3001698 10

C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.4E-33//161aa//32%//P54356

C-NT2RP3001716 C-NT2RP3001752

C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.8E-117//462aa//

55%//P52272 15

C-NT2RP3001844

C-NT2RP3001854//Homo sapiens mRNA; cDNA DKFZp564G013 (from clone DKFZp564G013).//0//1528bp// 99%//AL050011

C-NT2RP3001855//HOMEOBOX PROTEIN PKNOX1 (HOMEOBOX PROTEIN PREP-1).//8.1E-125//302aa//

20 60%//P55347

C-NT2RP3001898//"Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds."//0//1587bp//100%//AB000624

C-NT2RP3001931 C-NT2RP3001969//TRICHOHYALIN.//2.7E-11//442aa//23%//P37709

C-NT2RP3002002 25

C-NT2RP3002004//H.sapiens mRNA for FAST kinase.//1.50E-19211475bp//94%//X86779

C-NT2RP3002007//SAP1 PROTEIN.//1.1E-68//474aa//32%//P39955

C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//5.30E-25//139aa// 48%//Q09232

C-NT2RP3002045//"Homo sapiens mRNA for KIAA0899 protein, partial cds."//0//33 85bp//99%// 30

C-NT2RP3002056//"Homo sapiens Rb binding protein homolog mRNA, partial cds."//0//2374bp//99%// AF083249

C-NT2RP3002062//"Homo sapiens mRNA for KIAA0873 protein, partial cds."//0//3764bp//99%// AB020680

C-NT2RP3002081//"Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds. "//4.1E-233//1896bp//69%//AF111423

C-NT2RP3002097

C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%//Q12387

C-NT2RP3002142 40

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C-NT2RP3002146

C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//2.8E-253//474aa//93%//P15170

C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP7/1.9E-151//223aa//91%//Q02614

45 C-NT2RP3002166

C-NT2RP3002181

C-NT2RP3002244

C-NT2RP3002248

C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28%//P45978

50 C-NT2RP3002276

C-NT2RP3002304

C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE).// 3.70E-43//318aa//37%//P05792

C-NT2RP3002529//Homo sapiens mRNA for leucocyte vacuolar protein sorting.//0//2276bp//99%//AJ133421

C-NT2RP3002566 55

C-NT2RP3002587

C-NT2RP3002590

C-NT2RP3002631

- C-NT2RP3002650//"Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds."//0//2109bp//87%//AF165163
- C-NT2RP3002663//"Homo sapiens putative glycolipid transfer protein mRNA, complete cds."//8.10E-263//1243bp//97%//AF103731
- 5 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%//P13060
  - C-NT2RP3002763
  - C-NT2RP3002861
  - C-NT2RP3002911
  - C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2E-111//551aa//42%//Q04652
- 10 C-NT2RP3002953//"Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds."//0// 2388bp//99%//AF152498
  - C-NT2RP3002988//"Homo sapiens lkB kinase-b (IKK-beta) mRNA, complete cds."//1.8E-292// 1325bp//99%//AF080158
  - C-NT2RP3003008
- 15 C-NT2RP3003101//"Mouse mRNA for tetracycline transporter-like protein, complete cds."//3.6E-83// 807bp//72%//D88315
  - C-NT2RP3003204
  - C-NT2RP3003278
  - C-NT2RP3003282//"Homo sapiens dynamin (DNM) mRNA, complete cds."//0//2596bp//98%//L36983
- 20 C-NT2RP3003290//"Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds."//1.5e-310// 1468bp//82%//AB033922
  - C-NT2RP3003302
  - C-NT2RP3003313//"Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds."//0//2476bp//99%//AF117657
- 25 C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (R0(SS-A)) (R052).//1.3E-35//178aa//44%//Q62191
  - C-NT2RP3003344
  - C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07// 161aa//28%//P40084
- 30 C-NT2RP3003377
  - C-NT2RP3003385//"Mus musculus SKD3 mRNA, complete cds."//0//2133bp//85%//U09874
  - C-NT2RP3003490//"Homo sapiens mRNA for KIAA0725 protein, partial cds."//0//2437bp//99%//AB018268
- 35 C-NT2RP3003491//"Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds. "//5.6E-36//842bp//62%//AF091624
  - C-NT2RP3004206//CROOKED NECK PROTEIN.//1.4E-220//567aa//67%//P17886
  - C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%// AJ245820
- 40 C-NT2RP3004209//"Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds."//0// 2320bp//99%//AF126736
  - C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.7E-13//118aa//33%//P52734 C-NT2RP3004246
- C-NT2RP3004258//"Homo sapiens ZIS1 mRNA, complete cds."//0//1861bp//99%//AF065391 C-NT2RP3004262//"Homo sapiens heat shock protein hsp40-3 mRNA, complete cds."//2.4E-248//1126bp//100%//AF088982
  - C-NT2RP3004341
  - C-NT2RP3004378
- 50 C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1E-66//364bp//93%//AJ007798 C-NT2RP3004428
  - C-NT2RP3004451
  - C-NT2RP3004454//"Homo sapiens mRNA for KIAA0448 protein, complete cds."//0//2875bp//99%//AB007917
- 55 C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.6E-61//170aa//40%//Q01820
  - C-NT2RP3004498//"Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds."// 2E-249//1777bp//80%//U83176
  - C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.9E-295//893bp//92%//Y08260

C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.7E-37//190aa//39%//P40484 C-NT2RP3004534//"Mouse oncogene (ect2) mRNA, complete cds."//0//2075bp//87%//L11316 C-NT2RP4000528//NPL4 PROTEIN.//9.8E-86//515aa//37%//P33755 C-NT2RP4000907//"Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds."//0// 2127bp//86%//D45913 5 C-NT2RP4001029//"Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds."//0//1711bp// 90%//U20086 C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//0.000016// 186aa//29%//024076 C-NT2RP4001389//KES1 PROTEIN.//1.70E-31//342aa//34%//P35844 10 C-NT2RP4001442 C-NT2RP4001529//"Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds."/1.70E-255// 1148bp//90%//U20086 C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN).//1.10E-45//310aa//27%// P12868 15 C-OVARC1000106//"TROPOMYOSIN 1, FUSION PROTEIN 33."//0.000032//165aa//27%//P49455 C-OVARC1000198 C-OVARC1000682//"PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSI-DASE 1B)."//1.1E-209//293aa//95%//P39098 C-OVARC1000703 20 C-OVARC1000722//"Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds."//0//759bp//98%//AF038661 C-OVARC1000730 C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%//P25159 25 C-OVARC1000781 C-OVARC1000787 C-OVARC10008347/Homo sapiens mRNA for atopy related autoantigen CALCJ/2.8E-258//1183bp//99%//Y17711 C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199 C-OVARC1000850//"Homo sapiens PB39 mRNA, complete cds."//0//2095bp//99%//AF045584 C-OVARC1000862//M.musculus mRNA for FT1.//5.9E-226//1498bp//81%//Z67963 30 C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.2E-50//206aa//52%//P40484 C-OVA-RC1000883 C-OVARC1000886 C-OVARC1000912 C-OVARC1000915//"Homo sapiens histone deacetylase 5 mRNA, complete cds."//1.60E-121//591bp// 35 97%//AF132608 C-OVARC1000924 C-OVARC1000964 C-OVARC1000984 C-OVARC1001004 40 C-OVARC1001010 C-OVARC1001011 C-OVARC1001032 C-OVARC1001044 C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.9E-35//76aa//98%//P43490 45 C-OVARC1001068//"Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds."//0//1819bp// 99%//AF082657 C-OVARC1001074 C-OVARC1001092//" Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F185707 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))."//2E-214//769bp//97%// 50 AJ005897 C-OVARC1001107//"Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds."//6.1E-276//594bp//98%//AF167572 C-OVARC1001154//"Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds."//2.3E-296// 1561bp//93%//AF055008 55 C-OVARC1001161 C-OVARC1001167

C-OVARC1001170

- C-OVARC1001171//"Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds." //5.7E-151//436bp//92%//U94855
- C-OVARC1001173
- C-OVARC1001176
- 5 C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.1E-11//221aa//25%//P48510
  - C-OVARC1001188
  - C-OVARC1001232//"CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)."//5.10E-22//83aa//37%//Q10568
  - C-OVARC1001270
- 10 C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).// 0.0000014//224aa//26%//P25976
  - C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444
  - C-OVARC1001344
  - C-OVARC1001369
- 15 C-OVARC1001372//"Homo sapiens mRNA for KIAA0897 protein, partial cds."//0//840bp//97%// AB020704
  - C-OVARC1001391
  - C-OVARC1001399

20

- C-OVARC1001417//"Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170 mRNA, complete cds."//0//1715bp//99%//AF135802
- C-OVARC1001419//"Homo sapiens GOK (STIM1) mRNA, complete cds."//4.9E-48//586bp//69%// U52426
- C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111
- C-OVARC1001453
- 25 C-OVARC1001476//" Mus musculus YGR163w mRNA homologue, complete cds." //1.80E-187// 510bp//899//AB017616
  - C-OVARC1001480
  - C-OVARC1001489
  - C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE
- 30 PROTEIN 1).//0//777aa//91%//P98161
  - C-OVARC1001525
  - C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.4E-19//130aa//40%//P53081
  - C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%// AF031165
- 35 C-OVARC1001600
  - C-OVARC1001610//"Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds."//0//1870bp//99%//AF068302
  - C-OVARC1001702
  - C-OVARC1001703//"Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds."//3.5E-16//399bp//61%//AF133670
  - C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa//38%//Q62267
  - C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DI-AZEPAM BINDING INHIBITOR) (MA-DBI).//4.4E-40//195aa//41%//P07106
- 45 C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.3E-16//116aa//43%//Q13796
  - C-OVARC1001731//"TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2."//4E-122//282aa//85%//P08942
  - C-OVARC1001745
  - C-OVARC1001762//"N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-
- 50 AMINO, ACETYLTRANSFERASE 1).&guot;//6.4E-85//514aa//34%//P12945

  - C-OVARC1001767//"Homo sapiens mRNA for KIAA0675 protein, complete cds."//0//2083bp//99%//AB014575
- 55 C-OVARC1001768
  - C-OVARC1001791
  - C-OVARC1001795
  - C-OVARC1001802

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C-OVARC1001809//"Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds."//2.7E-190//
       1624bp//76%//AF068748
       C-OVARC1001828
       C-OVARC1001846
        C-OVARC1001861
5
        C-OVARC1001879
        C-OVARC1001880
        C-OVARC1001883
        C-OVARC1001916
        C-OVARC1001928
10
        C-OVARC1001942//"N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-
        AMINO, ACETYLTRANSFERASE 1)."//3.1E-81//497aa//35%//P12945
        C-OVARC1001943//"Mus musculus DEBT-91 mRNA, complete cds."//0//2035bp//87%//AF143859
        C-OVARC1001950
        C-OVARC1001987//"Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds."//
15
        2.3E-220//652bp//84%//AF061817
        C-OVARC1002050//"Homo sapiens mRNA for actin binding protein ABP620, complete cds."//0//
        1019bp//99%//AB029290
        C-OVARC1002082
        C-OVARC1002107
20
        C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRI-
        ER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.4E-52//306aa//35%//
        035913
        C-OVARC1002138//SAP1 PROTEIN.//7.6E-60//128aa//59%//P39955
25
         C-OVARC1002156
         C-OVARC1002158
        C-PLACE1000004//"Homo sapiens IDN3-B mRNA, complete cds."//0//2365bp//99%//AB019602
         C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.4E-17//185aa//32%//P08643
         C-PLACE1000048
         C-PLACE1000050
30
         C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.9E-54//190bp//94%//L22154
         C-PLACE1000081//"Human SEC7 homolog Tic (TIC) mRNA, complete cds."//0//2077bp//99%//
         U63127
         C-PLACE1000094
         C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//
 35
         1.8E-62//158aa//81%//P20290
         C-PLACE1000214
         C-PLACE1000236
         C-PLACE1000246
         C-PLACE1000292
 40
         C-PLACE1000308
         C-PLACE1000332
         C-PLACE1000453
         C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//
         P51522
 45
         C-PLACE1000599
         C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918
         C-PLACE1000653//"Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds."//
         0//1992bp//99%//AF180371
         C-PLACE1000656//" Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and
 50
          LLNLc110F1857Q7 (RZPD Berlin))."//2.1E-277//1260bp//99%//AJ005896
          C-PLACE1000706//"Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds."
          //0//1366bp//99%//AF119043
          C-PLACE1000712
          C-PLACE1000749
 55
          C-PLACE1000769//"Homo sapiens CGI-18 protein mRNA, complete cds."//0//1985bp//98%//
          AF132952
          C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
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CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734

```
C-PLACE1000849
        C-PLACE1000856//"Homo sapiens mRNA for KIAA0974 protein, partial cds."//0//1310bp//100%//
        AB023191
5
        C-PLACE1000931
        C-PLACE1000987//"Homo sapiens mRNA for KIAA0724 protein, complete cds."//0//1749bp//99%//
        AR018267
        C-PLACE1001010
        C-PLACE1001015
        C-PLACE1001024
10
        C-PLACE1001062//"Homo sapiens PAC clone DJ1049N15 from 7q31.2-7q32, complete sequence."//
        2.7E-32//470bp//71%//AC006020
        C-PLACE1001104
        C-PLACE1001168
        C-PLACE1001171//MYOTUBULARIN.//7.1E-84//198aa//73%//Q13496
15
        C-PLACE1001185//"Homo sapiens mRNA for KIAA0943 protein, partial cds."//0//1668bp//99%//
        C-PLACE1001238//"Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds."//
        2E-202//1333bp//80%//D14336
        C-PLACE1001280
20
        C-PLACE1001294//M.musculus GEG-154 mRNA.//4.3E-221//1057bp//78%//X7I642
        C-PLACE1001304//"Homo sapiens zinc finger protein dp mRNA, complete cds."//0//2421bp//99%//
         AF153201
         C-PLACE1001311
         C-PLACE1001323
25
         C-PLACE1001351
         C-PLACE1001414
         C-PLACE1001440
         C-PLACE1001456
         C-PLACE1001517//" Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1),
30
         complete cds."//4.60E-112//392bp//87%//AB002137
         C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.7E-130//244aa//99%//Q60809
         C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-118//429aa//48%//
         P51523
         C-PLACE1001634
35
         C-PLACE1001640
         C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.3E-66//174aa//45%//P91408
         C-PLACE1001705
         C-PLACE1001716
         C-PLACE1001720
40
         C-PLACE1001745
         C-PLACE1001748//"Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds."//0//2602bp//99%//
         AF061243
         C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein
         TRP6.//0//2900bp//99%//AJ006276
45
         C-PLACE1001799
         C-PLACE1001845//"Mus musculus cyclin ania-6a mRNA, complete cds."//3.30E-31//925bp//62%//
         AF159159
         C-PLACE1001897
         C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.5E-58//112aa//100%//
50
         076094
         C-PLACE1002157
         C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT
         SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591
         C-PLACE1002227
55
         C-PLACE1002259
         C-PLACE1002319
         C-PLACE1002395//"Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds."//7.9E-
```

```
100//966bp//75%//AB030505
        C-PLACE1002477
        C-PLACE1002493//" Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.
        "//1.7E-113//545bp//98%//AF042273
5
        C-PLACE1002500
        C-PLACE1002514
        C-PLACE1002532//HOMEOBOX PROTEIN DLX-5.//1.2E-152//289aa//96%//P70396
        C-PLACE1002537
        C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5E-99//386aa//48%//P45890
        C-PLACE10025 83//"GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE
10
        RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT)."//5.6E-34//
        76aa//98%//P39087
        C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//5.5E-17//76aa//56%//P45340
        C-PLACE1002625
        C-PLACE1002655//ADSEVERIN (SCINDERIN)(SC).//2.5E-278//543aa//92%//Q28046
15
        C-PLACE1002768
        C-PLACE1002782//"Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds."//3.8E-43//
        385bp//77%//U50927
        C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%//P53973
20
        C-PLACE1002853
        C-PLACE1002908//"Homo sapiens XGaIT-1 mRNA for galactosyltransferase I, complete cds."//0//
        1654bp//99%//AB028600
        C-PLACE1002962
        C-PLACE1002968
        C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%//Q49091
25
        C-PLACE1003025
        C-PLACE1003027//"Homo sapiens mRNA for KIAA0516 protein, partial cds."//2.1e-314//1417bp//
        100%//AB011088
        C-PLACE1003044//"Homo sapiens mRNA for KIAA0829 protein, partial cds."//0//1382bp//96%//
        AB020636
30
         C-PLACE1003176
         C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.9E-76//309aa//47%//
         Q15391
         C-PLACE1003256
         C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.9E-22//70aa7/47%//P21541
35
         C-PLACE1003343
         C-PLACE1003361
         C-PLACE1003366//"Homo sapiens otoferlin (OTOF) mRNA, complete cds."//1.4E-78//542bp//67%//
         AF107403
40
         C-PLACE1003373
         C-PLACE1003375
         C-PLACE1003394//"Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds."//2.30E-150//
         774bp//94%//M83680
         C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.3E-40//278aa//36%//P40556
         C-PLACE1003454
 45
         C-PLACE1003478
         C-PLACE1003516
         C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.1E-218//905bp//99%//X78136
         C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%//
 50
         Q09475
         C-PLACE1003528
         C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-
         ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
         NENT).//7.7E-68//404aa//33%//P32802
         C-PLACE1003566
 55
         C-PLACE1003584
         C-PLACE1003593
```

C-PLACE1003605//HAP5 TRANSCRIPTIONAL

```
ACTIVATOR.//0.00000023//82aa//35%//Q02516
        C-PLACE1003618
        C-PLACE1003638
        C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.6E-118//350aa//46%//P52742
        C-PLACE1003760//"Homo sapiens tetraspanin TM4-A mRNA, complete cds."//5.2E-289//1313bp//
5
        97%//AF133423
        C-PLACE1003768
        C-PLACE1003795
        C-PLACE1003886
        C-PLACE1003888//"Homo sapiens mRNA for KIAA1092 protein, partial cds."//0//2057bp//99%//
10
        C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//1.4E-243//
        584aa//74%//P17812
        C-PLACE1003915//"PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (AR-
        GININE- -TRNA LIGASE) (ARGRS)."//2.4E-108//581aa//40%//Q05506
15
        C-PLACE1004118
        C-PLACE1004256//"Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds."//
        2E-93//960bp//76%//AF115778
        C-PLACE1004274
        C-PLACE1004284
20
        C-PLACE1005331
        C-PLACE1005739//Homo sapiens mRNA; cDNA DKFZp564A032 (from clone DKFZp564A032).//0//2190bp//
        99%//AL050267
        C-PLACE1005828
        C-PLACE1005876//"CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT
25
        (CPSF 100 KD SUBUNIT)."//0//730aa//99%//Q10568
        C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.9E-42//224aa//43%//P54069
        C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
        (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2E-28//236aa//
        30%//P98110
30
        C-PLACE1007053
        C-PLACE1007068
        C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.3E-26//309aa//30%//Q04652
        C-PLACE1009921
        C-PLACE1010401
35
        C-PLACE1010856
        C-PLACE1010857
         C-PLACE1010917
         C-PLACE1010925
        C-PLACE1010926//"Homo sapiens mRNA for KIAA0554 protein, partial cds."//0//1160bp//100%//
40
        C-PLACE1010942//"Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds."//0//1440bp//
         99%//AF114487
         C-PLACE1010944
45
         C-PLACE1010954
        C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.3E-98//297aa//48%//P45890
         C-PLACE1011026
        C-PLACE1011046//"1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1
        (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154)."//0//646aa//97%//P10894
50
         C-PLACE1011054
         C-PLACE1011057
        C-PLACE1011109//"ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)."//1.50E-
         22//63aa//88%//Q07803
        C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.9E-71//190aa//44%//Q03532
55
         C-PLACE1011133
         C-PLACE1011143
         C-PLACE1011165
         C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.3E-89//167aa//100%//P03830
```

C-PLACE1011219//PROBABLEOXIDOREDUCTASE (EC 1.-.-.).//3.2E-12//212aa//29%//Q03326 C-PLACE1011221 C-PLACE1011263//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//2487bp// 99%//AL050390 5 C-PLACE1011325 C-PLACE1011332//"Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds."// 7.2E-151//697bp//99%//AF102265 C-PLACE1011340//"Homo sapiens IDN3-B mRNA, complete cds."//1.20E-74//380bp//97%// AB019602 C-PLACE1011399//"Homo sapiens CGI-72 protein mRNA, complete cds."//3.2E-90//427bp//99%// 10 C-PLACE1011433//"Homo sapiens mRNA for KIAA0530 protein, partial cds."//0//1946bp//99%// AB011102 C-PLACE1011452 C-PLACE1011465 15 C-PLACE1011472//"Homo sapiens mRNA for KIAA0712 protein, complete cds."//0//2022bp//99%// AB018255 C-PLACE1011477//"Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds."//0//2040bp//99%// AF065482 C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).// 20 4.90E-11//147aa//32%//P52178 C-PLACE1011520 C-PLACE1011563 C-PLACE1011567 C-PLACE1011576//"Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds."//0// 25 1791bp//82%//L11672 C-PLACE1011586 C-PLACE1011643 C-PLACE1011649 C-PLACE1011664//CROOKED NECK PROTEIN.//1.6E-187//505aa//64%//P17886 30 C-PLACE1011682 C-PLACE1011719 C-PLACE1011729 C-PLACE1011858//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//0//1490bp// 35 99%//AL050287 C-PLACE1011874 C-PLACE1011875//"Homo sapiens mRNA for KIAA0580 protein, partial cds."//4.1E-112//524bp// 100%//AB011152 C-PLACE1011923//"Homo sapiens serum-inducible kinase mRNA, complete cds."//0//2782bp//99%// 40 AF059617 C-PLACE1011982 C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.6E-42//104aa//49%// C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.1E-116//364aa//45%//P42566 45 C-PLACE2000017 C-PLACE2000021//"Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds."//2.7E-107//981bp//74%//AF082556 C-PLACE2000047 C-PLACE2000062//"Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type 50 lectin, complete cds, clone:HP01347."//6.3E-166//656bp//94%//AB015629 C-PLACE2000100 C-PLACE2000111 C-PLACE2000172 C-PLACE2000187 55 C-PLACE2000216//"Dog nonerythroid beta-spectrin mRNA, 3' end.&quot,//3.2E-253//1799bp//83%//L02897

C-PLACE2000246//"Homo sapiens mRNA for KIAA0795 protein, partial cds."//4.60E-172//796bp//

99%//AB018338

- C-PLACE2000317
- C-PLACE2000341//"Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds."/0//1554bp//99%//AF069307
- C-PLACE2000366
- 5 C-PLACE2000373//F-SPONDIN PRECURSOR.//8.6E-16//371aa//28%//P35446
  - C-PLACE2000394
  - C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//6.3E-37//90aa//98%//P10586
  - C-PLACE2000411//"Homo sapiens mRNA for KIAA1037 protein, partial cds."//0//2515bp//99%//AB028960
    - C-PLACE2000425

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- C-PLACE2000427//PROBABLE HELICASE MOT1.//1.2E-26//200aa//27%//P32333
- C-PLACE2000433
- C-PLACE2000438//"POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALAC-
- TEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALAC TOSAMINYLTRANSFERASE)(GALNAC-T1)."//2.1E-86//348aa//41%//Q10472
  - C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//2.5E-25// 165aa//40%//P33450
  - C-PLACE2000477//"Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds."//6.7E-127//671bp//94%//AF072733
  - C-PLACE3000009
  - C-PLACE3000020//"Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds."//0// 2253bp//99%//AF033861
  - C-PLACE3000103
- 25 C-PLACE3000142
  - C-PLACE3000145//TENSIN.//1E-108//277aa//75%//Q04205
  - C-PLACE3000156
  - C-PLACE3000157
  - C-PLACE3000197
- 30 C-PLACE3000208
  - C-PLACE3000226//"Homo sapiens mRNA for KIAA0962 protein, partial cds."//0//4805bp//99%//AB023179
  - C-PLACE3000242//"Homo sapiens mRNA for KIAA1114 protein, complete cds."//0//2786bp//96%//AB029037
- 35 C-PLACE3000363
  - C-PLACE3000405
  - C-PLACE3000416//"Homo sapiens mRNA for actin binding protein ABP620, complete cds."//1.80E-141//565bp//98%//AB029290
  - C-PLACE3000477
- 40 C-PLACE4000106//"Homo sapiens mRNA for KIAA0462 protein, partial cds."//0//6702bp//99%//
  AB007931
  - C-PLACE4000323
  - C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771
- 45 C-PLACE4000369//"Homo sapiens mRNA for KIAA1025 protein, partial cds."//0//4830bp//99%// AB028948
  - C-PLACE4000445//Homo sapiens mRNA; cDNA DKFZp434C212 (from clone DKFZp434C212).//0//2565bp//99%//AL080196
  - C-PLACE4000558//"Homo sapiens mRNA for KIAA0729 protein, partial cds."//0//1051bp//97%//
  - C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1) (UEGF-1).//9.3E-70//226aa//52%//P10079
  - C-PLACE4000593
  - C-PLACE4000612//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//7.1E-154//340aa//40%//P21414
  - C-PLACE4000670
  - C-THYRO1000026
  - C-THYRO1000085//"PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B."//2E-72//155aa//92%//

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Q06710
        C-THYRO1000107
        C-THYRO1000111
        C-THYRO1000132//" Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA,
        complete cds."//1.1E-159//824bp//95%//U97018
5
        C-THYRO1000156
        C-THYRO1000173//"Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.
        "//0//1713bp//99%//AF020797
        C-THYRO1000186
        C-THYRO1000187
10
        C-THYRO1000241
        C-THYRO1000279
        C-THYRO1000327//"Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds."
        //0//1567bp//99%//AF124145
15
        C-THYRO1000452
        C-THYRO1000471
        C-THYRO1000484
        C-THYRO1000502
        C-THYRO1000505
        C-THYRO1000585//"Homo sapiens protein associated with Myc mRNA, complete cds."//0//1901bp//
20
        99%//AF075587
         C-THYRO1000596
        C-THYRO1000662//"Homo sapiens XPV mRNA for DNA polymerase eta, complete cds."//0//2341 bp//
         99%//AB024313
         C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%//AJ132889
25
         C-THYRO1000715
         C-THYRO1000734
         C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//
         C-THYRO1000756//"ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC
30
         2.4.99.-) (ST6GALNACIII) (STY)."//1.8E-55//243aa//42%//Q64686
         C-THYRO1000777
         C-THYRO1000783//"Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete
         cds."//2.4E-157//1656bp//70%//U37373
         C-THYRO1000787
35
         C-THYRO1000793
         C-THYRO1000796
         C-THYRO1000843
         C-THYRO1000852//" Human branched chain aminotransferase precursor (BCATm) mRNA, nuclear gene en-
         coding mitochondrial protein, complete cds."//3.3E-147//790bp//93%//U68418
 40
         C-THYRO1000865
         C-THYRO1000895
         C-THYRO1000926//"Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.
         "//0//2387bp//99%//AF079529
         C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5E-83//566aa//
 45
         37%//P43550
         C-THYRO1000952
```

C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%//P35132

C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN 50 LIGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%//P52491 C-THYRO1001031

C-THYRO1001062

C-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//1.2E-67//245aa//62%//P98168

C-THYRO1001133 55

C-THYRO1001134//"Homo sapiens CGI-78 protein mRNA, complete cds.";//0//1898bp//99%// AF151835

C-THYRO1001173

	C-THYRO1001213
	C-THYRO1001321
	C-THYRO1001322
	C-THYRO1001365
5	C-THYRO1001401
	C-THYRO1001411
	C-THYRO1001434
	C-THYRO1001534
	C-THYRO1001541
10	C-THYRO1001559
	C-THYRO1001570
	C-THYRO1001595
	C-THYRO1001605
	C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//
15	99%//AJ002190
	C-THYRO1001656//"Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds."//4.1E-
	273//1947bp//82%//AF175968
	C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//0//1820bp//99%//
	AJ225089
20	C-THYRO1001673
	C-THYRO1001703//NIFR3-LIKE PROTEIN.//2.90E-32//282aa//32%//P45672
	C-THYRO1001706
	C-THYRO1001738//TUBULIN-TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.4E-20//217aa//30%//P38584
	C-THYRO1001745
25	C-THYRO1001793
	C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.4E-74//158aa//89%//P42128
	C-THYRO1001895
	C-THYRO1001907
	C-VESEN1000122
30	C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.4E-30//80aa//60%//P25916
	C-Y79AA1000059//"Homo sapiens immunophilin homolog ARA9 mRNA, complete cds."//2.9E-70//
	1040bp//65%//U78521
	C-Y79AA1000065
	C-Y79AA1000131
35	C-Y79AA1000181//"Homo sapiens CGI-01 protein mRNA, complete cds."//0//1858bp//99%//
	AF132936
	C-Y79AA1000202
	C-Y79AA1000214//"Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds."//7.1E-71//
	345bp//100%//AF081192
40	C-Y79AA1000230
	C-Y79AA1000258
	C-Y79AA1000268//"Mus musculus Nip21 mRNA, complete cds."//2.10E-50//648bp//64%//AF035207
	C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%//Q02910
	C-Y79AA1000328//SEL-10 PROTEIN.//0.000000067//219aa//25 %//Q93794
45	C-Y79AA1000355
	C-Y79AA1000368//REDUCED VIABILTTY UPON STARVATION PROTEIN 161.//4E-20//261 aa//27%//P25343
	C-Y79AA1000420
	C-Y79AA1000469//"Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, com-
	plete cds."//8.30E-252//1207bp//85%//U41736
50	C-Y79AA1000480
	C-Y79AA1000540
	C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE
	CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA
	C SUBUNIT).//0//652aa//98%//P17427
55	C-Y79AA1000574//Homo sapiens clone H17 unknown mRNA.//0//1932bp//99%//AF103801
	C-Y79AA1000627//"Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds."//2E-287//203
	Ibn//82%//AE060503

C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//5.80E-254//1477bp//84%//X69942

lbp//82%//AF060503

- C-Y79AA1000734//"Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds."// 0//1594bp//99%//AF093670
- C-Y79AA1000748//"Homo sapiens CGI-05 protein mRNA, complete cds."//1.9E-239//1367bp//91%// AF152097
- C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).// 5 4.9E-91//200aa//64%//Q61990
  - C-Y79AA1000774
  - C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTEDASE (EC 3.1.3.5).//3E-37//469aa//27%//P49902
  - C-Y79AA1000784//"Homo sapiens RanBP7/importin 7 mRNA, complete cds."//1.10E-236//1076bp// 99%//AF098799
    - C-Y79AA1000794//"Homo sapiens actin-associated protein 2E4/kaptin (2E4) mRNA, 2E4-1 allele, complete cds."//0//1610bp//99%//AF105369
    - C-Y79AA1000800//"Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds."//1.6E-284//1288bp//99%//AF072733
- C-Y79AA1000805 15

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- C-Y79AA1000824
- C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//5E-173//220aa//79%//P05209
- C-Y79AA1000850
- C-Y79AA1000962//"MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II)."// 4.2E-17//430aa//27%//Q99323
- C-Y79AA1000968//"Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds."//3.9E-248//1468bp//87%//U38253
- C-Y79AA1000976
- C-Y79AA1001023
- C-Y79AA1001041 25
  - C-Y79AA1001048//"ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD)."//3.1E-138//583aa//47%//P45953
  - C-Y79AA1001077
  - C-Y79AA1001078
- 30 C-Y79AA1001145
  - C-Y79AA1001177
  - C-Y79AA1001185
  - C-Y79AA1001211//" Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds. " //0//1435bp//99%//AF139658
- C-Y79AA1001228 35
  - C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HY-DROXYSTEROID DEHYDROGENASE 1).//7.7E-50//228aa//42%//P51657
  - C-Y79AA1001236//"Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin))."//0//1653bp//99%//AJ005892
- 40 C-Y79AA1001281
  - C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.000000023//193aa//30%// Q03309
  - C-Y79AA1001323//"Mus musculus mRNA for GSG1, complete cds."//3.3E-172//1171bp//83%//
- C-Y79AA1001391//HOMEOBOX PROTEIN HOX-A13 (HOX-1J).//1.2E-58//178aa//66%//P31271 45
  - C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.2E-13//230aa//32%//O83746 C-Y79AA1001402//" Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds. &guot;//8.50E-65//784bp//62%//AF083115
  - C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa//38%//P35132
    - C-Y79AA1001533//"Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds."// 4.5E-193//1333bp//80%//D14336
    - C-Y79AA1001541
  - C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KI-NASE) (PI4K-ALPHA).//7.5E-76//85aa//90%//P42356
    - C-Y79AA1001555
    - C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- AC-TIVATING ENZYME).//1.9E-40//482aa//27%//P27550

C-Y79AA1001585

C-Y79AA1001603//" POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC: POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)."//1.7E-84//313aa//48%//Q07537

5 C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.8E-91//209aa//41%//P52740

C-Y79AA1001665

C-Y79AA1001679//"Homo sapiens lambda-crystallin mRNA, complete cds."//3.4e-310//1430bp//98%//AF077049

C-Y79AA1001696//"Homo sapiens mRNA for KIAA1109 protein, partial cds."//0//1669bp//100%//AB029032

C-Y79AA1001705//"Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds. "//3.4E-47//626bp//68%//AF033120

C-Y79AA1001711//"Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds."//1.2E-258// 1185bp//99%//J04137

15 C-Y79AA1001781

10

C-Y79AA1001805

C-Y79AA1001827//"Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds."//0//1689bp//98%//AF177145

C-Y79AA1001846

20 C-Y79AA1001923

C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1E-10//94aa//47%//O42643

C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//52%//P42743

25 C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5E-163//752bp//99%//X86018

C-Y79AA1002089

C-Y79AA1002115

C-Y79AA1002125

C-Y79AA1002204

30 C-Y79AA1002208//ANKYRIN.//8.1E-34//188aa//38%//Q02357

C-Y79AA1002209//"Homo sapiens CGI-04 protein mRNA, complete cds."//0//1617bp//99%// AF132939

C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//7.10E-17//213aa//31%//P30620

C-Y79AA1002246//SYNAPTOTAGMIN V.//1.6E-28//286aa//32%//000445

35 C-Y79AA1002298

C-Y79AA1002307//"Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds."//0//1209bp//99%//

C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.9E-186//1130bp//82%//X67877

40 C-Y79AA1002351

45

55

C-Y79AA1002407

C-Y79AA1002433//"Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds."//0//1545bp//96%//AF152961

C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.5E-136//472aa//49%//Q05481

Homology Search Result Data 13.

[0333] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000042

C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1135bp//100%//

C-HEMBA1000150//H.sapiens gene for U5 snRNP-specific 200kD protein. J/2.50E-153//525bp//91% J/Z70200

C-HEMBA1000213

C-HEMBA1000243

```
C-HEMBA1000244
        C-HEMBA1000251
        C-HEMBA1000338
        C-HEMBA1000357
5
        C-HEMBA1000376
        C-HEMBA1000428
        C-HEMBA1000469
        C-HEMBA1000497
        C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa//
        25%//Q05481
10
        C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aa//32%//Q60865
        C-HEMBA1000575
        C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246
        C-HEMBA1000673
        C-HEMBA1000702
15
        C-HEMBA1000722
        C-HEMBA1000726
        C-HEMBA1000876
        C-HEMBA1000942
20
        C-HEMBA1000943
        C-HEMBA1000960
        C-HEMBA1000985
        C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE)
        (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493
25
        C-HEMBA1001020
        C-HEMBA1001024
        C-HEMBA1001026
        C-HEMBA1001051
        C-HEMBA1001060
        C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSORS.//1.50E-92//82aa//100%//P02461
30
        C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//
        432bp//94%//AF119043
        C-HEMBA1001099
        C-HEMBA1001121
         C-HEMBA1001123
35
         C-HEMBA1001208
         C-HEMBA1001213
         C-HEMBA1001226
         C-HEMBA1001247
40
         C-HEMBA1001299
         C-HEMBA1001319
         C-HEMBA1001323
         C-HEMBA1001327
         C-HEMBA1001361
45
         C-HEMBA1001375
         C-HEMBA1001377
         C-HEMBA1001383
         C-HEMBA1001391
         C-HEMBA1001411
50
         C-HEMBA1001432
         C-HEMBA1001433
         C-HEMBA1001435
         C-HEMBA1001442
         C-HEMBA1001463
         C-HEMBA1001515
55
         C-HEMBA1001522
         C-HEMBA1001557
         C-HEMBA1001566
```

```
C-HEMBA1001589
       C-HEMBA1001608
       C-HEMBA1001636
        C-HEMBA1001647
5
        C-HEMBA1001651
        C-HEMBA1001658
        C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E-09//101aa//35%//
        P54787
        C-HEMBA1001712
        C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OB-CADHERIN) (OSF-4).//
10
        1.10E-38//87aa//96%//P55288
        C-HEMBA1001745
        C-HEMBA1001750
        C-HEMBA1001784
15
        C-HEMBA1001791
        C-HEMBA1001803
        C-HEMBA1001820
        C-HEMBA1001835
        C-HEMBA1001888
        C-HEMBA1001912
20
        C-HEMBA1001915
        C-HEMBA1001918
        C-HEMBA1001940
        C-HEMBA1001942
25
        C-HEMBA1001964
        C-HEMBA1002022
        C-HEMBA1002039
        C-HEMBA1002100
        C-HEMBA1002113
30
        C-HEMBA1002119
        C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%//Q14847
        C-HEMBA1002160
        C-HEMBA1002162
        C-HEMBA1002166
        C-HEMBA1002185
35
        C-HEMBA1002204
        C-HEMBA1002328
        C-HEMBA1002337
        C-HEMBA1002348
40
        C-HEMBA1002381
        C-HEMBA1002486
        C-HEMBA1002498
        C-HEMBA1002538
        C-HEMBA1002552
        C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//
45
        68%//AF055993
        C-HEMBA1002558
        C-HEMBA1002621
        C-HEMBA1002629
50
        C-HEMBA1002645
        C-HEMBA1002659
        C-HEMBA1002661
        C-HEMBA1002666
        C-HEMBA1002678
55
        C-HEMBA1002679
        C-HEMBA1002712
        C-HEMBA1002716
        C-HEMBA1002742
```

```
C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7).//5.00E-37//268aa//34%//P06746
        C-HEMBA1002748
        C-HEMBA1002780
        C-HEMBA1002801
        C-HEMBA1002826
5
        C-HEMBA1002833
        C-HEMBA1002921
        C-HEMBA1002934
        C-HEMBA1002944
        C-HEMBA1002968
10
        C-HEMBA1003034
        C-HEMBA1003037
        C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN
        PRECURSOR (ALS).//1.30E-09//121aa//40%//P35858
        C-HEMBA1003078
15
        C-HEMBA1003083
        C-HEMBA1003086
        C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%//AF155096
        C-HEMBA1003133
        C-HEMBA1003142
20
        C-HEMBA1003166
        C-HEMBA1003197
        C-HEMBA1003202
        C-HEMBA1003220
        C-HEMBA1003229
25
        C-HEMBA1003276
        C-HEMBA1003278
        C-HEMBA1003328
         C-HEMBA1003373
         C-HEMBA1003597
30
         C-HEMBA1003598
         C-HEMBA1003656
         C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//
         423aa//47%//P34629
35
         C-HEMBA1003733
         C-HEMBA1003742
         C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)
         (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%//Q16665
         C-HEMBA1003803
         C-HEMBA1003854
40
         C-HEMBA1003926
         C-HEMBA1003939
         C-HEMBA1003987
         C-HEMBA1004012
         C-HEMBA1004015
 45
         C-HEMBA1004193
         C-HEMBA1004225
         C-HEMBA1004241
         C-HEMBA1004267
         C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%//AF155103
 50
         C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%//P22516
         C-HEMBA1004356//H.sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494
         C-HEMBA1004396
         C-HEMBA1004405
 55
         C-HEMBA1004433
         C-HEMBA1004538
         C-HEMBA1004542
         C-HEMBA1004573
```

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C-HEMBA1004577
        C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844
        C-HEMBA1004617
        C-HEMBA1004631
        C-HEMBA1004705
5
        C-HEMBA1004733
        C-HEMBA1004748
        C-HEMBA1004778
        C-HEMBA1004803
10
        C-HEMBA1004807
        C-HEMBA1004820
        C-HEMBA1004865
        C-HEMBA1004880
        C-HEMBA1004900
        C-HEMBA1004909
15
        C-HEMBA1004960
        C-HEMBA1004978
        C-HEMBA1004980
        C-HEMBA1004983
        C-HEMBA1004995
20
        C-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2212bp//99%//AB014548
        C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947
        C-HEMBA1005035
        C-HEMBA1005039
        C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%//P35290
25
        C-HEMBA1005050
        C-HEMBA1005062
        C-HEMBA1005066
        C-HEMBA1005075
30
        C-HEMBA1005079
        C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%//
        AF080561
        C-HEMBA1005123
        C-HEMBA1005149
35
        C-HEMBA1005152
        C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941
        C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%//
        Q00004
        C-HEMBA1005223
         C-HEMBA1005232
40
         C-HEMBA1005241
         C-HEMBA1005275
         C-HEMBA1005293
         C-HEMBA1005311
         C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581
45
         C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743
         C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//
         AF071787
         C-HEMBA1005374
         C-HEMBA1005382
50
         C-HEMBA1005411
         C-HEMBA1005426
         C-HEMBA1005443
         C-HEMBA1005447
55
         C-HEMBA1005497
         C-HEMBA1005500
         C-HEMBA1005506
         C-HEMBA1005508
```

```
C-HEMBA1005526
        C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.//0//
        1578bp//98%//AF191340
        C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA,
        complete cds.//1.00E-220//1014bp//99%//AF134157
5
        C-HEMBA1005552
        C-HEMBA1005568
        C-HEMBA1005588
        C-HEMBA1005593
10
        C-HEMBA1005606
        C-HEMBA1005616
        C-HEMBA1005627
        C-HEMBA1005670
        C-HEMBA1005679
        C-HEMBA1005699
15
        C-HEMBA1005705
        C-HEMBA1005732//Human mRNA for KIAA1293 gene, complete cds.//5.50E-102//317bp//98%//D14697
        C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM ACTIVATED NEU-
        TRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%//P00789
        C-HEMBA1005852
20
         C-HEMBA1005894
         C-HEMBA1005921
         C-HEMBA1006035
         C-HEMBA1006036
25
         C-HEMBA1006090
         C-HEMBA1006138
         C-HEMBA1006173
         C-HEMBA1006252
         C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836
         C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-130//332aa//62%//002193
30
         C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160
         C-HEMBA1006380
         C-HEMBA1006416
         C-HEMBA1006421
         C-HEMBA1006424
35
         C-HEMBA1006426
         C-HEMBA1006446
         C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//
         97%//P55786
         C-HEMBA1006486
 40
         C-HEMBA1006494
         C-HEMBA1006546
         C-HEMBA1006562
         C-HEMBA1006595
 45
         C-HEMBA1006597
         C-HEMBA1006631
         C-HEMBA1006639
         C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148
         C-HEMBA1006659
         C-HEMBA1006665
 50
         C-HEMBA1006676
         C-HEMBA1006695
         C-HEMBA1006709
         C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//
         91%//AF152492
 55
          C-HEMBA1006780
         C-HEMBA1006807//Homo sapiens mRNA for SPOP.//5.70E-125//1109bp//75%//AJ000644
          C-HEMBA1006824
```

```
C-HEMBA1006865
        C-HEMBA1006921
        C-HEMBA1006949
        C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase.//1.90E-80//
5
        447bp//89%//X74570
        C-HEMBA1007051
        C-HEMBA1007052
        C-HEMBA1007066
        C-HEMBA1007073
        C-HEMBA1007078
10
        C-HEMBA1007085
        C-HEMBA1007113
        C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds.//1.70E-252//1118bp//
        92%//AF125042
15
        C-HEMBA1007129
        C-HEMBA1007147
        C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%//AF076929
        C-HEMBA1007178
        C-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//1212bp//98%//D86987
        C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%//
20
        C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//2.00E-58//650bp//70%//J00060
         C-HEMBA1007251
         C-HEMBA1007288
         C-HEMBA1007322
25
         C-HEMBA1007341
         C-HEMBB1000050
         C-HEMBB1000054
         C-HEMBB1000059
         C-HEMBB1000089
30
         C-HEMBB1000113
         C-HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLA-
         SE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177
         C-HEMBB1000173
35
         C-HEMBB1000175
         C-HEMBB1000272
         C-HEMBB1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P37888
         C-HEMBB1000318
         C-HEMBB1000336
40
         C-HEMBB1000341
         C-HEMBB1000343
         C-HEMBB1000354
         C-HEMBB1000374
         C-HEMBB1000434
         C-HEMBB1000441
45
         C-HEMBB1000491
         C-HEMBB1000493
         C-HEMBB1000510
         C-HEMBB1000652
50
         C-HEMBB1000672
         C-HEMBB1000684
         C-HEMBB1000709
         C-HEMBB1000726
         C-HEMBB1000770
         C-HEMBB1000827
         C-HEMBB1000831
         C-HEMBB1000883
         C-HEMBB1000888
```

```
C-HEMBB1000893
        C-HEMBB1000913
        C-HEMBB1000996
        C-HEMBB1001004
5
        C-HEMBB1001047
        C-HEMBB1001060
        C-HEMBB1001114
        C-HEMBB1001119
        C-HEMBB1001133
10
        C-HEMBB1001142
        C-HEMBB1001177
        C-HEMBB1001208
        C-HEMBB1001209
        C-HEMBB1001249
15
        C-HEMBB1001253
        C-HEMBB1001254
        C-HEMBB1001271
        C-HEMBB1001304
        C-HEMBB1001317
20
        C-HEMBB1001348
        C-HEMBB1001394
        C-HEMBB1001410
        C-HEMBB1001424
        C-HEMBB1001426
        C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738
25
        C-HEMBB1001436
        C-HEMBB10014437/Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete
        cds.//3.00E-130//553bp//86%//AF062740
        C-HEMBB1001449
30
         C-HEMBB1001458
         C-HEMBB1001521
         C-HEMBB1001531
         C-HEMBB1001535
         C-HEMBB1001536
35
         C-HEMBB1001564
         C-HEMBB1001565
         C-HEMBB1001585
         C-HEMBB1001588
         C-HEMBB1001603
         C-HEMBB1001618
         C-HEMBB1001635
         C-HEMBB1001653
         C-HEMBB1001668
         C-HEMBB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//0//2035bp//99%//AB014546
45
         C-HEMBB1001685
         C-HEMBB1001695
         C-HEMBB1001707
         C-HEMBB1001735
         C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3
         P110).//4.60E-15//391aa//25%//P55884
50
         C-HEMBB1001747
         C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330
         C-HEMBB1001753
         C-HEMBB1001756
55
         C-HEMBB1001760
         C-HEMBB1001785
         C-HEMBB1001797
         C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167
```

```
C-HEMBB1001816
        C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA complete cds.//0//
        1514bp//99%//AF056209
        C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLCGF42.1 (FRAGMENT).//6.90E-11//87aa//35%//
        P18720
5
        C-HEMBB1001850
        C-HEMBB1001863
        C-HEMBB1001868
        C-HEMBB1001874
10
        C-HEMBB1001880
        C-HEMBB1001899
        C-HEMBB1001906
        C-HEMBB1001910
        C-HEMBB1001911
15
        C-HEMBB1001921
        C-HEMBB1001922
        C-HEMBB1001930
        C-HEMBB1001944
        C-HEMBB1001945
20
        C-HEMBB1001947
        C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.--)
        (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304
        C-HEMBB1001952
        C-HEMBB1001957
        C-HEMBB1001962
25
        C-HEMBB1001983
        C-HEMBB1001990
        C-HEMBB1001996
        C-HEMBB1002002
30
        C-HEMBB1002005
        C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYPIVC1).//2.70E-49//139aa//55%//P29981
        C-HEMBB1002043
        C-HEMBB1002045
        C-HEMBB1002049
        C-HEMBB1002050
35
        C-HEMBB1002068
        C-HEMBB1002092
        C-HEMBB1002139
        C-HEMBB1002142
        C-HEMBB1002190
40
        C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//
        44%//Q05481
        C-HEMBB1002218
45
        C-HEMBB1002232
        C-HEMBB1002247
        C-HEMBB1002249
        C-HEMBB1002266//NEURONAL PROTEIN. J/2.10E-46//121aa//76%//P41737
        C-HEMBB1002327
50
        C-HEMBB1002329
        C-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//1.10E-274//1249bp//99%//
        AJ010841
        C-HEMBB1002358
        C-HEMBB1002371
55
        C-HEMBB1002387
        C-HEMBB1002409
        C-HEMBB1002425
        C-HEMBB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692
```

```
C-HEMBB1002453
       C-HEMBB1002458
       C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%//U43885
       C-HEMBB1002489
       C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365
5
       C-HEMBB1002520
       C-HEMBB1002522
       C-HEMBB1002545
       C-HEMBB1002579
10
       C-HEMBB1002582
        C-HEMBB1002596
        C-HEMBB1002603
        C-HEMBB1002610
        C-HEMBB1002613
        C-HEMBB1002617
15
        C-HEMBB1002623
        C-HEMBB1002635
        C-HEMBB1002677
        C-HEMBB1002683
        C-HEMBB1002699
20
        C-HEMBB1002702
        C-MAMMA1000009
        C-MAMMA1000043
        C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN
        GP37].//1.90E-07//249aa//27%//P03396
25
        C-MAMMA1000057
        C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE-
        TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%//Q09860
        C-MAMMA1000092
        C-MAMMA1000103
30
        C-MAMMA1000117
        C-MAMMA1000129
        C-MAMMA1000133
        C-MAMMA1000155
35
        C-MAMMA1000175
        C-MAMMA1000198
        C-MAMMA1000241
        C-MAMMA1000251
        C-MAMMA1000254
        C-MAMMA1000287
40
        C-MAMMA1000307
        C-MAMMA1000331
        C-MAMMA1000339
        C-MAMMA1000340
         C-MAMMA1000348
45
         C-MAMMA1000356
         C-MAMMA1000360
         C-MAMMA1000402
         C-MAMMA1000414
50
         C-MAMMA1000431
         C-MAMMA1000444
         C-MAMMA1000458
         C-MAMMA1000500
         C-MAMMA1000522
 55
         C-MAMMA1000576
         C-MAMMA1000583
         C-MAMMA1000594
         C-MAMMA1000605
```

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C-MAMMA1000616
        C-MAMMA1000643
        C-MAMMA1000684//Homo sapiens 7-60 mRNA, complete cds.//0//2402bp//99%//AF109134
        C-MAMMA1000696
        C-MAMMA1000707
        C-MAMMA1000714
        C-MAMMA1000720
        C-MAMMA1000744
        C-MAMMA1000761
10
        C-MAMMA1000776
        C-MAMMA1000798
        C-MAMMA1000839
        C-MAMMA1000851
        C-MAMMA1000863
15
        C-MAMMA1000867
        C-MAMMA1000876
        C-MAMMA1000880
        C-MAMMA1000883
        C-MAMMA1000921
20
        C-MAMMA1000931
        C-MAMMA1000941
        C-MAMMA1000957
        C-MAMMA1000962
        C-MAMMA1000975
25
        C-MAMMA1000987
        C-MAMMA1001003
        C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R)
        (LUTEINIZING HOROMINE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%//Q90674
        C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC
30
        2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//2.60E-107//190aa//95%//Q15746
        C-MAMMA1001082
        C-MAMMA1001162
        C-MAMMA1001186
        C-MAMMA1001191
35
        C-MAMMA1001206
        C-MAMMA1001220
        C-MAMMA1001243
        C-MAMMA1001249
        C-MAMMA1001256
40
        C-MAMMA1001268
        C-MAMMA1001271
        C-MAMMA1001274
        C-MAMMA1001292
        C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP)
45
        (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN)
        (P50-RHOGAP).//2.20E-98//283aa//63%//Q07960
        C-MAMMA1001324
        C-MAMMA1001341
        C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%//P02750
50
        C-MAMMA1001397
        C-MAMMA1001408
        C-MAMMA1001420
        C-MAMMA1001442
       C-MAMMA1001452
55
        C-MAMMA1001465
        C-MAMMA1001487
        C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-
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TRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384

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C-MAMMA1001547
       C-MAMMA1001551
       C-MAMMA1001575
        C-MAMMA1001590
5
        C-MAMMA1001600
        C-MAMMA1001606
       C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%//AJ007989
        C-MAMMA1001663
        C-MAMMA1001670
10
        C-MAMMA1001671
        C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756
        C-MAMMA1001711
        C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653
        C-MAMMA1001744
        C-MAMMA1001745
15
        C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete
        cds.//0//2332bp//99%//AF117708
        C-MAMMA1001783
        C-MAMMA1001788
        C-MAMMA1001806
20
        C-MAMMA1001812
        C-MAMMA1001815
        C-MAMMA1001817
        C-MAMMA1001818
        C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148
25
        C-MAMMA1001824
        C-MAMMA1001851
        C-MAMMA1001854
        C-MAMMA1001864
30
        C-MAMMA1001878
        C-MAMMA1001890
        C-MAMMA1001907
        C-MAMMA1001908
        C-MAMMA1001931
        C-MAMMA1001969
35
        C-MAMMA1002011
        C-MAMMA1002032
        C-MAMMA1002041
        C-MAMMA1002047
        C-MAMMA1002056
40
         C-MAMMA1002058
         C-MAMMA1002078
         C-MAMMA1002082
         C-MAMMA1002084
         C-MAMMA1002093
45
         C-MAMMA1002094
         C-MAMMA1002118
         C-MAMMA1002125
         C-MAMMA1002132
50
         C-MAMMA1002140
         C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds7/1.70E-252//1170bp//99%//
         AF099664
         C-MAMMA1002145
         C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE
         1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR
 55
         B) (NKEF-B).//5.20E-61//60aa//90%//P32119
         C-MAMMA1002230
         C-MAMMA1002250
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C-MAMMA1002282
        C-MAMMA1002293
        C-MAMMA1002298
        C-MAMMA1002299
        C-MAMMA1002308
5
        C-MAMMA1002310
        C-MAMMA1002311
        C-MAMMA1002322
        C-MAMMA1002339
        C-MAMMA1002352
10
        C-MAMMA1002359
        C-MAMMA1002360
        C-MAMMA1002392
        C-MAMMA1002411
15
        C-MAMMA1002413
        C-MAMMA1002417
        C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE
        SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2).//1.10E-24//96aa//68%//Q14108
        C-MAMMA1002434
20
        C-MAMMA1002446
        C-MAMMA1002454
        C-MAMMA1002461
        C-MAMMA1002475
        C-MAMMA1002556
25
        C-MAMMA1002566
        C-MAMMA1002612
        C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640
        C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q07866
        C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030
        C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3e-317//
30
        1942bp//85%//AF018261
        C-MAMMA1002727
        C-MAMMA1002748
        C-MAMMA1002758
35
        C-MAMMA1002780
        C-MAMMA1002820
        C-MAMMA1002833
        C-MAMMA1002843
        C-MAMMA1002895
        C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742
40
        C-MAMMA1003004
        C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0//
        1533bp//99%//AF077952
        C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110
45
        C-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//0//3376bp//99%//D31886
        C-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//0//3551bp//99%//AB014590
        C-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//0//3035bp//96%//AB014561
        C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775 C-NT2RM1000499
        C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aai/28%//
50
        Q99383
        C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//
        52%//Q05481
        C-NT2RM2001592//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3471bp//99%//AB028990
        C-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//0//1632bp//99%//AB014518
55
        C-NT2RM2001637
        C-NT2RM2001641
        C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%//Q07230
        C-NT2RM2001699
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- C-NT2RM2001706
- C-NT2RM2001718
- C-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2892bp//99%//AB007931
- C-NT2RM2001805
- 5 C-NT2RM4000086
  - C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%//P10962
  - C-NT2RM4000414
  - C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%//Q04652
  - C-NT2RM4000634
- 10 C-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//0//1412bp//100%//AB028992 C-NT2RM4000783
  - C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%//P02750 C-NT2RM4000971
  - C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//50%//Q05481
  - C-NT2RM4001092//ZINC FINGER PROTEIN GLO3.//3.10E-24//265aa//33%//P38682
  - C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//1.10E-48//218aa//43%//Q03532 C-NT2RM4001569
  - C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.// 8.10E-300//1395bp//98%//M37712
- 20 8.10E-300//1395bp C-NT2RM4001905

15

30

50

- C-NT2RM4001938//Homo sapiens mRNA for KIAA0898 protein, partial cds.//0//2234bp//99%//AB020705
- C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-TRNA LIGASE) (ASPRS).// 1.90E-31//80aa//52%//P36419
- 25 C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%// AF072758
  - C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0// 2550bp//99%//AF176085
  - C-NT2RM4002109//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2572bp//99%//AF071592
  - C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%//AF035940
  - C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%//AF030430 C-NT2RM4002390
  - C-NT2RM4002398
- 35 C-NT2RM4002420
  - C-NT2RM4002534
  - C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%//AF022962
  - C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).// 4.60E-78//921bp//69%//X85019
- 40 C-NT2RP1000358//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//0//1938bp// 88%//AL050019
  - C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-ZYME 1).//8.20E-83//345aa//47%//Q61068
- 45 C-NT2RP1000609//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2165bp//99%//AL050118
  - C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANSPORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721
  - C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//0// 1687bp//99%//AF145020
  - C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//98%//AF047020
  - C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%//AF064094 C-NT2RP1000916
- 55 C-NT2RP1000944
  - C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//2085bp//99%//
  - C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%//Q06218

C-NT2RP1001	11	13
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C-NT2RP1001173//Homo sapiens mRNA; cDNA DKFZp566D1146 (from clone DKFZp566D1146).//0//2333bp//99%//AL080222

C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%//

5 U79139

C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%//M34192

C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0// 2006bp//100%//AF081513

10 C-NT2RP1001311

C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%// AF126799

C-NT2RP2000001//Homo sapiens mRNA for KIAA1111 protein, partial cds.//0//3188bp//99%//AB029034 C-NT2RP2000027

15 C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%//002675

C-NT2RP2000198

C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa//34%//P41238

20 C-NT2RP2000551

C-NT2RP2000644

C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955

C-NT2RP2000678

C-NT2RP2000715

25 C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%// U80811

C-NT2RP2000970

C-NT2RP2001347

C-NT2RP2001460//TRICHOHYALIN.//1.00E-14//521aa//24%//P37709

C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLO-CASE OF OUTER MEMBRANE 40 KD SUBUNTD.//6.10E-12//184aa//31%//P24391
C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%//U97067
C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-NA, complete cds.//0//1287bp//99%//AF058718

35 C-NT2RP2001677

C-NT2RP2001678

C-NT2RP2001720

C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-

40 ZYME 1).//7.90E-52//220aa//44%//Q61068

C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%//P51523

C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009

C-NT2RP2001861

45 C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//014754

C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%//P55008

C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%//

50 C-NT2RP2001936

C-NT2RP2001943

C-NT2RP2001946

C-NT2RP2002032

C-NT2RP2002033

55 C-NT2RP2002041

C-NT2RP2002047

C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226// 1301bp//88%//U87306

C-NT2RP2002124//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1772bp//95%//AB029020 C-NT2RP2002172 C-NT2RP2002219 C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%//AF005418 C-NT2RP2002316 C-NT2RP2002373 C-NT2RP2002439 C-NT2RP2002475 C-NT2RP2002546 C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%// 10 C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%//U19181 C-NT2RP2002643 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%//AF041107 15 C-NT2RP2002736 C-NT2RP2002740 C-NT2RP2002741//Homo sapiens mRNA for Neurobiastoma, complete cds.//9.90E-54//964bp//64%//D89016 C-NT2RP2002752 C-NT2RP2002753 C-NT2RP2002857 20 C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-TEIN).//1.90E-11//132aa//38%//Q13829 C-NT2RP2003073 C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%//AJ132545 25 C-NT2RP2003206 C-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//0//2870bp//98%//X74794 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186// 1551bp//77%//AF023657 C-NT2RP2003237 C-NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%//AF176069 30 C-NT2RP2003280 C-NT2RP2003293 C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.50E-13//302aa//26%// C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-35 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-ZYME 1),//9.60E-78//346aa//43%//061068 C-NT2RP2003456 C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//0//1746bp// 40 95%//M12783 C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1764bp// 99%//AF125158 C-NT2RP2003559 C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).// 2.10E-59//270aa//46%//P19474 45 C-NT2RP2003581 C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//9.40E-243//1624bp// 82%//AJ006215 C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete 50 cds.//2.1e-313//978bp//99%//AF098786 C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//1.80E-72//350bp//100%// AJ132637 C-NT2RP2003727 C-NT2RP2003751 C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.50E-63//253aa//50%// Q09201 C-NT2RP2003825

C-NT2RP2003871

	C-NT2RP2003885
	C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1) (NIMA-RELATED PROTEIN KI-
	NASE 1).//6.10E-183//387aa//87%//P51954
	C-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//0//2866bp//98%//AB007916
5	C-NT2RP2003988
	C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//
	2.30F-53//141aa//78%//P20290
	C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLA-
	SE).//5.40E-30//319aa//31%//Q01513
10	C-NT2RP2004142
	C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%//Y12781
	C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//3.80E-52//397bp//82%//
	AF003998
	C-NT2RP2004207
45	C-NT2RP2004226
15	C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%//
	AB015982
	C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//
	9.90E-12//427aa//26%//P19246
20	C-NT2RP2004270//PROTEIN PTM1 PRECURSOR.//1:40E-16//334aa//24%//P32857
20	C-NT2RP2004321
	C-NT2RP2004339
	C-NT2RP2004347
	C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp//
25	99%//AB028069
20	C-NT2RP2004399
	C-NT2RP2004400
	C-NT2RP2004412
	C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.//0//2321bp//86%//AF155739
30	C-NT2RP2004490
	C-NT2RP2004523
	C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%//
	AF090190
	C-NT2RP2004580
35	C-NT2RP2004587//Homo sapiens mRNA for KIAA0888 protein, partial cds.//0//2886bp//100%//AB020695
	C-NT2RP2004594
	C-NT2RP2004681
	C-NT2RP2004709
	C-NT2RP2004710//Homo sapiens mRNA for KIAA1014 protein, partial cds.//0//2587bp//100%//AB023231
40	C-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//0//1774bp//99%//AB020691
	C-NT2RP2004767
	C-NT2RP2004775
	C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//1.00E-
	228//1666bp//75%//U56732
45	C-NT2RP2004962
	C-NT2RP2004982
	C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//
	1.80E-99//376aa//43%//P19474
	C-NT2RP2005018
50	C-NT2RP2005020
	C-NT2RP2005022
	C-NT2RP2005031
	C-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//0//4069bp//99%//AB014564 C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26) (2-5A-DEPENDENT RNAASE) (RNASE
**	L) (RIBONUCLEASE 4) (FRAGMENT).//0.000000022//139aa//35%//Q05921
55	L) (RIBONUCLEASE 4) (FRAGMENT).//0.0000000022/1139aa/133 /ai/(2032 1 C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//2769bp//98%//AJ007509
	C-NT2RP2005254

C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds.//0//1643bp//

- 99%//AF124735
- C-NT2RP2005336//TRICHOHYALIN.//5.40E-10//545aa//22%//P37709
- C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).//2.10E-124//636aa// 38%//P32660
- 5 C-NT2RP2005360
  - C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN.//5.30E-63//410aa//40%//P22059
  - C-NT2RP2005454
  - C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//1.20E-130//608bp//99%//AF070652
- 10 C-NT2RP2005476//Human p190-B (pl90-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032
  - C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.00000015//279aa//26%//P35418
  - C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742
  - C-NT2RP2005501
  - C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1).//5.50E-70//393aa//39%//P11171
- 15 C-NT2RP2005600//Homo sapiens mRNA for KIAA1020 protein, partial cds.//0//2554bp//99%//AB028943 C-NT2RP2005645
  - C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.//2.60E-10//175aa//27%// O92834
  - C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//3.00E-63//323aa//39%//Q62158
- 20 C-NT2RP2005741
  - C-NT2RP2005806
  - C-NT2RP2005815
  - C-NT2RP2005841
  - C-NT2RP2005882
- 25 C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-FERASE).//1.50E-67//388aa//44%//P25500
  - C-NT2RP2006103
  - C-NT2RP2006166
  - C-NT2RP2006258
- 30 C-NT2RP2006261
  - C-NT2RP2006321
  - C-NT2RP2006454
  - C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295// 1193bp//99%//AF113538
- 35 C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%//P32559 C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755
  - C-NT2RP3000418
  - C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//2.90E-1511319aa//26%//P37908
- 40 C-NT2RP3000487
  - C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X16667
  - C-NT2RP3000526
  - C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.70E-11//90aa//42%//Q13562
  - C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0//2232bp//82%//AB012265
- 45 C-NT2RP3000628
  - C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.40E-24// 155aa//37%//Q10149
  - C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.).//8.30E-108//331aa//50%//P27448
- 50 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E-46//73aa//98%//P39027
  - C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.00E-201//584aa//54%//Q05481
  - C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.90E-11//631aa//23%//
- 55 C-NT2RP3001245//Homo sapiens mRNA for KIAA0923 protein, complete cds.//0//2659bp//99%//AB023140 C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.70E-10//540aa// 23%//P32380
  - C-NT2RP3001356

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C-NT2RP3001383
        C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538
        C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//1.40E-76//
        388aa//32%//P46821
        C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0//1788bp//99%//AF113534
        C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.10E-
        240//902bp//99%//AF054177
        C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//6.90E-132//
        774bp//88%//AF008554
        C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14141
10
         C-NT2RP3001739
         C-NT2RP3001777
         C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.20E-14//242aa//24%//Q00808
         C-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//0//3747bp//99%//AB014575
15
         C-NT2RP3001944
         C-NT2RP3002033
        C-NT2RP3002054
         C-NT2RP3002063//Homo sapiens mRNA for KIAA1033 protein, partial cds.//0//2830bp//99%//AB028956
         C-NT2RP3002099
20
         C-NT2RP3002102
         C-NT2RP3002147
         C-NT2RP3002163
         C-NT2RP3002173
         C-NT2RP3002255
        C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYN-
25
         THETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE).//8.60E-49//243aa//43%//Q58767
         C-NT2RP3002343
         C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase
         (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396
         C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG)(P1-CDC21).//8.60E-
30
         79//416aa//34%//P33991
         C-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//0//3811bp//99%//AB014578
         C-NT2RP3002545//Homo sapiens mRNA; cDNA DKFZp586G0518 (from clone DKFZp586G0518).//0//2499bp//
         99%//AL050092
         C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//5.80E-40//161aa//
35
         C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60)
         (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19/173aa//28%//P11598
         C-NT2RP3002603
         C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//
40
         90aa//42%//P38660
         C-NT2RP3002659
         C-NT2RP3002660
         C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.//0//1596bp//98%//AF151903
45
         C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kifib), complete cds.//1.10E-93//1205bp//69%//D17577
```

C-NT2RP3002701 C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%//Q24371

C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-232//1282bp//85%//AF030430

50 C-NT2RP3002876

C-NT2RP3002877

C-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//0//2085bp//94%//AB018314 C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%//D89053 C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.90E-52//899bp//64%//AB029333

C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mR-55 NA, complete cds.//0//2656bp//99%//AF084555

C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%//Q02357

C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%//P23645

- C-NT2RP3003078
- C-NT2RP3003139
- C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%//AF07773 8
- 5 C-NT2RP3003150
  - C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//5.70E-09//169aa//
  - C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-210//1851bp//76%//AF110267
- 10 C-NT2RP3003210
  - C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-187//1750bp//75%//U20286
  - C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%//AB030656
  - C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//2366bp//99%//
- 15 AF098462 C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))/(RO(SS-A)).// 4.20E-86//366aa//48%//P19474
  - C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170//585aa//54%//064948
- 20 C-NT2RP3003311
  - C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45//782bp//65%//U90653
  - C-NT2RP3003427
  - C-NT2RP3003543
- 25 C-NT2RP3003552
  - C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30// 191aa//40%//P40529
  - C-NT2RP3003564
  - C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0//3131bp//94%//
- 30 AF106681
  - C-NT2RP3003621
  - C-NT2RP3003625
  - C-NT2RP3003656 C-NT2RP3003659/HES1 PROTEIN.//5.90E-22//229aa//27%//P35843
- 35 C-NT2RP3003686
  - C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446
  - C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%//P24014
  - C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%// U28164
- 40 C-NT2RP3003795

45

55

- C-NT2RP3003805
- C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%//Q07590
- C-NT2RP3003819
- C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%//P02720
- C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete cds.//2.2e-316//1436bp//99%//AB020523
- C-NT2RP3003833
- C-NT2RP3003842
- 50 C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%//
  AB019435
  - C-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//0//2557bp//99%//AB018343 C-NT2RP3003876
  - C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//2.20E-20//76aa//64%//Q09332
  - C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0//2191bp//99%//AF086628
  - C-NT2RP3003989

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C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1)
        (KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263
        C-NT2RP3004070
        C-NT2RP3004145
5
        C-NT2RP3004215
        C-NT2RP3004253
        C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61 %//AF007871
        C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//
10
        C-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0//1778bp//99%//AC003982
        C-NT2RP3004503
        C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//
        P51523
        C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferas e (GlcNAc6ST),
        complete cds.//0//2393bp//99%//AB014679
15
        C-NT2RP4000023
        C-NT2RP4000218
        C-NT2RP4000424
        C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.70E-141//511aa//43%//Q99676
        C-NT2RP4001447
20
        C-NT2RP4001841
        C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-85//489aa//43%//P55194
        C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-168//601aa//52%//067618
        C-NT2RP4002075
25
        C-NT2RP4002083
        C-OVARC1000001/Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//
        99%//AB029290
        C-OVARC1000008
        C-OVARC1000017
30
        C-OVARC1000058
        C-OVARC1000068
        C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//
        727bp//67%//AF156957
        C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761
35
        C-OVARC1000109
        C-OVARC1000114
        C-OVARC1000145
        C-OVARC1000240
        C-OVARC1000302
40
        C-OVARC1000408
        C-OVARC1000414
        C-OVARC1000440
        C-OVARC1000442
        C-OVARC1000496
45
        C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2)
        (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//015349
        C-OVARC1000557
        C-OVARC1000578
        C-OVARC1000622
50
        C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888
        C-OVARC1000681
        C-OVARC1000700
        C-OVARC1000724
        C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11//
55
        74aa//37%//P49596
        C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED
        PROTEIN) (GRP 75).//3.90E-46//78aa//98%//035501
        C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//1.30E-32//170aa//34%//P37440
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C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.0000054//135aa//28%//P03398
        C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aaaa//49%//P32943
        C-OVARC1000960
        C-OVARC1000971
        C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%//Q06527
5
        C-OVARC1001000
        C-OVARC1001029
        C-OVARC1001040
        C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN
        EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%//P42566
10
        C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//5.1e-310//1588bp//93%//
        AF051782
        C-OVARC1001118
        C-OVARC1001129
        C-OVARC1001169
15
        C-OVARC1001240
        C-OVARC1001261
        C-OVARC1001339
        C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%//P09058
        C-OVARC1001357
20
        C-OVARC1001442
        C-OVARC1001611
        C-OVARC1001813
        C-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//0//1760bp//99%//AF054174
25
        C-OVARC1002143
        C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-
        REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%//P31213
         C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-
         09//207aa//30%//Q91854
         C-PLACE1000014
30
         C-PLACE1000078
         C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//2041bp//87%//
         C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.70E-07//251aa//24%//P23645
         C-PLACE1000814
35
         C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-153//326aa//64%//P52742
         C-PLACE1001007
         C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds.//4.00E-300//
         1355bp//100%//AB024301
40
         C-PLACE1001088
         C-PLACE1001136
         C-PLACE1001241
         C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-228//827bp//99%//
         AF009615
45
         C-PLACE1001395
         C-PLACE1001740
         C-PLACE1001746
         C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//7.50E-16//
         319aa//26%//P37908
 50
         C-PLACE1002066
         C-PLACE1002115
         C-PLACE1002213
         C-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//0//1657bp//98%//AB018271
         C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp//99%//U69274
         C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0//2092bp//84%//U69262
 55
         C-PLACE1002499
         C-PLACE1002578
```

	C-PLACE1002772
	C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201
	C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50E-203//396aa//86%/
	P51522
5	C-PLACE1002993
•	C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete
	cds_//8.50E-44//225bp//100%//AF032387
	•
	C-PLACE1003205
	C-PLACE1003249 C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSORS.//1.70E-23//594aa//33%//P28481
10	
	C-PLACE1003553
	C-PLACE1003592
	C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-93//270aa//66%/
	P46975
15	C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793
	C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//6.20E-282/
	1316bp//98%//AF053305
	C-PLACE1003870
	C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS
20	FERASE).//3.70E-222//651aa//66%//P25500
	C-PLACE1003892
	C-PLACE1003900
	C-PLACE1004336
	C-PLACE1004384
25	C-PLACE1004425
	C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.90E-56//276aa//41%/
	P51522
	C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds.//2.10E
	16//402bp//62%//U90878
30	C-PLACE1004518
	C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.//3.50E-274//1305bp//97%//AF132954
	C-PLACE1004681
	C-PLACE1004693
	C-PLACE1004716//Homo sapiens HSPC038 protein mRNA, complete cds.//2.70E-103//586bp//91%//AF125099
35	C-PLACE1004815
	C-PLACE1004836
	C-PLACE1004838
	C-PLACE1004840
	C-PLACE1004900
40	C-PLACE1004985
	C-PLACE1005085
	C-PLACE1005086
	C-PLACE1005108
	C-PLACE1005146
45	C-PLACE1005409
	C-PLACE1005453
	C-PLACE1005477
	C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288
	C-PLACE1005595
50	
50	C-PLACE1005603 C-PLACE1005639
	C-PLACE1005639  C-PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//2.00E-118//378bp//98%
	AF162680
	C-PLACE1005799 C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482
55	
	C-PLACE1005884
	C-PLACE1005968

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C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%//AF151852
        C-PLACE1006017
        C-PLACE1006037
        C-PLACE1006076
5
        C-PLACE1006143
        C-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//1489bp//100%//AB014548
        C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMA-
        LEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//
        4.60E-117//147aa//80%//P21796
        C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%//U76374
10
        C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//
        1.30E-18//460aa//24%//Q00547
        C-PLACE1006371
        C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- AC-
        TIVATING ENZYME).//1.20E-83//313aa//49%//P27550
15
        C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0//
        2170bp//99%//AF191338
        C-PLACE1006521
        C-PLACE1006534//Homo sapiens mRNA; cDNA DKFZp564G1964 (from clone DKFZp564G1964).//1.70E-192//
20
        883bp//99%//AL110144
        C-PLACE1006617
        C-PLACE1006640
        C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//
        6.20E-63//191aa//43%//P13688
         C-PLACE1006760
25
         C-PLACE1006779
         C-PLACE1006805
         C-PLACE1006815
         C-PLACE1006867
30
         C-PLACE1007045
         C-PLACE1007097
         C-PLACE1007111
         C-PLACE1007112
         C-PLACE1007140//Homo sapiens mRNA for KIAA1009 protein, complete cds.//0//3492bp//99%//AB023226
35
         C-PLACE1007218
         C-PLACE1007454
         C-PLACE1007478
         C-PLACE1007677
         C-PLACE10077057/Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//
40
         82%//AB033922
         C-PLACE1007737
         C-PLACE1007743
         C-PLACE1007852//Homo sapiens mRNA for KIAA0878 protein, complete cds.//1.00E-232//1174bp//94%//
         AB020685
45
         C-PLACE1007877
         C-PLACE1008045
         C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179
         C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.).//3.00E-25//208aa//37%//Q03326
         C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077
50
         C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808
         C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PRO-
         TEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN- 10).//2.20E-23//94aa//47%//Q05315
         C-PLACE1008331
         C-PLACE1008369
55
         C-PLACE1008392
         C-PLACE1008405
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C-PLACE1008584
        C-PLACE1008625
        C-PLACE1008630
        C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN
        H2).//5.20E-90//483aa//38%//002668
5
        C-PLACE1008715
        C-PLACE1008748
        C-PLACE1008757
        C-PLACE1008798
10
        C-PLACE1008851
        C-PLACE1008947
        C-PLACE1009039
        C-PLACE1009048
        C-PLACE1009050
        C-PLACE10091137/Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//
15
        0//2529bp//99%//AF035586
        C-PLACE1009150
        C-PLACE1009200
        C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P29675
        C-PLACE1009298//Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds.//0//2262bp//99%//
20
        C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%//P14922
        C-PLACE1009398//ZINC FINGER PROTEIN 135.//6.20E-97//361aa//51%//P52742
        C-PLACE1009410
        C-PLACE1009477//Homo sapiens mRNA for KIAA0684 protein, partial cds.//6.50E-148//592bp//99%//AB014584
25
        C-PLACE1009493
        C-PLACE1009539
        C-PLACE1009595
        C-PLACE1009637
30
        C-PLACE1009639
        C-PLACE1009798//RLR1 PROTEIN.//1.60E-18//270aa//23%//P53552
        C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-).//6.50E-28//
        209aa//38%//P43510
        C-PLACE1009888
        C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds.//0//1730bp//99%//AF038963
35
        C-PLACE1009947
        C-PLACE1010069
        C-PLACE1010089//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1554bp//100%//AB029020
        C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).//
40
        5.10E-27//371aa//28%//Q14246
        C-PLACE1010270
        C-PLACE1010562
        C-PLACE1010579//Homo sapiens PTB domain adaptor protein CED-6 mRNA, complete cds.//9.30E-299//
        1362bp//99%//AF200715
45
        C-PLACE1010624
        C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and
        S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907
        C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-)
         (DUGT),//1.80E-222//808aa//52%//Q09332
        C-PLAC.E1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160
50
        C-PLACE1010761
        C-PLACE1010802 C-PLACE1010833//CALTRACTIN (CENTRIN).//0.0000001//154aa//28%//P41209
        C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-25//583aa//
        23%//P35580
55
        C-PLACE1010916
        C-PLACE1010947
        C-PLACE1010965
        C-PLACE1011032
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C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019
        C-PLACE1011056//HISTONE H1, GONADAL.//6.80E-13//154aa//37%//P02256
        C-PLACE1011090//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522).//0//880bp//
        99%//AL050159
        C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663
5
        C-PLACE1011214
        C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//
        701bp//99%//AF153604
        C-PLACE1011273
10
        C-PLACE1011291
         C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587
         C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN
         H2).//1.70E-78//383aa//39%//Q61703
         C-PLACE1011503
         C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (30ST3B1) mRNA,
15
         complete cds.//0//1559bp//99%//AF105377
         C-PLACE1011646//Homo sapiens clone 25059 mRNA sequence.//5.00E-223//1035bp//99%//AF131752
         C-PLACE1011650
         C-PLACE1011675
20
         C-PLACE1011725
         C-PLACE1011749
         C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE
         B) (NMMHC-B).//1.30E-15//409aa//27%//P35580
         C-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//0//1163bp//100%//AB018256
25
         C-PLACE2000006
         C-PLACE2000007//Homo sapiens mRNA for KIAA0913 protein, partial cds.//0//1968bp//97%//AB020720
         C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//
         212aa//35%//P10586
         C-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C), mRNA, complete cds.//4.60E-
         291//1167bp//89%//L08505
30
         C-PLACE2000061
         C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%//AF027219
         C-PLACE2000097
         C-PLACE2000103
35
         C-PLACE2000115
         C-PLACE2000124
         C-PLACE2000140
         C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%//O15736
         C-PLACE2000176
         C-PLACE2000223
         C-PLACE2000235
         C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%//P23098
         C-PLACE2000302
         C-PLACE2000347
45
         C-PLACE2000359
         C-PLACE2000371//TENSIN.//2.90E-78//561aa//37%//Q04205
         C-PLACE2000379
         C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PRO-
         TEIN) (12E7).//1.60E-14//180aa//39%//P14209
         C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE)
50
         (LEURS).//9.90E-229//821aa//54%//Q09996
         C-PLACE2000450
         C-PLACE2000455
         C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//1979bp//90%//Y17267
55
         C-PLACE3000070
         C-PLACE3000119
         C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC15.//1.90E-08//281 aa//22%//P22224
```

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C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1)
        mRNA, complete cds.//0//2043bp//99%//AF170084
        C-PLACE3000148
        C-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.10E-75//382bp//99%//
        AB014572
        C-PLACE3000160
        C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742
        C-PLACE3000194
        C-PLACE3000199
        C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0//
10
        1862bp//98%//AF105020
        C-PLACE3000230
        C-PLACE3000244/PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aay/92%/P53995
        C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0//4583bp//
15
        83%//AF143946
        C-PLACE3000276
        C-PLACE3000310
        C-PLACE3000320
        C-PLACE3000331
        C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
20
        DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23 %//P08640
         C-PLACE3000352
         C-PLACE3000353//Homo sapiens mRNA; cDNA DKFZp586H0623 (from clone DKFZp586H0623).//0//2456bp//
        99%//AL096739
25
         C-PLACE3000362
         C-PLACE3000365
         C-PLACE3000388
         C-PLACE3000413
         C-PLACE3000425
         C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE
30
         B) (NMMHC-B).//2.90E-54//626aa//29%//P35580
         C-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//
         P46100
         C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0//4661bp//
35
         99%//AF165281
         C-PLACE4000089
         C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aa//88%//
         AF091234
         C-PLACE4000129
40
         C-PLACE4000147
         C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746
         C-PLACE4000211//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds.//1.70E-262//1217bp//98%//
         AF000422
         C-PLACE4000222
         C-PLACE4000269//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3787bp//99%//AB028990
45
         C-PLACE4000270
         C-PLACE4000300
         C-PLACE4000387
         C-PLACE4000392
         C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5142bp//90%//Z70200
50
         C-PLACE4000450//Homo sapiens TTF-I interacting peptide 5 mRNA, partial cds.//2.70E-261//1217b.p//98%//
         AF000422
         C-PLACE4000465
         C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIV-
55
         ITY) (TRANSCRIPTION FACTOR NTF-1).//5.70E-60//254aa//44%//P13002
```

C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//6340bp//87%//Y17267

431aa//29%//O60100

C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//

EP 1 074 617 A2 C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%//AF034800 C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-TRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655 C-THYRO1000034//TRICHOHYALIN.//9.40E-10//176aa//30%//P37709 C-THYRO1000070 C-THYRO1000072//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799 C-THYRO1000092 C-THYRO1000121//Homo sapiens mRNA for KIAA1116 protein, complete cds.//0//2159bp//99%//AB029039 C-THYRO1000124 C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%//AJ005698 C-THYRO1000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//0//1409bp//98%//AB014552 C-THYRO1000206 C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%// P51523 C-THYRO1000253 C-THYRO1000270 C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068 C-THYRO1000320 C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//P17563 C-THYRO1000368 C-THYRO1000381 C-THYRO1000387 C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299// 1325bp//99%//AF072864 C-THYRO10003957/Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857 C-THYRO1000401 C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663 C-THYRO1000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).// 4.20E-98//408aa//42%//P19474 C-THYRO1000558 C-THYRO1000570 C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%// AF140360 C-THYRO1000625 C-THYRO1000637

35

5

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25

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50

C-THYRO1000676

C-THYRO1000684//Homo sapiens mRNA for KIAA0872 protein, complete cds.//0//2131bp//99%//AB020679

C-THYRO1000712

C-THYRO1000805 40

C-THYRO1000815

C-THYRO1000855

C-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).// 7.50E-57//315aa//43%//P32322

C-THYRO1000988 45

C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%//P31948 C-THYRO1001120//Mus musculus FX-induced thymoma transcript (FXI-T1) mRNA, complete cds.//1.90E-92// 1479bp//66%//U38252

C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTSZ) gene, exons 4, 5, and 6 and complete cds; and

TH1 gene partial sequence.//3.80E-100//478bp//99%//AF136276

C-THYRO1001262

C-THYRO1001271

C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%//P45701

C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%//AF121861 55 C-THYRO1001347

C-THYRO1001363//Homo sapiens mRNA; cDNA DKFZp56400423 (from clone DKFZp56400423).//0//2173bp// 99%//AL080120

C-THYRO1001374//Homo sapiens mRNA forKIAA0707 protein, partial cds.//0//1700bp//99%//AB014607 C-THYRO1001403 C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%//P30427 C-THYRO1001406//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//1676bp//98%// 5 AF078850 C-THYRO1001426 C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN. TYPE B) (NMMHC-B).//2.70E-171//559aa//59%//P35580 C-THYRO1001480 C-THYRO1001487 10 C-THYRO1001584 C-THYRO1001661 C-THYRO1001746 C-THYRO1001772 15 C-THYRO1001854 C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81 %// C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%//AF126484 C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0//1515bp//99%// 20 AF123534 C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0//2644bp//81%//AB030835 C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//0//2048bp//93%//X84692 C-Y79AA1000410 C-Y79AA1000539 C-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.00E-302//1375bp//99%// 25 AF091080 C-Y79AA1000802 C-Y79AA1000827 C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757 30 C-Y79AA1000969 C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4.70E-151//985bp//87%//U52962 C-Y79AA1001061 C-Y79AA1001068 C-Y79AA1001216 C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//996bp//99%//AJ011738 35 C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).// 2.50E-14//410aa//24%//Q00547 C-Y79AA1001692/Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.//1.40E-78// 40 227aa//40%//Q01820 C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%// C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTI-VATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133 45 C-Y79AA1002210/YTUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-TEIN).//0.0000018//140aa7/25%//Q13829 C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17// 146aa//35%//016264 C-Y79AA1002220 50 C-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//0//3168bp//99%//AB014592 C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384 C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%// C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879 55 C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//

C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725

86%//U49385

C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//

```
51%//Q05481
        C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-310//
        1444bp//98%//AF129534
5
        C-HEMBA1000290
        C-HEMBA1000459
        C-HEMBA1000505
        C-HEMBA1001196//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%//
        .104088
        C-HEMBA1002503
10
        C-HEMBA1002508
        C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//0//2432bp//99%//
        AJ011972
        C-HEMBA1003480
        C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.40E-110//242aa//
15
         C-HEMBA10036451/TTPD PROTEIN.//2.40E-10//289aa//23%//015736
         C-HEMBA1003646//Homo sapiens mRNA for KIAA1013 protein, partial cds.//0//3049bp//99%//AB023230
         C-HEMBA1003667
         C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-
20
         09//611aa//22%//P23253
         C-HEMBA1003827
         C-HEMBA1003838
         C-HEMBA1004055
         C-HEMBA1004056
25
         C-HEMBA1004086
         C-HEMBA1004335
         C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%//Q99471
         C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-
         TEIN).//3.10E-51//152aa//40%//Q61221
30
         C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%//AF201333
         C-HEMBA1004507
         C-HEMBA1004638
         C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%//P18583
         C-HEMBA1004709
35
         C-HEMBA1004860
         C-HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.//1.90E-11//376bp//63%//AJ250308
         C-HEMBA1005472
         C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%//002193
         C-HEMBA1005572
40
         C-HEMBA1005780
         C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%//
         C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%//Q61001
         C-HEMBA1006124
 45
         C-HEMBA1006461
         C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-
         ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%//P25716
         C-HEMBA1006617
         C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%//015509
 50
         C-HEMBA1006779
         C-HEMBA1006796
          C-HEMBA1006812
         C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%//
 55
          C-HEMBA1007174//Homo sapiens mRNA for KIAA1065 protein, complete cds.//0//1079bp//97%//AB028988
          C-HEMBB1000240
          C-HEMBB1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%//P22516
```

```
C-HEMBB1000335
        C-HEMBB1000337
        C-HEMBB1000554
        C-HEMBB1000573
5
        C-HEMBB1000749
        C-HEMBB1000774
        C-HEMBB1000835
        C-HEMBB1001197
        C-HEMBB1001315
10
        C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//
        27%//Q05481
        C-HEMBB1001500
        C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092
        C-HEMBB1001619
15
        C-HEMBB1001630
        C-HEMBB1001665
        C-HEMBB1001684//Homo sapiens mRNA for KIAA1108 protein, partial cds.//0//2348bp//99%//AB029031
        C-HEMBB1001812
        C-HEMBB1001834
20
        C-HEMBB1001869
        C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN | PRECURSOR (BIGLYCAN) (PG-S 1).//5.40E-75//
        241aa//48%//P47853
        C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR)
        (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549
25
        C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%//P37709
        C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//
        874bp//86%//U47742
        C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-
        OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME
30
        64E).//6.90E-132//561aa//50%//Q24574
        C-HEMBB1001925
        C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%//Y08715
        C-HEMB81002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163
        C-HEMBB1002152
35
        C-HEMBB1002300
        C-HEMBB1002381
        C-HEMBB1002383
        C-HEMBB1002534
        C-MAMMA1000143
40
        C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//
        P51523
        C-MAMMA1000227
        C-MAMMA1000257
        C-MAMMA1000264
45
        C-MAMMA1000270
        C-MAMMA1000279
        C-MAMMA1000372
        C-MAMMA1000559
        C-MAMMA1000752
50
        C-MAMMA1000760
        C-MAMMA1000778
        C-MAMMA1000855
        C-MAMMA1000859
        C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN
55
        H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-141//576aa//37%//Q06033
        C-MAMMA1000940
        C-MAMMA1001073
```

C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6e-312//1596bp//94%//

```
AF067420
       C-MAMMA10011987/Homo sapiens eps15RmRNA, partial cds.//0//2253bp//99%//AB015346
        C-MAMMA1001202
        C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%//P12978
5
        C-MAMMA1001252
        C-MAMMA1001296
        C-MAMMA1001502
        C-MAMMA1001630
        C-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.30E-39//160aa//55%//P49910
10
        C-MAMMA1001683
        C-MAMMA1001715
        C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, par-
        tial cds.//0//1603bp//99%//AF095687
        C-MAMMA1001760
        C-MAMMA1001769
15
        C-MAMMA1001785
        C-MAMMA1001848
        C-MAMMA1001874
        C-MAMMA1001956
20
        C-MAMMA1002009
        C-MAMMA1002033
        C-MAMMA1002155
        C-MAMMA1002498
        C-MAMMA1002545
25
        C-MAMMA1002571
        C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3:2.1.3)(GLUCAN 1,4-ALPHA- GLUCOSI-
        DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640
        C-MAMMA1002590
        C-MAMMA1002617//ZINC FINGER PROTEIN 135.//7.60E-89//252aa//57%//P52742
        C-MAMMA1002618
30
        C-MAMMA1002636
        C-MAMMA1002646
        C-MAMMA1002665
        C-MAMMA1002708
        C-MAMMA1002728
35
         C-MAMMA1002744
        C-MAMMA1002764
         C-MAMMA1002765
         C-MAMMA1002830
         C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECUR-
40
         SOR (CTPT).//4.90E-10//334aa//22%//P52178
         C-MAMMA100285 8//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590
         C-MAMMA1002880
         C-MAMMA1002892
45
         C-MAMMA1002909
         C-MAMMA1002941
         C-MAMMA1002947
         C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//
         P40343
         C-MAMMA1002973
50
         C-MAMMA1002987
         C-MAMMA1003003
         C-MAMMA1003026//Homo sapiens HSPC057 mRNA, complete cds.//0//1773bp//98%//AF161542
         C-MAMMA1003031
         C-MAMMA1003089
 55
         C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).//
         1.00E-07//362aa//23%//P39843
```

C-NT2RM1000272

	C-NT2RM1000341
	C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein.//3.00E-158//733bp//99%//AJ238097
	C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//3.40E-177//814bp//
	99%//AF103731
5	C-NT2RM1000623//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
·	C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1).//5.60E-08//187aa//
	27%//P49695
	C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%//AF084458
	C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%//
10	AF082516
	C-NT2RM1001082
	C-NT2RM1001112
	C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.20E-28//805bp//61%//
	AF053091
15	C-NT2RM2001360//Homo sapiens clone C40 unknown mRNA.//1.00E-250//1136bp//100%//AF103798
13	C-NT2RM2001797//Homo sapiens mRNA; cDNA DKFZp572C163 (from clone DKFZp572C163); partial cds.//0//
	2300bp//100%//AL110217
	C-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//
	2249bp//99%//AF044195
20	C-NT2RM4002504
	C-NT2RP1000409
	C-NT2RP1000460//Homo sapiens mRNA for KIAA1068 protein, partial cds.//0//3199bp//99%//AB028991
	C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//9.70E-196//901bp//
	99%//AF173378
25	C-NT2RP1000796
	C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%//
	P51522
	C-NT2RP2001214
	C-NT2RP2001214  C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//
30	45%//Q05481 C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds.//0//3712bp//99%//AB024334
	C-NT2RP2002056
	C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0//1644bp//98%//
	X65634
35	C-NT2RP2002333
	C-NT2RP2002677
	C-NT2RP2002755
	C-NT2RP2002843
	C-NT2RP2003101
40	C-NT2RP2003668
	C-NT2RP2003799
	C-NT2RP2004095
	C-NT2RP2004300
	C-NT2RP2004675
45	C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETERO-
40	CHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN).//4.20E-09//804aa//
	22%//Q61687
	C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.10E-308//1437bp//98%//
	AF045583
50	C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%//Q14444
	C-NT2RP2005726
	C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYL-

C-NT2RP2005980

C-NT2RP2006184//Homo sapiens mRNA for KIAA0918 protein, partial cds.//0//4235bp//99%//AB020725

C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%//Q13131

C-NT2RP2006554

TRANSFERASE).//4.40E-55//358aa//42%//P51005

C-NT2RP3000584

C-NT2RP3001115

C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58// 1138bp//63%//AF193613

5 C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E- 22//227aa//33%//P08458

C-NT2RP3002330//Homo sapiens eRFS mRNA, complete cds.//0//2443bp//99%//U87791

C-NT2RP3002402

C-NT2RP3002484//Homo sapiens mRNA for KIAA0998 protein, partial cds.//1.20E-124//597bp//98%//AB023215 C-NT2RP3002512

10 C-NT2RP3002713

C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.00E-07//70aa//41%//P17564

C-NT2RP3002799

C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%//Q31125

15 C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%// P51026

C-NT2RP3002955

C-NT2RP3002985

C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//

20 82%//U78090

C-NT2RP3003121

C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc fmger protein, complete cds.//0//1998bp//91%//AB011414

C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%//

25 AF071592

C-NT2RP3003155

C-NT2RP3003157

C-NT2RP3003185//TROPOMYOSIN 1, FUSION PROTEIN 33.//2.80E-06//402aa//23%//P49455

C-NT2RP3003264

30 C-NT2RP3003346

C-NT2RP3003403

C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//743bp//90%//AF071317

C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%//P53009

35 C-NT2RP3003572

C-NT2RP3003576

C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%//AB013885 C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//2.20E-13//146aa//42%//P14209

40 C-NT2RP3003680//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154); complete cds.//0// 2047bp//95%//AL080155

C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds.//9.00E-238//1529bp//84%//U71294 C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//924bp//89%//AF130457

45 C-NT2RP3003828

C-NT2RP3003932

C-NT2RP3003992//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564Cl 86).//0//2739bp//99%//AL050019

C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%//X84692

50 C-NT2RP3004028

C-NT2RP3004041

C-NT2RP3004051

C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0//1806bp//99%//X76091

C-NT2RP3004093

55 C-NT2RP3004095

C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-229//1560bp//78%//AF126747

C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-

```
DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640
        C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948
        C-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1J/1.30E-14//242aa//24%//Q00808
        C-NT2RP3004332
5
        C-NT2RP3004349
        C-NT2RP3004470
        C-NT2RP4000035
        C-NT2RP4000049
        C-NT2RP4000102
10
        C-NT2RP4000167
        C-NT2RP4000515
        C-NT2RP4000517
        C-NT2RP4000519
        C-NT2RP5003512//Homo sapiens mRNA for KIAA1291 protein, partial cds.//0//1980bp//99%//AB033117
15
        C-OVARC1000092
        C-OVARC1000533
        C-OVARC1000678
        C-OVARC1000689//Homo sapiens mRNA; cDNA DKFZp434C1415 (from clone DKFZp434C1415); partial cds.//
        0//2032bp//99%//AL133014
20
        C-OVARC1000802
        C-OVARC1000890
        C-OVARC1000891
         C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp//
        82%//AB005549
25
         C-OVARC1001072
         C-OVARC1001117
        C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192
         C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%//
        X62083
         C-OVARC1001329
30
         C-OVARC1001341
         C-OVARC1001376
         C-OVARC1001496//Horno sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//
35
         C-OVARC1001873
         C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15)
         (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-
         ZYME).//1.60E-81//212aa//70%//P34547
         C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-
40
         241//1124bp//98%//AF135421
         C-PLACE1001036//Homo sapiens mRNA for KIAA1017 protein, complete cds.//0//2117bp//99%//AB023234
         C-PLACE1001076
         C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%//P52742
         C-PLACE1001366
45
         C-PLACE1001545
         C-PLACE1001608
         C-PLACE1002004
         C-PLACE1002256
         C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233
         C-PLACE1002591//CORONIN-LIKE PROTEIN P57.//4.40E-70//208aa//66%//P31146
50
         C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%//
         AF079765
         C-PLACE1003383
         C-PLACE1003864
         C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN.//5.20E-47//577aa//25%//P10267
55
         C-PLACE1004913
         C-PLACE1004979
```

C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6e-313//1413bp//99%//AF132950

```
C-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2431bp//99%//AB011148
        C-PLACE1005128
        C-PLACE1005162
        C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//
5
        96%//AF113539
        C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4* (PBP 4*) (PBP 4A).//1.10E-09//93aa//31%//P32959
        C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//
        7.60E-97//1287bp//67%//AJ010046
        C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).//
10
        6.80E-09//267aa//30%//P29128
        C-PLACE1005611//Mus musculus mRNA for mDjIO, complete cds.//2.00E-33//379bp//66%//AB028860
        C-PLACE1005802
        C-PLACE1005850
        C-PLACE1005898
        C-PLACE1005932
15
        C-PLACE1006129//Homo sapiens HSPC057 mRNA, complete cds.//0//2849bp//98%//AF161542
        C-PLACE1006360
        C-PLACE1006795
        C-PLACE1006878//TRNA-SPUCING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-
        NUCLEASE).//1.90E-08//122aa//36%//P16658
20
        C-PLACE1007557
        C-PLACE1007807
         C-PLACE1008181
         C-PLACE1008426//Homo sapiens mRNA for KIAA1288 protein, partial cds.//0//3311bp//99%//AB033114
25
         C-PLACE1008455
         C-PLACE1008941
         C-PLACE1009935
         C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.20E-18//467aa//30%//P46804
         C-PLACE10118967/Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%//U61969
30
         C-PLACE2000003
         C-PLACE2000132
         C-PLACE2000170
         C-PLACE2000335
35
         C-PLACE3000124
         C-PLACE3000158
         C-PLACE3000207
         C-PLACE3000221
         C-PLACE3000271
40
         C-PLACE3000304
         C-PLACE3000322
         C-PLACE3000341
         C-PLACE3000373
         C-PLACE3000399
45
         C-PLACE3000401
         C-PLACE3000402
         C-PLACE3000406
         C-PLACE3000475
         C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
         DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640
         C-PLACE4000093
         C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%//
         AF146689
         C-PLACE4000131//Homo sapiens mRNA; cDNA DKFZp586J0917 (from clone DKFZp586J0917); partial cds.//0//
         1612bp//97%//AL117455
55
         C-PLACE4000247
         C-PLACE4000250
         C-PLACE4000252
```

C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5143bp//90%//Z70200

C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201 C-PLACE4000320 C-PLACE4000344 5 C-PLACE4000367 C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- AC-TIVATING ENZYME).//7.20E-22//54aa//62%//Q01576 C-PLACE4000411//Homo sapiens mRNA; cDNA DKFZp586D0624 (from clone DKFZp586D0624); partial cds.// 0//2159bp//98%//AL117654 10 C-PLACE4000487 C-PLACE4000494 C-PLACE4000521 C-PLACE4000548//Homo sapiens mRNA for KIAA0947 protein, partial cds.//0//4864bp//99%//AB023164 C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//2384bp//99%//AF047690 15 C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%// AB021663 C-THYRO1000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//0//3711bp//99%//AB018333 C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%// 20 AF118566 C-THYRO1001142 C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa// 62%//005481 C-THYRO1001320 C-THYRO1001537//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522); partial cds.// 25 0//1010bp//98%//AL050159 C-THYRO1001602 C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%//Q04652 C-THYRO1001828 C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%// 30 AF157833 C-Y79AA1001167 C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0// 4708bp//99%//AF055084 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149 35 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415 C-HEMBA1006092 C-HEMBA1006406 C-HEMBB1000790 40 C-HEMBB1000917 C-HEMBB1002280 C-MAMMA1000802 C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%// P20931 45 C-MAMMA1002597 C-MAMMA1002868 C-NT2RP2003161 C-NT2RP2003339 C-NT2RP3001282 50 C-PLACE1001761 C-PLACE1004491 C-PLACE1004686 C-PLACE1005574 C-PLACE1006382 C-PLACE1006792 C-PLACE3000455 C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0//2567bp//88%//AF030430 C-THYRO1000916

- C-HEMBA1000327
- C-HEMBB1000637
- C-HEMBB1001967
- C-MAMMA1000266
- 5 C-NT2RP2002979
  - C-PLACE1007866
  - C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE PAK-GAMMA (EC 2.7.1.-) (GAMMA-PAK)
  - (P21-ACTIVATED KINASE 2) (PAK-2) (PAK65) (S6/H4 KINASE).//9.80E-25//155aa//45%//Q13177
  - C-PLACE4000156//ZINC FINGER PROTEIN 132.//7.10E-151//476aa//46%//P52740
- 10 C-THYRO1001637
  - C-MAMMA1002215
  - C-MAMMA1002721
  - C-NT2RP2002070
- 15 Homology search result 14.

30

- [0334] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, as and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared.
- 20 Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.
  - C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.90E-250//554aa//85%//061712
  - C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)
- 25 (LEURS).//6.40E-99//457aa//45%//Q09996
  - C-HEMBA1000020//Homo sapiens beta 2 gene.//7.50E-264//1194bp//95%//X02344
  - C-HEMBA1000030//Homo sapiens ARF GTPase-activating protein GITI mRNA, complete cds.//0//1759bp//99%//AF124490
  - C-HEMBA1000129//HYPOTHETICAL HEUCASE C8A4.08C IN CHROMOSOME I.//3.80E-25//166aa//36%//Q09884
  - C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0/1135bp//100%//
  - C-HEMBA1000150//Homo sapiens putative RNA helicase mRNA, complete cds.//5.20E-213//525bp//99%//
- 35 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).// 1.90E-12//368aa//24%//P08553
  - C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5.00E-16//166aa//36%//P35584
  - C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE D.//2.90E-14//303aa//25%//P35662
  - C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.40E-12//125aa//31 %//P48555
- C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%//AJ011738 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1.00E-86//146aa//56%//Q61221
  - C-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.10E-254//1440bp//87%// AF030131
- 45 C-HEMBA1000304//Rattus norvegicus Ca2<sup>+</sup>-dependent activator protein (CAPS) mRNA, complete cds.//5.10E-131//712bp//91%//U16802
  - C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.20E-49//107aa//91%//035594
  - C-HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%//
    - C-HEMBA1000369//Homo sapiens mRNA for PICK1, complete cds.//0//1949bp//98%//AB026491
    - C-HEMBA1000411//ANKYRIN.//5.70E-12//127aa//38%//Q02357
    - C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.30E-45//481aa//29%//Q04652
    - C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2.00E-22//188aa//31%//P22279
- 55 C-HEMBA1000518//PECANEX PROTEIN.//2.10E-19//227aa//38%//P18490
  - C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.40E-44//292aa//36%//Q01755
  - C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAG-MENTS).//2.60E-12//73aa//41%//P02826

- C-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//2.20E-194//663bp//83%// D89340
- C-HEMBA1000555//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//7.90E-226// 1501bp//83%//AF156529
- 5 C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa// 25 %//Q05481
  - C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aabp//32%//Q60865
  - C-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.10E-144//602bp//77%//AF045573
- C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%//P23246
  C-HEMBA1000592//Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds.//0//1465bp//99%//AF121856
  C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.80E-55//179aa//61%//O43295
  C-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.20E-156//1366bp//76%//U35776
- C-HEMBA1000851//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0//1862bp//99%// AF173868
  - C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1.00E-78//119aa//87%//P51689 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN)// 1.60E-30//127aa//40%//P43366
- 20 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHRO-MOSOME X.//1.00E-10//288aa//23%//Q19124
  - C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%//P06493
  - C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID)(FRAGMENT).//
- 25 1.40E-12//131aa//38%//Q01485 C-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.//4.80E-169//786bp//
  - 99%//U06088
  - C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//1.50E-92//82aa//100%//P02461
    C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//
- 30 432bp//94%//AF119043

- C-HEMBA1001088//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//3.50E-50// 176aa//57%//P48059
- C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065)(HA0946) (FRAGMENT).//1.50E-116//197aa//58%//Q06730
- C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.80E-79//179aa//80%//P51646
  C-HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.//0//1511bp//99%//AF112221
  C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733
  C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%//Q60401
- 40 C-HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.//9.60E-258//682bp// 94%//AF153686
  - C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.40E-133//614bp//99%//AF057358
  - C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.90E-64//104aa//82%//P17081
- 45 C-HEMBA1001405//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//5.60E-25//863bp//60%// AF053091
  - C-HEMBA1001446//Homo sapiens rap2 interacting protein x mRNA, complete cds.//9.20E-55//719bp//68%// AF112221
  - C-HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.//4.20E-290//2008bp//81%//AF205599
  - C-HEMBA1001476//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%// J04088
  - C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.70E-16//63aa//61%//P18850
- 55 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.90E-37//399aa//29%//P29166 C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.30E-53//110aa//100%//P19065
  - C-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//808bp//97%//AJ012449

- C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.90E-156//348aa//83%//Q14141
- C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%// P42803
- C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.60E-10//155aa//28%// Q63679
  - C-HEMBA1001651//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 1 (CYTADHERENCE ACCESSORY PROTEIN 1).//6.20E-07//362aa//24%//Q50365
  - C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.60E-36//365aai/33%//P33450
- 10 C-HEMBA1001672//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//1707bp//98%//AF072247
  - C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//5.40E-09//101aa//35%//P54787
  - C-HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.//3.70E-78//200bp//100%//AB029042
    - C-HEMBA1001723//Homo sapiens G protein beta subunit mRNA, partial cds.//3.10E-267//1212bp//99%// AF195883
    - C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OBCADHERIN) (OSF-4).// 1.10E-38//87aa//96%//P55288
- 20 C-HEMBA1001744//SCY1 PROTEIN.//9.90E-32//481aa//25%//P53009
  - C-HEMBA1001746//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//7.60E-59//998bp//64%//AF098066
  - C-HEMBA1001804//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0// 1637bp//99%//AF125158
- 25 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.80E-11//206aa//36%//P11675
  C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.90E-135//459aa//52%//Q99676
  C-HEMBA1001822//Mus musculus Ese2L protein mRNA, complete cds.//1.90E-235//1329bp//89%//AF132479
  C-HEMBA1001824//Homo sapiens nuclear protein NP94 mRNA, complete cds.//1.40E-199//1180bp//89%//AF159025
- 30 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.60E-64//221aa//55%//Q07230 C-HEMBA1001866//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//5.70E-51//234aa//41%//Q09332 C-HEMBA1001869//TRITHORAX PROTEIN.//9.60E-05//166aa//27%//P20659
  - C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//
- 35 9.30E-36//395aa//26%//Q63342

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- C-HEMBA1001913//GCN20 PROTEIN.//2.30E-81//158aa//50%//P43535
  - C-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//0// 1850bp//99%//AF000145
  - C-HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.//0//1721bp//99%//AF155114
- 40 C-HEMBA1002035//Homo sapiens BAZ1A mRNA for bromodomain adjacent to zinc finger domain 1A, complete cds.//0//2149bp//99%//AB032252
  - C-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.30E-271//1583bp//88%//U92703
  - C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%//Q02357
- C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%//Q14847 C-HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.//1.10E-153//1059bp//82%//AF178669 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.40E-51//180aa//56%//
  - P79293
    C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6.00E-13//190aa//36%//
    P43694
  - C-HEMBA1002212//TYROSINE-PROTEIN KINASE-2 (EC 2.7.1.112) (FRAGMENT).//3.00E-17//267aa//29%//P18161
  - C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.20E-199//392aa//89%//P47226 C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED
- 55 NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%//P46087
  C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.10E-46//302bp//90%//AF125537
  - C-HEMBA1002341//P53-BINDING PROTEIN 2 (53BP2) (FRAGMENT).//3.80E-55//109aa//96%//Q62415
  - C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//

- 1847bp//99%//AF092563
- C-HEMBA1002417/mGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//1.00E-121//489aa// 52%//P39447
- C-HEMBA1002419//TRICHOHYALIN.//1.90E-09//299aa//24%//P22793
- 5 C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.20E-24//109aa//55%//Q00994 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.50E-50//199aa//61%//P98175 C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.10E-12//285aa//
  - 31%//P17437

- C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.80E-53//257aa//36%//P48732
- C-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//0//2432bp//99%//
  AJ011972
  - C-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//0//1605bp//97%//AF016903
  - C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//68%//AF055993
- 15 C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//6.80E-305//951bp//99%// AF075587
  - C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7).//5.00E-37//268aa//34%//P06746
  - C-HEMBA1002768//Mus musculus formin binding protein 17 mRNA, partial cds.//7.80E-237//1522bp//85%//AB011126
- 20 C-HEMBA1002770//Rattus norvegicus mRNA for TIP120, complete cds.//2.90E-176//1024bp//88%//D87671 C-HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, complete cds.//3.40E-54//319bp//76%//AF153879 C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2e-314//1437bp//99%//AF071185
  - C-HEMBA1002818//Homo sapiens mRNA for fibulin-4.//2.00E-304//1383bp//99%//AJ132819
- 25 C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME n.//1.50E-44//188aa// 52%//Q09297
  - C-HEMBA1002935//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.30E-15//371aa// 25%//Q05481
  - C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2.00E-34//300aa// 34%//P16157
  - C-HEMBA1002951//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//4.40E-06//324aa// 24%//P32380
  - C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).// 1.20E-27//63aa//100%//P14646
- C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.80E-25//534aa//24%//Q02224
  C-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//1.40E-171//1552bp//75%//U20286
  - C-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA,//0//1558bp//99%// AF054182
- 40 C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR (ALS).//1.30E-09//121aa//40%//P35858
  - C-HEMBA1003077//SLIT PROTEIN PRECURSOR.//2.60E-15//199aa//31%//P24014
  - C-HEMBA1003096//Mouse 19.5 mRNA, complete cds.//5.60E-117//1139bp//72%//M32486
  - C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%//AF155096
- 45 C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.50E-51//221aa//33%//P41940
  - C-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//0//1583bp//99%//AJ005670
  - C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANS-
- 50 FERASE (EC 2.1.1.61), J/5.90E-74//134aa//53%//P44551
  - C-HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//8.50E-87// 285bp//90%//AF129534
  - C-HEMBA1003235//TROPOMYOSIN.//2.30E-06//109aa//33%//Q02088
  - C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.20E-41//245aa//42%//Q06548
- 55 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6.00E-11//239aa//32%//P32506
  - C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.40E-229// 1043bp//99%//AB024436
  - C-HEMBA1003291//SNF1-RELATED PROTEIN KINASE KIN10 (EC 2.7.1.-) (AKIN10)7/6.20E-28//126aa//51%//

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- C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.00E-08//248aa//23%//Q02224
- C-HEMBA1003408//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (VERSION 1).// 7.80E-13//297aa//30%//P18616
- 5 C-HEMBA1003417//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds.//1.50E-255//1179bp//99%//AF095192
  - C-HEMBA1003418//TRICHOHYALIN.//8.70E-19//281aa//31%//P37709
  - C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%//AB013139
  - C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41).//2.40E-110//242aa// 58%//P00736
    - C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (TSLET-2).//8.80E-189//360aa//96%//P50480 C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.10E-68//251aa//52%//P53384
    - C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-I).//1.20E-31//71aa//100%//P16874
- 15 C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A))(RO(SS-A)).//
  7.90E-49//279aa//32%//P19474
  - C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.90E-206//445aa//74%//Q13330
  - C-HEMBA1003581//TALIN.//4.40E-45//52aa//98%//P26039
  - C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.40E-10// 118aa//35%//P19682
  - C-HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.//0//1713bp//99%//AB026125
  - C-HEMBA1003617//Homo sapiens ubiquitin-like product Chap1/Dsk2 mRNA, complete cds.//6.90E-178//501bp//97%//AB015344
  - C-HEMBA1003645//TIPD PROTEIN.//2.40E-10//289aa//23%//O15736
- 25 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.20E-75//151aa//99%//Q13207
  - C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-09//611aa//22%//P23253
  - C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//423aa//47%//P34629
- 30 C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//2.00E-73//526aa//32%//Q13105
  - C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.10E-59//249aa//47%//P53973
  - C-HEMBA1003742//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.// 1.70E-44//501bp//67%//AF037339
  - C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN)
  - (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%//Q16665 C-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//5.80E-
  - 81//511bp//86%//U17343 C-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.10E-190// 1204bp//84%//AF084259
- 40 C-HEMBA1003805//Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds.//0//988bp// 95%//AF090402
  - C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).//8.10E-31//134aa//52%//P40484
  - C-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//1.20E-105//1192bp//70%//AF030430 C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.80E-16//
- 45 89aa//46%//P16372
  - C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//8.50E-221//1188bp//78%//AF091234
  - C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT).//1.60E-166//416aa//72%//Q14141
  - C-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//3.90E-208//951 bp//99%//AF067855
- 50 C-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//8.40E-60//243aa//39%// P34529
  - C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13.//6.20E-30//208aa//37%//P51153
  - C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2.//1.50E-12//258aa//29%//P40991
  - C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%//U50748
- 55 C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//5.70E-217//1217bp//88%//
  AF095927
  - C-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN CL-6).//2.00E-43//98aa//84%//Q08755

- C-HEMBA1004275//Homo sapiens PHD-finger protein (GRC5) mRNA, complete cds.//1.10E-152//1403bp//69%// AF043725
- C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds.//4.80E-257//738bp//99%//AF092094
- 5 C-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//0//1982bp// 99%//AF022795
  - C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%//AF155103 C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.30E-93//357aa//42%//Q99676
  - C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%//Q99471
- 10 C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%//P22516

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- C-HEMBA1004356//H.sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%//X77494
- C-HEMBA1004389//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0// 1437bp//99%//AF125158
- C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CY-CLOPHILIN-10).//3.20E-32//148aa//52%//P52017
- 15 CLOPHILIN-10).//3.20E-32//148aa//52%//P52017
  C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//3.10E-51//152aa//40%//Q61221
  - C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%//AF201333
  - C-HEMBA1004509//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THI-
- OLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME ,4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//200aa//28%//Q13107
  - C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds.//1.2e-316//1445bp//99%// AF089841
  - C-HEMBA1004573//Homo sapiens mRNA for HELG protein.//2.00E-59//483bp//68%//AJ277291
- 25 C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%//AF193844 C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%//P18583
  - C-HEMBA1004697//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMMHC) (FRAGMENT).//2.90E-05//303aa//21%//P35749
  - C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUTTIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743
  - C-HEMBA1004752//Homo sapiens mRNA for LAK-4p, complete cds.//4.60E-109//650bp//89%//AB002405
  - C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds.//9.10E-34//515bp//66%//U49082
  - C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds.//2.60E-246//1249bp//94%//
- 35 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.40E-111//314aa//58%//P08547
  - C-HEMBA1004795//CDC4-UKE PROTEIN (FRAGMENT).//3.80E-69//198aa//66%//P50851
  - C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//8.20E-154//317aa//94%//
  - C-HEMBA1004889//Human C3f mRNA, complete cds.//6.70E-24//341aabp//26%//U72515
- 40 C-HEMBA1004929//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.50E-05//148aa//24%// P25386
  - C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.30E-27//65aa//100%//Q16401 C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEURO FILAMENT PROTEIN) (NF-H).// 0.00000096//286aa//23%//P12036
- 45 C-HEMBA1004973//ZINC-BINDING PROTEIN A337/4.10E-08//121aa//33%//Q02084
  - C-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//0//1813bp//99%//AF041474
  - C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%//AF132947
  - C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%//P35290
  - C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%//
  - C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%//AF132941
  - C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%//Q00004
  - C-HEMBA1005206//Drosophila simulans anon73Bl gene and Su(P) gene.//1.90E-11//376bp//63%//AJ250308
- 55 C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.30E-10//189aa//25%//P39929
  - C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%//AJ007581
  - C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%//P52743
  - C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%//

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- C-HEMBA1005394//Mus musculus pantothenate kinase 1 beta (panKlbeta) mRNA, complete cds.//3.90E-126// 1097bp//75%//AF200357
- C-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//2.00E-213//537bp//99%//AF041248
  - C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%//O02193 C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.10E-154//285aa//99%//Q60809
  - C-HEMBA1005530//Homo sapiens anaphase-promoting complex\_subunit 7 (APC7) mRNA, complete cds.//0// 1578bp//98%//AF191340
- C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA, 10 complete cds.//1.00E-220//1014bp//99%//AF134157
  - C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%//P39929
  - C-HEMBA1005576//Mus musculus mRNA for plexin 2, complete cds.//1.20E-122//870bp//82%//D86949
  - C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, complete cds.//0//1721bp//100%//AF133270
- C-HEMBA1005582//TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL TRO-15 POMYOSIN).//0.00000009//213aa//27%//P09492
  - C-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).//2.30E-54//562aa//29%//P34036
  - C-HEMBA1005621//Homo sapiens Mad2-like protein mRNA, complete cds.//8.00E-211//962bp//99%//AF072933
  - C-HEMBA1005666//Homo sapiens mRNA for DIPB protein.//8.60E-147//685bp//99%//AJ249128
- C-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) 20 (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3).//2.10E-37//98aa//81 %//Q15768 C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).// 4.40E-17//167aa//34%//P25296
- C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEU-TRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%//P00789 25
  - C-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.60E-15//76aa//51%// P51522
  - C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%// AF082516
- C-HEMBA1006031//Homo sapiens mRNA for putative phospholipase, complete cds.//0//1413bp//99%//AB019435 30 C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%//Q61001
  - C-HEMBA1006067//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//8.20E-12//297bp//64%//AF098066
  - C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25 %//Q93794
- C-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//0//155 lbp// 35
  - C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.90E-19//215aa//39%//P05142
  - C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.60E-23// 151aa//37%//P16372
- C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR.//0.00000002// 40 62aa//53%//P42698
  - C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836
  - C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.30E-123//200aa//73%//P10265
  - C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-FERASE).//1.00E-210//490aa//77%//P25500
  - C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2.//0.000000012//176aa// 30%//P32505
  - C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-).//4.20E-12//215aa//23%//P70473
  - C-HEMBA1006309//Homo sapiens aspartyl aminopeptidase mRNA, complete cds.//5.30E-169//774bp//100%// AF005050
  - C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds.//3.70E-225//1189bp//88%//AF076183
  - C-HEMBA1006344//RADIXIN.//1.50E-31//333aa//28%//P26043
  - C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-130//332aa//62%//O02193
- C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160 55
  - C-HEMBA1006398//Human L1 element L1.6 putative pi 50 gene, complete cds.//2.00E-277//1729bp//85%// U93563
  - C-HEMBA1006445//Homo sapiens putative tumor supressor NOEY2 mRNA, complete cds.//1.40E-270//1224bp//

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- C-HEMBA1006474//40 KD PROTEIN.//1.40E-39//292aa//34%//Q01552
- C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//97%//P55786
- 5 C-HEMBA1006507//DIAPHANOUS PROTEIN HOMOLOG 2.//1.40E-46//316aa//32%//O60879
  - C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%//P25716
  - C-HEMBA1006559//Mus musculus PRAJA1 (Praja1) mRNA, complete cds.//2.80E-206//1107bp//83%//U06944
- C-HEMBA1006583//Drosophila melanogaster Scribble (scrib) mRNA, complete cds.//1.70E-63//1002bp//65%//
  AF190774
  - C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.00000069//109aa//38%//Q58323
  - C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%//O15509
  - C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148
- 15 C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMC1-TFG2 INTERGENIC REGION.//3.30E-22//241aa//31%//P53196
  - C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).// 0.000000043//111aa//40%//Q01485
  - C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//91%//AF152492
  - C-HEMBA1006807//Homo sapiens mRNA for SPOP.//5.70E-125//1109bp//75%//AJ000644
  - C-HEMBA1006877//OXYSTEROL-BINDINGPROTEIN.//2.00E-59//378aa//39%//P16258
  - C-HEMBA1006885//Homo sapiens gene for Proline synthetase associated, complete cds.//0//1467bp//96%//AB018566
- 25 C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%// U35832
  - C-HEMBA1006941//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds.//2.10E-271// 1234bp//99%//AF118649
  - C-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.60E-143//740bp//94%//
- 30 AF004828

- C-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/l-4)GlcNAc alpha-2.3-sialytransferase.//1.90E-80//447bp//89%//X74570
- C-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (UC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A).//2.40E-188//391aai/89%//Q90828
- 35 C-HEMBA1007087//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//8.30E-27//253aa//30%//Q10568
  - C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds.//1.70E-252//1118bp//92%//AF125042
  - C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%//AF076929
- C-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds.//3.80E-271//642bp//99%//AF062085
  C-HEMBA1007194//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.//0// 1588bp//99%//AF139658
  - C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%//
- 45 C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//2.00E-58//650bp//70%//J00060
  - C-HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds.//5.00E-58//330bp//95%// AF176707
  - C-HEMBA1007300//Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds.//0//1519bp//99%//AF127479
- 50 C-HEMBA1007301//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//6.20E-18//115aa//33%//P13941
  - C-HEMBB1000036//Homo sapiens CGI-51 protein mRNA, complete cds.//0//1665bp//99%//AF151809
  - C-HEMBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.80E-187// 1582bp//80%//AF084928
  - C-HEMBB1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC
- 55 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.90E-22//426aa//25%//P11799
  - C-HEMBB1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521
  - C-HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177

- C-HEMBB1000217//Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.//0// 1038bp//99%//AF090385
- C-HEMBB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEEDB.5.// 2.70E-12//112aa//47%//Q09530
- 5 C-HEMBB1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%//P22516

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- C-HEMBB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHRO-MOSOME V.//6.10E-09//242aa//26%//Q23256
- C-HEMBB1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P37888
- C-HEMBB1000593//Homo sapiens transfemn receptor 2 alpha (TFR2) mRNA, complete cds.//1.30E-107//503bp//99%//AF067864
- C-HEMBB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.10E-19//232aa//28%//P78970
- C-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.20E-28//273aa//31%//P27671 C-HEMBB1000693//Homo sapiens neuroan1 mRNA, complete cds.//0//2952bp//94%//AF040723
- 15 C-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.20E-130//692bp//93%//
  - C-HEMBB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847
  - C-HEMBB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.// 1.20E-126//613bp//97%//AF111105
- 20 C-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.// 5.10E-54//232aa//43%//P39956
  - C-HEMBB1000831//Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA, complete cds.//5.80E-60//301bp//99%//AF126008
  - C-HEMBB1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa// 31%//P29122
  - C-HEMBB1000927//Homo sapiens A-type potassium channel modulatory protein 2 (KCHIP2) mRNA, complete cds.//1.30E-126//592bp//99%//AF199598
  - C-HEMBB1000947//Homo sapiens clone HAW100 putative ribonuclease III mRNA, complete cds.//0//2292bp// 99%//AF116910
- 30 C-HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.40E-120//580bp//67%//AF099974 C-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.60E-18//178aa//30%//P28575
  - C-HEMBB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-73//230aa//45%// P51523
- 35 C-HEMBB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.90E-19//264aa//34%//P46087
  - C-HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.60E-52//331bp//80%//AF010144
  - C-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.40E-307//1447bp//97%//AF034803
- 40 C-HEMBB1001112//Homo sapiens sec61 homolog mRNA, complete cds.//6.00E-145//961 bp//83 %//AF077032 C-HEMBB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435 C-HEMBB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.20E-210//1835bp//76%//AF110267
  - C-HEMBB1001175//ANKYRIN.//7.00E-11//169aa//31%//Q02357
- 45 C-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.40E-93//196aa//54%//P46938
  - C-HEMBB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.80E-284//713bp//100%//AF089897
  - C-HEMBB1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7.00E-43//394aa//34%//P16157
- 50 C-HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//7.80E-46//163aa//51%//P46719
  - C-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.20E-79//196aa//80%//P17081
  - C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.30E-129//724bp//86%//U92703
  - C-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.// 2.10E-65//458bp//79%//D63850
    - C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//4.60E-06//124aa//37%//P98175
    - C-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.10E-58//292bp//99%//AF097441

- C-HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757 C-HEMBB1001429//Homo sapiens leucine aminopeptidase mRNA, complete cds.//0//1933bp//99%//AF061738 C-HEMBB1001443//Rattus norvegicus pyruvate dehydrogenase phosphatase isoenzyme 1 mRNA, complete cds.//3.00E-130//553bp//86%//AF062740
- 5 C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa// 27%//Q05481
  - C-HEMBB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%//Q28092 C-HEMBB1001564//VACUOLAR ATP SYNTHASE SUBUNIT H (EC 3.6.1.34) (V-ATPASE H SUBUNIT) (V-ATPASE M9.2 SUBUNIT) (9.2 KD MEMBRANE ACCESSORY PROTEIN).//9.60E-32//80aa//78%//O15342
- 10 C-HEMBB1001673//Homo sapiens gene for new zinc finger protein, complete cds.//0//1919bp//99%//AB012770 C-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3 P110).//4.60E-15//391aa//25%//P55884
  - C-HEMBB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//1.70E-16//84aa//47%//Q03330
  - C-HEMBB1001802//Human desmin mRNA, complete cds.//0//1523bp//98%//U59167
- C-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//0//
  1514bp//99%//AF056209
  - C-HEMBB1001839//GASTRULA ZINC FINGER PROTEIN XLCGF42.1 (FRAGMENT).//6.90E-11//87aa//35%//P18720
  - C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//5.40E-75//241aa//48%//P47853
  - C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR) (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%//Q61549
  - C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%//P37709

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- C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//874bp//86%//U47742
  - C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//6.90E-132//561aa//50%//Q24574
  - C-HEMBB1001950//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.----)
- (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//31%//P54304
  C-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYPIVC1).//2.70E-49//139aa//55%//P29981
  C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%//Y08715
  - C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%//P56163
    C-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN
- 35 KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2).//8.70E-61//77aa//74%//P55144
  - C-HEMBB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//44%//Q05481
    - C-HEMBB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%//P41737
  - C-HEMBB1002342//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds.//1.50E-229// 1045bp//99%//AF118649
  - C-HEMBB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%//P34692
  - C-HEMBB1002477//Human Grb2-associated binder-1 mRNA, complete cds.//7.70E-258//774bp//99%//U43885
  - C-HEMBB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42%//P48365
  - C-HEMBB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5.00E-28//266aa//33%//P27544
- 45 C-HEMBB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//0//1417bp//99%//AF089749
  - C-HEMBB1002607//Homo sapiens vitamin D3 receptor interacting protein (DRIP80) mRNA, complete cds.//2.00E-136//660bp//98%//AF105421
  - C-HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.//7.80E-285//841bp//96%//AF132961
  - C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5).//8.20E-198//868bp//99%//
- C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN GP37].//1.90E-07//249aa//27%//P03396
  - C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.50E-90//323aa//48%//P47226
  - C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE-
- 55 TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%//Q09860
  C-MAMMA1000173//Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete cds.//
  2.60E-164//1044bp//87%//AF197060
  - C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%//

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- C-MAMMA1000284//P.walti mRNA for rnp associated protein 55.//2.20E-109//864bp//76%//X99836
- C-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//0//1466bp// 99%//AB015132
- 5 C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//2.00E-30//119aa//
  53%//Q09232
  - C-MAMMA1000612//Homo sapiens G protein beta subunit mRNA, partial cds.//8.30E-178//1992bp//84%//AF195883
  - C-MAMMA1000625//GYP7 PROTEIN.//2.10E-41//198aa//40%//P48365
- 10 C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.).//4.40E-33//250aa// 33%//P42660
  - C-MAMMA1000684//Homo sapiens opioid growth factor receptor mRNA, complete cds.//0//2391bp//99%// AF172451
  - C-MAMMA1000713//L-RBULOKINASE (EC 2.7.1.16).//7.70E-17//246aa//29%//P94524
- 15 C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.00E-77//395aa//45%//O14646
  - C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%//AJ011779
  - C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//9.00E-299// 1033aa//55%//P87115
- 20 C-MAMMA1000824//ACTIN.//6.20E-20//284aa//28%//P53500
  - C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.80E-40//101aa//54%//O27540
  - C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (TTI HEAVY CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.00E-141//576aa//37%//Q06033 C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%//AJ250711
- 25 C-MAMMA1001008//Homo sapiens aspartic-like protease mRNA, complete cds.//2.50E-276//1263bp//99%// AF117892
  - C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HOROMINE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%//Q90674
  - C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN]//2.60E-107//190aa//95%//Q15746
  - C-MAMMA1001041//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//1.60E-16//113aa//41%//Q01082
    - C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99%//AJ237946
    - C-MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds.//1.30E-181//397bp//98%//AF151830
- 35 C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6e-312//1596bp//94%// AF067420
  - C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4.00E-49//125aa//68%//P51521
  - C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%//Q09273
  - C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%//Q92338
- 40 C-MAMMA1001198//Homo sapiens eps15R mRNA, partial cds.//0//2253bp//99%//AB015346
  - C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%//P12978
  - C-MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.//2.30E-271//1414bp//89%// AF184275
  - C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.10E-52//630aa// 30%//P34537
  - C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//2.20E-98//283aai/63%//Q07960
  - C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%// P20931
    - C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%//P02750 C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//6.50E-129//260aa//92%//P52623
- C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-TRAL PROTEINASE) (CANP) (MU-TYPE).//5.70E-55//86aa//97%//P07384
  - C-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.50E-276//1561bp//90%//M61764
    - C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6.//5.20E-189//871bp//99%//AJ007989
    - C-MAMMA1001633//ZINC FINGER PROTEIN 165.//6.30E-39//160aa//55%//P49910

- C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ).//0.00000058//29aa//100%//P47756 C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//0//1603bp//99%//AF095687
- C-MAMMA1001735/TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V).//5.90E-240//445aa//97%//P09653
- 5 C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8.50E-32//171aa// 36%//P21573
  - C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2 (KCNK6) mRNA, complete cds.//0//2332bp//99%//AF117708
  - C-MAMMA1001754//Homo sapiens Vacuolar proton pump subunit SFD alpha isoform mRNA complete cds.//0// 1987bp//99%//AF112204
    - C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.80E-45//351aa//38%// Q58556
    - C-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.60E-200//1272bp//79%//X85991
    - C-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//1.30E-198//1157bp//80%//Y13148
- 15 C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.60E-77//507aa//38%//Q07230
  - C-MAMMA1001868//TRICHOHYALIN.//2.70E-19//359aa//25%//P22793

B) (NKEF-B).//5.20E-61//60aa//90%//P32119

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- C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.//1.70E-252//1170bp//99%// AF099664
- C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//6.00E-66//157aa//70%//P15880 C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURAL KILLER CELL ENHANCING FACTOR
- C-MAMMA1002219//Rattus norvegicus rexo70 mRNA, complete cds.//1.30E-181//861bp//98%//AF032667
- C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).//8.80E-217//310aa//86%//PP70541
- C-MAMMA1002268//Mus musculus sphingosine kinase (SPHKIa) mRNA, partial cds.//1.00E-190//1624bp//76%// AF068748
- C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase activating protein.//1.10E-214//881bp//97%//
- 30 C-MAMMA1002329//M.musculus mRNA for semaphorin B.//3.80E-45//332bp//84%//X85991
  - C-MAMMA1002351//Mus musculus dynactin subunit p25 (p25) mRNA, complete cds.//4.30E-119//773bp//86%//
  - C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//1.50E-07//206aa//29%//Q02926
  - C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2).//1.10E-24//96aa//68%//Q14108
  - C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(\*) SYNTHETASE (EC 6.3.5.1).//1.00E-11//128aa// 36%//P47623
  - C-MAMMA1002485//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//1822bp//99%// AF098462
- 40 C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//1.20E-34//
  337aa//31%//P43571
  - C-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.// 0//1910bp//99%//AF065214
  - C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.60E-19//666aa//23%//P08640
  - C-MAMMA1002617//ZINC FINGER PROTEIN 135.//7.60E-89//252aa7/57%//P52742
    - C-MAMMA1002619//PROBABLE UBIQUTTIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUTTIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUTTINATING ENZYME).//9.50E-16//159aai/37%//Q09931
- 50 C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640
  - C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q07866
  - C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030
  - C-MAMMA1002655//Homo sapiens mRNA for ganglioside sialidase, complete cds.//0//1515bp//99%//AB008185
  - C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL-AC-
- 55 TIVATING ENZYME).//1.10E-45//618aa//26%//P27550
  - C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3e-317// 1942bp//85%//AF018261
  - C-MAMMA1002769//Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete cds.//

2.20E-25//330bp//77%//AF011794

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- C-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//2.60E-58//373bp//81%// U58883
- C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECUR-
- 5 SOR (CTPT).//4.90E-10//334aa//22%//P52178
  - C-MAMMA1002858//Rat cMG1 mRNA.//3.70E-238//1147bp//92%//X52590
  - C-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERESTING NEW CYS-HIS PROTEIN).//1.40E-160//305aa//85%//P48059
  - C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN).//5.70E-30//214aa// 35%//P48060
    - C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742
    - C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.//1.10E-05//69aa//42%//
    - C-MAMMA1003011//HISTONE MACRO-H2A.1.//2.70E-123//370aa//66%//Q02874
- 15 C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7).//7.40E-46//332aa//36%//P06746
  - C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//1.90E-13//108aa//33%//P23851
  - C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds.//0// 1533bp//99%//AF077952
- 20 C-MAMMA1003057//MD6 PROTEIN.//3.10E-225//419aa//97%//Q60584
  - C-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//1.10E-234// 1178bp//86%//AF071316
  - C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//2.20E-105//217aa//89%//P46735
  - C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//4.30E-218//996bp//99%//Y15062
- 25 C-MAMMA1003150//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECUR-SOR.//5.00E-13//592aa//24%//P47179
  - C-MAMMA1003166//Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds.//3.10E-158// 592bp//97%//AF123052
  - C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110
- 30 C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-) (ORF4) (ORF2).//2.90E-14//299aa//25%//P37596
  - C-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.//0//3106bp//89%//D87671
  - C-NT2RM1000080//UNC-1 PROTEIN.//5.90E-25//211aa//31%//Q21190
  - C-NT2RM1000086//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//8.40E-52//364aa// 32%//P34537
    - C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).// 1.00E-07//362aa//23%//P39843
    - C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).//1.20E-10//150aa//28%//P87072
- 40 C-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.80E-110//516bp//99%//AF044959
  - C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.30E-38//469aa//27%//P49902 C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CAL-
- CINEURIN REGULATORY SUBUNIT).//1.20E-10//150aai/28%//P87072

  C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.10E-10//94aai/47%//O42643
  - C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2476bp//99%//AJ245820
  - C-NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.//2.00E-126//592bp//99%//
  - C-NT2RM1000252//H.sapiens E-MAP-115 mRNA.//9.70E-35//569bp//64%//X73882
  - C-NT2RM1000256//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.// 0//3012bp//99%//AB016789
  - C-NT2RM1000257//MAGO NASHI PROTEIN.//7.90E-69//143aa//91%//P49028
- C-NT2RM1000260//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP100 mRNA, complete cds.//0//2766bp//99%//AF055995
  - C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V- ATPASE 28 KD ACCESSORY PROTEIN).//1.50E-106//118aa//97%//P39942

- C-NT2RM1000354//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//7.40E-245//2101bp//68%//AF111423
- C-NT2RM1000355//Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds.7/0//1599bp//99%//AF152462
- 5 C-NT2RM1000377//Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds.//3.20E-196//
  1016bp//94%//AF179212
  - C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.// 0.00000019//67aa//31%//P53915
  - C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
- 10 C-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.40E-185// 1486bp//81%//AF084928
  - C-NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A.//3.00E-17//927bp//58%//AJ132700 C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein.//3.00E-158//733bp//99%//AJ238097
  - C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//3.40E-177//814bp//
  - C-NT2RM1000555//UNR PROTEIN.//0//678aa//98%//P18395

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- C-NT2RM1000563//TRANSMISSION-B LOCKING TARGET ANTIGEN S230 PRECURSOR.//0.0000068//199aa//30%//Q08372
- C-NT2RM1000623//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
- 20 C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
  - C-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds.//5.70E-210//960bp//99%// AF038957
  - C-NT2RM1000666//DNA-BINDING PROTEIN A.//2.20E-09//165aa//34%//P16989
  - C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein.//0//3104bp//99%//AJ132440
- 25 C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//5.60E-08//187aa// 27%//P49695
  - C-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//0//3524bp//99%//AF027208
  - C-NT2RM1000746//Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds.//6.70E-227// 1043bp//99%//AF141310
- 30 C-NT2RM1000770//DXS6673E PROTEIN.//1.40E-39//194aa//48%//Q14202
  - C-NT2RM1000772//VEGETATABLE INCOMPATIBILITY PROTEIN HET-E-1.//7.30E-15//280aa//27%//Q00808
  - C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-indl gene).//1.10E-98//571bp//89%// Z97207
  - C-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//0//3524bp//99%//AF027208
- 35 C-NT2RM1000826//UNR PROTEIN.//0//678aa//98%//P18395
  - C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541 bp//99%//AF08445 8
  - C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//9.70E-42//333aa//36%//P16157
  - C-NT2RM1000852//Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds.//0// 2206bp//99%//AF077033
  - C-NT2RM1000874//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.// 1.40E-244//1113bp//99%//AF043733
  - C-NT2RM1000882//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//4.30E-122//1394bp//69%// AF126799
- 45 C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%// AF082516
  - C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.80E-56//630aa//30%//P34537
  - C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//1020aa//89%//P70700
  - C-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR).//8.90E-26//229aa//29%//P02583
  - C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//1.00E-15//266aa// 26%//P46577
  - C-NT2RM1001003//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//0//2230bp// 99%//AF030233
    - C-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.60E-13//119aa//36%//
    - C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%//

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- C-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODEESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148).//8.30E-47//259aa//35%//P08487
- 5 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa// 52%//Q05481
  - C-NT2RM1001102//Human HEM45 mRNA, complete cds.//2.30E-27//482bp//63%//U88964
  - C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//5.60E-06//239aa//27%//P54197
  - C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.20E-144//362aa//71%//P25167
  - C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTER-MEDIATE CHAIN).//0.00000043//136aa//31%//P54703
    - C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).// 1.30E-36//160aa//40%//P50102
    - C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%//AF067223
    - C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//3.60E-19//181aa//34%//P14918
- 20 C-NT2RM2000322//SPERMIDINE SYNTHASE (EC 2.5.1.16) (PUTRESCINE AMINOPROPYLTRANSFERASE) (AMINOPROPYLTRANSFERASE).//8.10E-06//167aa//29%//O48660
  - C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.//1.80E-14//245aa//29%//P11274
  - C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//0//1506bp//99%// U48251
- 25 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLE-OTIDE//1.70E-68//419aa//36%//P50849
  - C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-NENT).//1.60E-54//344aa//33 %//P32802
- 30 C-NT2RM2000407//Mus musculus semaphorin VIa mRNA, complete cds.//9.70E-201//826bp//84%//AF030430 C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//1.00E-222//237aa//89%//Q08469
  - C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION.//1.00E-07// 157aa//28%//P36113
- 35 C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-).//8.90E-06//377aa//24%// P22211
  - C-NT2RM2000490//SYNAPTOTAGMIN (P65).//1.80E-13//166aa//34%//P41823
  - C-NT2RM2000502//Rattus norvegicus W307 mRNA, complete cds.//1.70E-58//381bp//86%//U78304
  - C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%//AF061243
- 40 C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.30E-12//282aa//32%//P17437
  - C-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//0//2519bp//96%//AF032108
  - C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).// 1.70E-187//741aai/46%//P73505
- 45 C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.80E-60//384aa//40%//P53973
  - C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.// 0//2712bp//99%//AF156487
  - C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds://4.90E-70//838bp//69%//AF179221
- 50 C-NT2RM2000609//Homo sapiens CTL1 gene.//0//1559bp//99%//AJ245620
  - C-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//2.60E-106//1069bp//74%//U35776
  - C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.40E-32//319aa//35%//Q08170
- 55 C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.70E-142//285aa//90%//P32391
  - C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.80E-23//184aa// 36%//Q15404
  - C-NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.//0//1731bp//99%//AF121141

- C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.90E-103//249aa//73%//P28160 C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.70E-53//266aa//43%//P41877
- C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//9.50E-279//545aa// 98%//P23514
  - C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.70E-200//927bp//99%//AB015046
  - C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.20E-154//285aa//99%//Q60809
  - C-NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1554bp//99%//AF100757 C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.40E-15//266aa//
- 10 C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III.//2.40E-15//266aa//
  26%//P46577
  - C-NT2RM2001105//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.20E-28//805bp//61%// AF053091
  - C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.30E-20//267aa//35%//P05143
- 15 C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5).//1.50E-07//95aa//35%// P48724
  - C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//3.60E-10//
    177aa//32%//P97924
  - C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMI-DOHYDROLASE).//1.30E-180//328aa//99%//P13264
  - C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.60E-166//312aa//98%// P53995
  - C-NT2RM2001324//ZYXIN.//6.80E-55//200aa//41%//Q04584

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- C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-08//334aa//22%//Q00808
- 25 C-NT2RM2001424//Homo sapiens mRNA for EIB-55kDa-associated protein.//0//1621bp//99%//AJ007509 C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.40E-121// 437aa//57%//P52569
  - C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.90E-27//90aa//42%//P38660
- 30 C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//
  4.30E-61//312aa//44%//P19474
  - C-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//3.10E-156//909bp//88%//AF032667 C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein.//0//3114bp//99%//AJ132440
  - C-NT2RM2001613//Homo sapiens sec61 homolog mRNA, complete cds.//0//2601 bp//99%//AF084458
- 35 C-NT2RM2001632//KES1 PROTEIN.//1.40E-31//342aa//34%//P35844
  - C-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145).//1.20E-142//566aa//56%//P52591
  - C-NT2RM2001648//Homo sapiens sec61 homolog mRNA, complete cds.//0//2421 bp//99%//AF084458
  - C-NT2RM2001652//Homo sapiens guanine nucleotide exchange factor mRNA, complete cds.//0//2608bp//99%//
  - C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN.//3.40E-39//161aa//34%//P20107
  - C-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA complete cds.//0// 2471bp//99%//AF044195
  - C-NT2RM2001668//Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending in intron 11, complete cds.//6.20E-16//464bp//62%//AFQ83391
    - C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%//Q07230
    - C-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds.//0// 1843bp//94%//U21155
    - C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//4.60E-20//253aa// 30%//Q09674
    - C-NT2RM2001698//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.//6.20E-253// 1170bp//99%//AB028600
    - C-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT).//5.70E-130//536aa//49%//P50544
- 55 C-NT2RM2001716//Homo sapiens BPTF mRNA for bromodomain PHD finger transcription factor, complete cds.//
  0//1774bp//98%//AB032251
  - C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-

ZYME).//7.20E-16//381aa//27%//Q09931

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- C-NT2RM2001743//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//0//1498bp//99%//AF011792
- C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.80E-11//119aa//36%//Q92609
- 5 C-NT2RM2001760//Homo sapiens sec61 homolog mRNA, complete cds.//0//2379bp//99%//AF084458
  - C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.40E-154//394aa//64%//P52742
  - C-NT2RM2001782//Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds.//0// 1470bp//99%//AF135422
  - C-NT2RM2001785//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//0//2150bp//99%// AF126799
  - C-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0// 2249bp//99%//AF044195
  - C-NT2RM2001823//CHD1 PROTEIN.//1.80E-106//631aa7/39%//P32657
  - C-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//0//2415bp//97%//AF013759
- C-NT2RM2001886//PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2 (EC 3.1.13.4) (PAB1P-DEPENDENT POLY(A)-NUCLEASE).//3.00E-54//337aa//39%//P53010
  - C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.10E-26//204aa//34%//P28692
  - C-NT2RM2001930//M.musculus mRNA for semaphorin G.//5.20E-135//894bp//83%//X97818
  - C-NT2RM2001935//Homo sapiens single-strand selective monofunctional uracii DNA glycosylase mRNA, complete cds.//0//1454bp//99%//AF125182
  - C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.70E-27//216aa//34%// P28320
  - C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.0000001// 212aa//23%//P38250
- 25 C-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//0//1658bp//98%// AF089816
  - C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.90E-39//253aa//35%// P37838
  - C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.30E-10//232aa// 28%//Q12730
  - C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME L//3.10E-12//206aa// 30%//Q09782
  - C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).// 2.90E-08//83aa//44%//P40796
- 35 C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.10E-89// 425aa//41%//P46837
  - C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.// 0//1959bp//99%//AB016789
  - C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa// 24%//Q07878
    - C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).// 5.00E-62//104aa//57%//Q61990
    - C-NT2RM2002091//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//7.10E-29//805bp//61 %//
- 45 C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%//AJ010840 C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0// 1868bp//99%//AF030435
  - C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.90E-13// 487aa7/26%//P49695
- 50 C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8.00E-31//105aa//47%//P47805
  C-NT2RM2002145//Homo sapiens erythrobiast macrophage protein EMP mRNA, complete cds.//8.50E-191//
  1524bp//81%//AF084928
  - C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.10E-155//381aa//72%//P25167
- 55 C-NT2RM4000030//LAS1 PROTEIN.//5.60E-12//184aa//32%//P36146
  - C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.000008//112aa//31%//Q06003
  - C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.50E-81//251aa//53%//P52742
  - C-NT2RM4000139//R.norvegicus trg mRNA.//2.30E-114//1161bp//72%//X68101

- C-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE-TRNA LIGASE) (THRRS).//1.20E-157//321aa//61%//P26639
- C-NT2RM4000156//H.sapiens HPBRII-7 gene.//3.60E-21//785bp//60%//X67336
- C-NT2RM4000167//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//1946bp//99%//AJ271784
- 5 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.80E-13//686aa//23%// P25386
  - C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.20E-75//439aa//41%//P16381 C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).//4.90E-32//170aa//41%//Q16600 C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%//P10962
- 10 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.10E-27//633bp//64%//L20303
  - C-NT2RM4000233//Mus musculus semaphorin Via mRNA, complete cds.//3.40E-231//1395bp//86%//AF030430 C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.20E-276//1124bp//97%//M99438
- 15 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%//
  AJ132637
  - C-NT2RM4000354//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.50E-21//208aa//35%//Q24371 C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.90E-80//213aa//75%//P35292
  - C-NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//2156bp//87%//AF195418
- 20 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%//AJ133769
  - C-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds.//4.10E-271// 2085bp//77%//AF062476
  - C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//8.00E-20//393aa// 24%//Q10297
- C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2092bp//99%//AF097025 C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.80E-11//242aa//31%//P04280 C-NT2RM4000496//SAP1 PROTEIN.//8.30E-53//434aa//29%//P39955
  - C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H)
- 30 (FRAGMENT).//1.10E-11//394aa//24%//P16884 C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.40E-89//389aa//43%//Q07230
  - C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%//Q04652
  - C-NT2RM4000595//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//8.70E-15//403aa//30%//
- 35 C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-09//108aa//31%//Q00808 C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE—COA LIGASE) (ACYL- ACTIVATING ENZYME).//2.70E-146//420aa//60%//P27550
  - C-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//3.00E-68//297aa//40%//P51178
- 40 C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL13747/1.20E-28//180aa//30%//P74168

- C-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.00E-136// 1104bp//77%//AF022789
- C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000041//207aa//29%//P52154 C-NT2RM4000734//Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds.//0//2071bp//99%//AF221712
- C-NT2RM4000741//Homo sapiens hSGT1 mRNA for hSgt1p, complete cds.//0//2184bp//99%//D88208
- C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.90E-125//301aa//53%//Q99676 C-NT2RM4000798//Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA, complete cds.//0//2603bp//99%//AF084521
- 50 C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).//1.10E-24//138aa//44%//P40682
  - C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//6.70E-22//250aa//29%//P02750 C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//50%//Q05481
- 55 C-NT2RM4001047//MO25 PROTEIN.//8.00E-140//333aa//80%//Q06138
  C-NT2RM4001054//Homo sapiens sec61 homolog mRNA, complete cds.//3.10E-190//1315bp//81%//AF077032
  - C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME IJ/0.000000032// 165aa//33%//Q09820

- C-NT2RM4001092//ZINC FINGER PROTEIN GLO37/3.10E-24//265aa//33%//P38682
- C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II.//5.90E-86//292aa//48%//Q09417
- C-NT2RM4001140//HOMEOBOX PROTEIN MSH-D.//1.00E-11//103aa//38%//Q01704
- 5 C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//4.10E-197//445aa//78%//Q27969
  - C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//1.10E-48//218aa//43%//Q03532
  - C-NT2RM4001200//ZINC FINGER PROTEIN 135.//9.50E-135//375aa//60%//P52742
  - C-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//0//2310bp//99%//
- 10 C-NT2RM4001217//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds.//3.10E-148//1445bp// 72%//U65079
  - C-NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//4.30E-55//289bp//77%//AF129131
  - C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-UKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K).//3.50E-35//124aa//65%//P54676
  - C-NT2RM4001316/ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3)
  - (MCAD).//2.30E-31//334aa//30%//P08503 C-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.80E-39//728bp//64%//D89016
  - C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1.00E-28//171aa//37%//P32626
- 20 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//8.10E-30//265aa//33%//P53742
  - C-NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//0//2300bp//99%//AF155103
  - C-NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds.//0//2524bp//99%//AB019494
  - C-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.20E-237//1079bp//99%//AF098799
  - C-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//0//1962bp//87%//AF020526
  - C-NT2RM4001412//Homo sapiens nGAP mRNA, complete cds.//0//1918bp//99%//AF047711
  - C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE-TRNA LIGASE) (ILERS).//
- 30 1.40E-118//444aa//46%//P73505

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- C-NT2RM4001483//ZINC FINGER PROTEIN 136.//5.10E-106//357aa//55%//P52737
- C-NT2RM4001566//NECDIN.//9.80E-44//227aa//41%//P25233
- C-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.50E-284// 1082bp//90%//AF071317
- 35 C-NT2RM4001592//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION.//7.60E-56// 213aa//49%//P31380
  - C-NT2RM4001597//M.musculus red-1 gene./12.10E-171//1414bp//78%//X92750
  - C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3)J/2.60E-32//203aa//39%//Q12600
  - C-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3).// 1.50E-93//278aa//38%//Q13368
  - C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//2.70E-84// 410aa//42%//P37339
    - C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.90E-141//354aa//72%//Q14141
  - C-NT2RM4001731//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//0//1922bp//100%//
    - C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.).//4.10E-186//639aa//58%//Q05512
    - C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.90E-66//311aa//35%//Q03164
    - C-NT2RM4001810//AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN
- 50 CORE PROTEIN) (CSPCP) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 1).//5.10E-07// 263aa//30%//P16112
  - C-NT2RM4001813//LECTIN BRA-2.//0.00000048//114aa//30%//P17346
  - C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.// 8.10E-300//1395bp//98%//M37712
- 55 C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)7/2.90E-55//325aa//37%//P28160 C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.90E-161//481aa//56%//
  - C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.50E-22//126aa//46%//P79779

- C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.30E-244//1248bp//94%// Y17711
- C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.50E-23//184aa// 36%//Q15404
- C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.90E-09//268aa//26%//P47486 5 C-NT2RM4001930//Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds.//0//1930bp//99%//AF102851
  - C-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//0//2087bp//99%//AF098162 C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.60E-261//1563bp//84%//X99330
- C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.80E-112//457aa//47%// 10 P51523

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- C-NT2RM4001987//NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140].//3.20E-17//281aa//30%//P16170
- C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 INTERGENIC REGION.//6.90E-94//589aa//35%//P42935
  - C-NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.//1.90E-53//1585bp//60%//AF104260
  - C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-TRNA LIGASE) (ASPRS).// 1.90E-31//80aa//52%//P36419
  - C-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//1865bp//99%// U82267
  - C-NT2RM4002066//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds.//1.50E-211//1123bp//71 %//AF117755
  - C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%// AF072758
- C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.80E-105//556aa//41 %//Q04652 25 C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0// 2550bp//99%//AF176085 C-NT2RM4002109//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//2572bp//99%//AJ271784
  - C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%//P24014
- C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%//AF035940 30 C-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, complete cds.//0//2671bp//99%//AF084535 C-NT2RM4002174//MRPPROTEIN.//9.10E-68//264aa//51%//P21590 C-NT2RM4002189//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
  - DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//6.20E-33//688aa//27%//P08640 C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%//AF030430
- 35 C-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//3.00E-37//122aa// 72%//Q07803
  - C-NT2RM4002213//Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds.//0// 2452bp//100%//AF157028
- C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.70E-19//147aa//41%//P40809 C-NT2RM4002251//ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANS-FERASE (EC 2.4.1.101) (N-GLYCOSYLOLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYL-TRANSFERASE I) (GNT- I) (GLCNAC-T I).//2.20E-36//320aa//38%//P27808 C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.000000001//154aa//33%//P48778
- C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL-AC-45 TIVATING ENZYME).//1.30E-29//275aa//30%//P27095
  - C-NT2RM4002438//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//1.10E-49//611 bp//70%//
  - C-NT2RM4002460//ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20].//0.0000016//226aa//24%//P51515
  - C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.90E-15//366aa//27%//Q00808 C-NT2RM4002532//PROTEIN HOM1.//2.00E-16//276aa//28%//P55137
  - C-NT2RM4002558//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//0//1797bp//99%// AF055899
- C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%//AF022962 55 C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T2).// 4.60E-78//921bp//69%//X85019
  - C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.70E-68//236aa//58%//P54815

- C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-TRNA UGASE) (ASPRS).// 2.30E-101//488aa//45%//O32038
- C-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//0//1747bp//99%//AB013385
- C-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1652bp//99%//AJ012449
- 5 C-NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.//5.90E-150//1025bp//82%//
  AF193608
  - C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%//X98834
  - C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4.00E-116//296aa//51%//P93471
  - C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.50E-50//181aa//60%//P51859
- 10 C-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//3.40E-270// 951bp//98%//AF011792
  - C-NT2RP1000202//ANKYRIN.//1.00E-25//302aa//34%//Q02357
  - C-NT2RP1000272//Mus musculus mRNA for neural specific sr protein NSSR 2, complete cds.//1.40E-267// 1155bp//87%//AB015895
- 15 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.30E-275//1249bp//99%//AF053551
  - C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.70E-47//155aa//58%//P32447
  - C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.70E-15//162aa//30%//P25343
  - C-NT2RP1000363//R.norvegicus LL5 mRNA7/7.90E-262//1175bp//83%//X74226
- 20 C-NT2RP1000376//Homo sapiens Ca2+-independent phospholipase A2 long isoform (iPLA2) mRNA, complete cds.//0//2252bp//96%//AF102989
  - C-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.90E-153//230aa//99%//P55161
  - C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.80E-94//1019bp//63%//AF111423
  - C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.40E-10//227aa//25%//Q08257
  - C-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//3.80E-19//149aa//36%//P17624
  - C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.60E-94//
- 30 254aa//47%//P34580

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- C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.50E-240//445aa//97%//P09653
- C-NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.//7.5e-315//1445bp//99%// AF039688
- C-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB).//3.60E-30//534aa//23%//P33194 C-NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.//6.50E-171//516bp//99%//U47101
- C-NT2RP1000522//UBIQUTIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-ZYME 1).//8.20E-83//345aa//47%//Q61068
- 40 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.10E-27//193aai/35%//P49020
  - C-NT2RP1000574//HOMEOBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.50E-75//151aa//94%// P97367
  - C-NT2RP1000630//NECDIN.//2.40E-44//227aa//41%//P25233
- 45 C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANS-PORTING POLYPEPTIDE).//1.20E-78//483aa//31%//P46721
  - C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P) mRNA, complete cds.//0// 1687bp//99%//AF145020
  - C-NT2RP1000733//Human mRNA for GSPT1-TK protein,complete cds.//0//2057bp//99%//E14379
- 50 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%//AF101434
  - C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein PO mRNA, complete cds.//9.70E-196//901bp//99%//AF173378
  - C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-OPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%//O35566
  - C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.20E-83//334aa//50%//Q07960
  - C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase Al (PDE9A) mRNA, complete cds.//0//1494bp//99%//

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- C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//98%//AF047020
- C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-OPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%//O35566
  - C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%//AF064094
  - C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.20E-20//306aa//33%//Q09531
  - C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.70E-19//343aa//25%//Q13823
- 10 C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds.//4.60E-105//504bp//99%//U39317
  - C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.40E-23//370aa//28%//Q04652
  - C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.40E-19//343aa//25%//Q13823
  - C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.50E-236//966bp//99%// M17885
    - C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.90E-299//554aa//99%//P19338
    - C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.20E-78// 1529bp//61%//L01790
    - C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%// P51522
    - C-NT2RP1001033//Homo sapiens delta-tubulin mRNA, complete cds.//2.10E-285//1290bp//100%//AF201333 C-NT2RP1001073//Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.//8.10E-107//504bp//99%//AF182291
    - C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//2085bp//99%//
    - C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%//Q06218 C-NT2RP1001113//Homo sapiens CTL2 gene.//0//2790bp//98%//AJ245621
    - C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%// U79139
- 30 C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%// M34192
  - C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0// 2006bp//100%//AF081513
  - C-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//0//2020bp//99%//AF029914
- 35 C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024 C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.80E-38//258aa//32%//Q12024
  - C-NT2RP1001310//Homo sapiens mitochondrial carrier homolog 1 isoform a mRNA, partial cds; nuclear gene for mitochondrial product.//0//1732bp//99%//AF176006
  - C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%// AF126799
    - C-NT2RP1001361//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//6.50E-116//541bp//100%//AF070652
    - C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION.//2.70E-22// 284aa//25%//P40074
- 45 C-NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1782bp//99%//AF210052 C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.90E-141//396aa//67%//P91917
  - C-NT2RP1001449//Mus musculus Gng31g mRNA, complete cds.//7.20E-165//800bp//87%//AF069954
  - C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.20E-137//629bp// 100%//AJ005257
- 50 C-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.//2.10E-158//755bp//86%//L11316
  - C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.20E-40//261aa//27%//Q08891
  - C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%//P42803
  - C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-OPROTEIN SFA-1) (CD151 ANTIGEN).//1.60E-30//232aa//30%//O35566
    - C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.80E-121//271aa//89%//P47758
    - C-NT2RP1001665//CALMODUUN.//0.00000051//83aa//30%//P02594

- C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.80E-17//79aa// 55%//O34136
- C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.40E-177//726aa//47%// P51523
- C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)7/1.80E-22//184aa// 34%//Q01730
  - C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.// 0//1390bp//98%//AF061749
  - C-NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.//0// 2245bp//99%//AF155109
  - C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EP-SILON).//9.40E-16//45aa//100%//P49446
  - C-NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//3546bp//99%//AF195418
  - C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.40E-51// 383aa//32%//P33450
  - C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene).//7.90E-20//265bp//73%//
  - C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%//AB018356
  - C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.50E-117//541aa//42%//
  - C-NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//0//1490bp//99%// AF175966
  - C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN
- ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.40E-226//423aa//99%//P35585 25
  - C-NT2RP2000153//GAR2 PROTEIN.//9.80E-23//311aa//28%//P41891

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- C-NT2RP2000157//MLO2 PROTEIN.//2.60E-11//62aa//40%//Q09329
- C-NT2RP2000161//DIS3 PROTEIN HOMOLOG.//4.10E-35//184aa//44%//Q17632
- C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%//O02675
- 30 C-NT2RP2000195//Homo sapiens androgen induced protein (AIG-1) mRNA, complete cds.//7.80E-152//704bp//
  - C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1).//0.000043//103aa//28%//P35568
  - C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.40E-21//210aa//33%//P56558
  - C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//9.70E-41//278aa//36%//P40556 C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (AI 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA).//
- 7.10E-12//213aa//23%//P35251 C-NT2RP2000270//Human putative G-protein coupled receptor (SH120) mRNA, complete cds.//1.30E-242// 40 1043bp//99%//U78723
  - C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.60E-27//576aa// 25%//Q10297
  - C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.30E-186//256aa//60%//Q99676
- C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.30E-279// 45 1193bp//99%//U82381
  - C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111// 226aa//92%//P08760
  - C-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds.//0//2331bp//
    - C-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//0//1886bp//99%//L28010
    - C-NT2RP2000420//ZINC FINGER PROTEIN 165.//8.50E-33//155aa//52%//P49910
    - C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp// 99%//AF102265
- C-NT2RP2000448//KES1 PROTEIN.//8.70E-54//392aa//38%//P35844 55
  - C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa// 34%//P41238
  - C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%//P39955

- C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.30E-27//349aa//32%// O01577
- C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE-TRNA LIGASE)//2.70E-100// 488aa//44%//O32038
- 5 C-NT2RP2000764//NIFS PROTEIN.//6.60E-36//252aa//42%//P12623
  - C-NT2RP2000809//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0// 3347bp//99%//AF095195
  - C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//5-.60E-08//179aa//29%// Q99104
- 10 C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120).//1.10E-07//96aa//29%// P13466
  - C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//7.90E-08//172aa//28%//P26174
  - C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%// U80811
- 15 C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%//O60841
  - C-NT2RP2000892//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%//AB006135
  - C-NT2RP2000931//MATRIN 3.//2.40E-289//467aa//95%//P43244
  - C-NT2RP2000943//Homo sapiens sec24D protein mRNA, complete cds.//0//2767bp//99%//AF130464
  - C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%//AB024704
- 20 C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE).// 5.80E-46//222aai/45%//Q20939
  - C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.20E-118//430aa//54%//P50232
  - C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%//AJ132440
  - C-NT2RP2001168//VERPROLIN.//1.50E-09//143aa//33%//P37370
- 25 C-NT2RP2001174//GASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT).//6.00E-10//88aa//38%// P18722
  - C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//45%//Q05481
  - C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMMHC).//
- 30 2.20E-10//366aa//28%//P14105

- C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT).//4.40E-91//179aa//99%//P28663
- C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN.//8.30E-39//161aa//34%//P20107
- C-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
- 35 TEIN).//5.50E-116//311aa//71%//Q13829
  - C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.00E-11//403aa//25%//Q02817
  - C-NT2RP2001392//MTTOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//8.40E-192//581aa//54%//P93647
  - C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein.//0//2068bp//99%//Y18004
- C-NT2RP2001397//Homo sapiens mRNA for cyclin B2, complete cds.//1.9e-316//1428bp//100%//AB020981
  C-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds.//9.00E-112//742bp//82%//U76759
  C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds.//0//3712bp//99%//AB024334
  C-NT2RP2001460//TRICHOHYAUN.//1.00E-14//521aa//24%//P37709
  - C-NT2RP2001511//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//3.20E-297//2206bp//75%//AF093097
    - C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1.//0//2502bp//99%//Y14494 C-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.// 0//2326bp//99%//AF035586
    - C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//27%//Q60992
- 50 C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME I.//8.20E-29//294aa// 31%//Q09837
  - C-NT2RP2001597//RYANODINE RECEPTOR, CARDIAC MUSCLE.//0.000000036//127aa//36%//P30957
  - C-NT2RP2001601//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1748bp//99%//AF196304
- 55 C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLO-CASE OF OUTER MEMBRANE 40 KD SUBUNIT).//6.10E-12//184aa//31%//P24391
  - C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%//U97067
  - C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mR-

- NA, complete cds.//0//1287bp//99%//AF058718
- C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE), (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).//1.10E-47//126aa//53%//P42897
- C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-ZYME 1).//7.90E-52//220aa//44%//Q61068
  - C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DI-PHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSTRANSFERASE (EC 2.5.1.10)) (KIAA0032).//5.40E-47//96aa/797%//P14324
- 10 C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%// P51523
  - C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%//P53009
  - C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%//O14754
  - C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER
- 15 MOLECULE 1).//1.20E-45//141aa//65%//P55008
  - C-NT2RP2001883//Homo sapiens CGI-01- protein mRNA, complete cds.//0//2306bp//99%//AF132936
  - C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%//
  - C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.30E-38//395aa//30%//P53946
- 20 C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.70E-177// 1538bp//74%//AF062378
  - C-NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha mRNA, complete cds.//2.00E-38//435bp//67%//AF090989
  - C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//6.50E-129//279aa//
- 25 85%//Q08469
  - C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).// 1.70E-47//247aa//52%//P35331
  - C-NT2RP2002046//Homo sapiens mRNA for transcription factor.//0//1664bp//99%//AJ130894
  - C-NT2RP2002058//Homo sapiens WD repeat protein WDR3 (WDR3) mRNA, complete cds.//0//2510bp//99%//
- 30 AF083217

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- C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226// 1301bp//88%//U87306
- C-NT2RP2002078//PECANEX PROTEIN.//1.80E-09//195aa//32%//P18490
- C-NT2RP2002079//HISTONE HI, GONADAL.//4.40E-11//214aa//34%//P02256
- 35 C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//33 89bp//99%//AJ007509 C-NT2RP2002105//H.sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0//1644bp//98%// X65634
  - C-NT2RP2002124//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-
- 40 TOUS NUCLEAR PROTEIN HOMOLOG).//4.30E-44//155aa//37%//Q13107
  - C-NT2RP2002185//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%//AF176069
  - C-NT2RP2002193//Homo sapiens PIAS3 mRNA for protein inhibitor of activatied STAT3, complete cds.//0// 2809bp//99%//AB021868
  - C-NT2RP2002252//Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.//0//3118bp//91%//L38621
- 45 C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%//AF005418 C-NT2RP2002270//AF-9 PROTEIN.//1.20E-07//74aa//36%//P42568
  - C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%//Y16521
  - C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.40E-254//1158bp//99%//AB015594
  - C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.30E-240// 1105bp//99%//AF038958
  - C-NT2RP2002408//Homo sapiens mRNA for TOLLIP protein.//3.20E-210//1136bp//93%//AJ242972
  - C-NT2RP2002442//HESA PROTEIN.//2.80E-14//163aa//30%//P46037
  - C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//6.50E-07//171aa//27%//P30620
  - C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%// AB005289
  - C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//4.60E-144//537aa//49%//Q02386
  - C-NT2RP2002520//Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds.//3.70E-34//668bp//61%//AF105427

- C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//6.20E-19//288aa// 26%//Q11073
- C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%// P51523
- 5 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.50E-35//181aa// 42%//P12815
  - C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%//U19181 C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH).//2.80E-08//109aa//37%//P19076
- 10 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.).//1.70E-51//326aa//38%// P55345
  - C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II.//1.90E-14//210aa// 30%//O14345
  - C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//4.90E-85//489aa//43%//P55194
- 15 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%//AF041107 C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%//D89016 C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.80E-10//203aa//27%//P29764
  - C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN.//0.000039//206aa//23%//P14922
- 20 C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.90E-136//623bp// 100%//AF038392
  - C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHRO-MOSOME II.//4.10E-87//395aa//40%//Q18964
  - C-NT2RP2002939//ZINC FINGER PROTEIN 136.//5.40E-70//282aa//42%//P52737

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- 25 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.60E-80//147aa//100%//P51669 C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//1.00E-08//98aa//36%//P10129 C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//
  - C-N12RP2002986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul containing protein, complete cus.//o//220986//Homo sapiens mRNA for Reich moul cus.//o//220986//Homo sapiens may sapiens m
  - POLYMERASE I SUBUNIT 2) (RPA135).//0//716aa//91%//P70700 C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//L90E-11//132aa//38%//Q13829
  - C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//2.30E-82//642bp//68%// AF079765
  - C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.40E-38//539aa//25%//Q04652 C-NT2RP2003137//UBIQUITIN.//0.000026//70aa//30%//P13117
  - C-NT2RP2003157//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.30E-13//185aa//38%//Q08170
- C-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//0//2091bp//99%//D67025
   C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%//AJ132545
  - C-NT2RP2003177//Homo sapiens recombination and sister chromatid cohesion protein homolog (hrec8) mRNA, partial cds.//0//1641bp//99%//AF006264
  - C-NT2RP2003228//H.sapiens PI-Cdc21 mRNA.//0//2870bp//98%//X74794
- 45 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186// 1551bp//77%//AF023657
  - C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978
  - C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811
- 50 C-NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.//0//1789bp//99%//AF176069
  - C-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//1.90E-16//145aa//43%//P30771
  - C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE).//4.20E-88//374aa//47%//Q23400
- 55 C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 meidating protein, complete cds.//0//1526bp//99%//
  - C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC).//2.20E-199//550aa//70%//Q07866
  - C-NT2RP2003308//CROOKED NECK PROTEIN.//5.40E-244//622aa//67%//P17886

- C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.60E-14//332aa//32%//P26337
- C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG.//0.000022//261aa// 24%//P48754
- 5 C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor.//0//1509bp//99%//AJ133769
  C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.50E-13//302aa//26%//
  P25386
  - C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//9.60E-78//346aa//43%//Q61068
  - C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5.00E-131//269aa//91%// P38378
  - C-NT2RP2003466//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//0//2194bp//99%//AF126799
- 15 C-NT2RP2003480//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//3012bp// 99%//AF125158
  - C-NT2RP2003506//NADPH-CYTQCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//5.40E-14//106aa//46%//P04175
  - C-NT2RP2003513//Homo sapiens mRNA for paralemmin.//0//2137bp//97%//Y14770

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- 20 C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//0//1746bp// 95%//M12783
  - C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1764bp//99%//AF125158
  - C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.70E-17// 148aa//34%//P74261
  - C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)).// 2.10E-59//270aa//46%//P19474
  - C-NT2RP2003596//Mus musculus Fas-apoptosis inhibitory molecule (Faim) mRNA, complete cds.//4.80E-82// 530bp//85%//AF130367
- 30 C-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//0//2442bp//99%//
  AF030233
  - C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//9.40E-243//1624bp//82%//AJ006215
  - C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete cds.//2.1e-313//978bp//99%//AF098786
    - C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//1.80E-72//350bp//100%//AJ132637
    - C-NT2RP2003713//Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds.//0//2018bp//99%//
- 40 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.40E-29//85aa//72%//Q05481
  - C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.70E-75//147aa//93%//P51669
  - C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//869aa//80%//P53620
  - C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.//5.50E-63//253aa//50%// Q09201
  - C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//3.70E-21//137aa//43%//Q11076
- 50 C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).// 0.00000016//117aa//29%//Q91955
  - C-NT2RP2003871//Homo sapiens transposon-derived Buster1 transposase-like protein gene, complete cds.//0// 2807bp//99%//AF205601
  - C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//6.10E-183//387aa//87%//P51954
    - C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.50E-23//200aa//30%//O09175
    - C-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8.//1.40E-16//664aa7/20%//

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- C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).// 2.30E-53//141aa//78%//P20290
- C-NT2RP2004041//SYNAPSINS IA AND B.//0.00000074//159aa//32%//P17599
- 5 C-NT2RP2004066//Mus musculus Msx2 interacting nuclear target protein mRNA, complete cds.//2.70E-288// 1994bp//81%//AF156529
  - C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.40E-30//319aa//31%//Q01513
- C-NT2RP2004170//Homo sapiens mRNA for transducin (beta) like 1 protein.//1.10E-138//1236bp//74%//Y12781

  C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).//

  5.60E-31//424aa//28%//Q07231
  - C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//3.80E-52//397bp//82%//AF003998
  - C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/threonine kinase, complete cds.//0//2272bp//99%//AB015982
  - C-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//0//3044bp//99%//AB015718
    C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//
    9.90E-12//427aal/26%//P19246
  - C-NT2RP2004245//Mus musculus pantothenate kinase 1 beta (panKlbeta) mRNA, complete cds.//6.40E-117// 1122bp//72%//AF200357
  - C-NT2RP2004270//PROTEIN PTM1 PRECURSOR.//1.40E-16//334aa//24%//P32857
  - C-NT2RP2004366//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS 13.//1.30E-51//505aa// 29%//007878
  - C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.30E-15// 126aa//39%//P38120
  - C-NT2RP2004392//MNN4 PROTEIN7/1.40E-11//143aa//27%//P36044
  - C-NT2RP2004396//Homo sapiens mRNA for activator of S phase Kinase, complete cds.//5.40E-243//1108bp// 99%//AB028069
  - C-NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.//0//2321bp//86%//AF155739
- C-NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds.//0//2075bp//99%//AF180920
  C-NT2RP2004538//Mus musculus kinesin-like protein KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86%//
  - C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//3.00E-117//625aa//40%//
    Q09903
- 35 C-NT2RP2004587//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//
  7.30E-07//352aa//23%//P07197
  - C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.50E-233//1061bp//99%//AJ006291 C-NT2RP2004681//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).// 2.60E-07//426aa//23%//P19246
- 40 C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME I.//5.60E-64//616aa// 33%//Q92355
  - C-NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds.//1.50E-280//1464bp//85%// U40750
  - C-NT2RP2004732//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).// 7.30E-07//352aa//23%//P07197
  - C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.30E-26//190aa//41%//P38692
  - C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE TRNA LIGASE) (LEURS).//9.50E-73//153aa//59%//Q10490
- C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC
   6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.70E-135//414aa//62%//P53588
   C-NT2RP2004816//H58 PROTEIN.//9.00E-173//327aa//98%//P40336
  - C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETERO-CHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN).//4.20E-09//804aa// 22%//Q61687
  - C-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2103bp//99%//AB007144
  - C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%//P13692
  - C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//1.00E-

228//1666bp//75%//U56732

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- C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8.//3.30E-47//353aa//30%//Q12386
- C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).// 1.80E-99//376aa//43%//P19474
- 5 C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%//AJ011779
  C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.30E-47//155aa//59%//P32447
  C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME)
  (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE).//4.00E-91//218aa//44%//
  Q92089
- 10 C-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA).//2.00E-173//273aa//57%//P34466
  - C-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%// X98743
  - C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//0.000000022//139aa//35%//Q05921
  - C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//0.00E-01//1437bp//98%//
  - C-NT2RP2005162//Homo sapiens aspartyl aminopeptidase mRNA, complete cds.//0//1615bp//99%//AF005050 C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//0//2769bp//98%//AJ007509
- 20 C-NT2RP2005204//Homo sapiens SUMO-1-activating enzyme E1N subunit (SUA1) mRNA, complete cds.//0// 1262bp//99%//AF090385
  - C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, complete cds.//0//2087bp//99%//AF097025
    C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0/2122bp//99%//D89053
  - C-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//0//2992bp//99%//AF060219
  - C-NT2RP2005315//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.//1.90E-170//780bp//100%//AF036144
  - C-NT2RP2005325//Homo sapiens LIM-homeodomain protein HLHX2 (LHX2) mRNA, complete cds.//0//1643bp//99%//AF124735
- 30 C-NT2RP2005336//TRICHOHYALIN.//5.40E-10//545aa//22%//P37709
  - C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 5 (EC 3.6.1.38).//2.10E-124//636aa// 38%//P32660
  - C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%//AF072247
- 35 C-NT2RP2005360//Homo sapiens sentrin/SUMO-specific protease (SENP1) mRNA, complete cds.//1.30E-52//753bp//67%//AF149770
  - C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.20E-39//224aa//35%//Q13823
  - C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN.//5.30E-63//410aa//40%//P22059
  - C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.20E-13//185aa//38%//Q08170
  - C-NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds.//4.10E-202//962bp//98%//
    AF113540
  - C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds.//1.20E-13 0//608bp//99%//AF070652
- C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3.00E-44//252aa//41%//P38127
  C-NT2RP2005476//Human pl90-B (pl90-B) mRNA, complete cds.//3.40E-108//668bp//88%//U17032
  C-NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.//1.80E-175//1102bp//83%//
  - C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.00000015//279aa//26%//P35418
- 50 C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-146//398aa//59%//P52742
  - C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.20E-81//166aa//88%//P36876 C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%//AF151803
  - C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0// 3994bp//99%//AF092563
    - C-NT2RP2005525//Mus musculus kanadaptin mRNA, complete cds.//2.40E-304//1687bp//85%//AF035526
    - C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1).//5.50E-70//393aa//39%//P11171
    - C-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1560bp//98%//AJ012449

- C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2.00E-20//181aa//36%//Q39366
- C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1.00E-46//576bp//70%//AF062529
  - C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYC-OSYLASE) (GUANINE INSERTION ENZYME).//8.20E-23//164aa//28%//O32053
  - C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9e-313//1455bp//98%//AF062085
- C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(\*) SYNTHETASE (EC 6.3.5.1).//1.00E-11//128aa// 36%//P47623
  - C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.20E-13//74aa//45%//P56101
  - C-NT2RP2005669//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds.// 1.60E-248//1129bp//99%//AF043733
  - C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.40E-200//908bp//99%//AF089814
  - C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR.//2.60E-10//175aa//27%//
  - C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//3.00E-63//323aa//39%//Q62158 C-NT2RP2005712//Homo sapiens myosin X (MYO10) mRNA, partial cds.//0//2681 bp//99%//AF132022
  - C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%//Q14444
    - C-NT2RP2005722//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//2545bp//99%//AB011414
      - C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN).//3.00E-09// 169aa//28%//P38074
- 25 C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%//
  AF068868
  - C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%// AF082516
  - C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.70E-61//374aa//38%//P47943
- 30 C-NT2RP2005767//G.gallus PB1 gene.//5.00E-163//1158bp//81%//X90849

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- C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.// 2.70E-180//656bp//99%//AF151351
- C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITO-CHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-
- BINDING PROTEIN) (SABP).//2.10E-213//249aa//85%//Q02038

  C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYL-TRANSFERASE).//4.40E-55//358aa//42%//P51005
  - C-NT2RP2005784//Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds.//0// 2191bp//92%//AF155120
- 40 C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//2.30E-39// 318aa//31%//P40004
  - C-NT2RP2005835//SHP1 PROTEIN.//1.80E-28//208aa//32%//P34223
  - C-NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds.//3.50E-52//1091bp//59%//AB039669
  - C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5.00E-11//155aa//34%// P48837
  - C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-FERASE),//1.50E-67//388aa//44%//P25500
  - C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.50E-13//185aa//38%//Q08170
- 50 C-NT2RP2006071//Homo sapiens adaptor protein APPL mRNA, complete cds.//5.80E-120//1257bp//64%//
  AF169797
  - C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.10E-214//1026bp//97%//X96484
  - C-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//0//1669bp//88%// U49055
- 55 C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2.00E-59//
  388aa//32%//P46821
  - C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.80E-274//1236bp//99%//AF035262 C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEOBOX PROTEIN (RATHKE POUCH HOMEO BOX).//

3.40E-07//50aa//50%//Q61658

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- C-NT2RP2006456//Homo sapiens leucine-rich glioma-inactivated protein precursor (LGI1) mRNA, complete cds.// 1.30E-37//484bp//65%//AF055636
- C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266
- 5 C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%//Q13131
  - C-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//3.10E-272//1220bp//95%//AF038966
  - C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYPIIG1) (P450-NMB) (OLFACTIVE).//4.20E-134//486aa//50%//P24461
  - C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%//P09543
  - C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295// 1193bp//99%//AF113538
- 15 C-NT2RP3000031//HISTONE DEACETYLASE HDA1.//1.10E-71//350aa//42%//P53973
  C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%//P32559
  C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%//P33755
  C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.20E-150//490a
  - C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.20E-150//490aa//53%//Q05481
- 20 C-NT2RP3000068//SON OF SEVENLESS PROTEIN HOMOLOG 1 (SOS-1) (MSOS-1).//2.20E-06//165aa//27%//
  Q62245
  C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCCP)].//1.90E-123//436aa//50%//
- 25 C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%//P13692 C-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.90E-11//721aa//23%//P08640 C-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-84//453aa//42%//Q04652
  - C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334 C-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, pi 30, complete cds.//0//2730bp//82%// D29766
    - C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%//AJ242978
    - C-NT2RP3000333//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%//AB006135
- C-NT2RP3000341//Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.50E-246//1124bp//99%//AF106622
  C-NT2RP3000350//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2392bp//99%//AF120334
  C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%//P08760
- 40 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%//AB019219
  - C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.10E-107//206aa//99%//P35293
  - C-NT2RP3000393//Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.//5.80E-266//1373bp//86%//AF061817
- C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)//
  1.70E-139//679aa//41%//O43143
  - C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%//AF071185 C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//2.90E-15//319aa//26%//P37908
- 50 C-NT2RP3000441//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//3.40E-42//645bp//67%//AF098066
  - C-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//0//1934bp//99%//X16667
  - C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.80E-28//536aa//27%//P28160
  - C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.90E-12//192aa//30%//
- 55 P15151
  C-NT2RP3000562//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//2165bp//99%//
  AF093097
  - C-NT2RP3000578//HES1 PROTEIN.//1.30E-22//229aa//27%//P35843

- C-NT2RP3000590//UVS-2 PROTEIN.//1.30E-22//458aa//24%//P33288
- C-NT2RP3000596//TRICHOHYALIN.//2.50E-17//304aa//28%//Q07283
- C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.70E-11//90aa//42%//Q13562
- C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0//2232bp//82%//AB012265
- 5 C-NT2RP3000624//Rattus norvegicus mRNA for SECIS binding protein 2 (sbp2 gene).//5.80E-234//1562bp//81%//
  AJ251245
  - C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.00E-140//499aa//46%//P51523
  - C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.40E-24// 155aa//37%//Q10149
    - C-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//4.10E-165//371aa//49%// P10895
    - C-NT2RP3000753//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//
- 15 2.00E-10//565aa//24%//P12036

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- C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7.00E-28//176aa//34%//Q94650
- C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.50E-36//417aa//31%//Q61982
- C-NT2RP3000826//Homo sapiens mRNA for seven transmembrane protein TM7SF3, complete cds.//0//2522bp//99%//AB032470
- 20 C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//8.30E-108//331aa// 50%//P27448
  - C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.90E-69//1611bp//61%//U53445
  - C-NT2RP3000869//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.//2.60E-138// 1673bp//67%//AF227209
  - C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.70E-87//175aa//98%//Q03426
  - C-NT2RP3000917//DHP1 PROTEIN.//1.00E-193//428aa//55%//P40848
  - C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.// 2.70E-185//585bp//88%//AF015264
- 30 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E-46//73aa//98%//P39027
  - C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000006//78aa//48%//P25159
  - C-NT2RP3001055//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds.//3.80E-38//462bp//70%//AF225902
  - C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.00E-201//584aa// 54%//Q05481
  - C-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//7.10E-47//537bp//74%//AF060219
  - C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds.//1.70E-94//787bp//66%//
- 40 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3.00E-44//260aa//40%//P55201
  - C-NT2RP3001111//Homo sapiens TRF-proximal protein mRNA, complete cds.//1.50E-149//731bp//97%//
  - C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//2.90E-11//631aa//23%// P25386
- 45 C-NT2RP3001120//ZINC FINGER, PROTEIN 136.//7.80E-170//512aa//58%//P52737
  - C-NT2RP3001140//F-SPONDIN PRECURSOR.//9.90E-238//419aa//96%//P35446
  - C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%//P52154
  - C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%//AJ006266
  - C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION.//1.70E-10// 196aa//27%//P53154
  - C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa//33%// P35663
  - C-NT2RP3001221//GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//1.90E-31//353aa//30%//P80193
- 55 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.20E-166//395aa//51%//P14873
  - C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.70E-10//540aa//23%//P32380

- C-NT2RP3001268//Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.//0//3606bp//99%// AF198358
- C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.// 1.30E-99//669bp//83 %//Y18101
- 5 C-NT2RP3001307//Gallus gallus RPE65 mRNA, complete cds.//4.20E-29//530bp//63%//AB017594
  - C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).//2.40E-16//175aa//28%//P51508
  - C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PRO-TEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//3.60E-25//129aa//34%//P32089
  - C-NT2RP3001383//Mus musculus ARL-6 interacting protein-6 (Aip-6) mRNA, partial cds.//3.40E-40//355bp//79%//AF133913
    - C-NT2RP3001384//Homo sapiens mRNA for LA95 protein.//0//1214bp//99%//AJ243467
    - C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.30E-61//374aa//36%//P49711
    - C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52%//P53538

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- C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%//P53009
- 15 C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1.00E-16//77aa//46%//O33529
  - C-NT2RP3001427//WERNER SYNDROME HEUCASE HOMOLOG.//2.70E-10//159aa//33%//O09053
  - C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.40E-128//152aa//99%//P 12270
  - C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITY ANTIGEN MODIFIER 2).//3.20E-90//157aa//59%//P36371
- 20 C-NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds.//4.60E-20//792bp//59%// AF205831
  - C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.10E-13//87aa//43%//P11632
  - C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%//U13395
  - C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.// 0//2295bp//99%//AF064801
    - C-NT2RP3001527//Human Sp140 protein (Sp140) mRNA, complete cds.//4.30E-290//793bp//93%//U63420
    - C-NT2RP3001529//SPO0B-ASSOCIATED GTP-BINDING PROTEIN.//1.00E-61//345aa//42%//P20964
    - C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II.//9.10E-10//158aa// 31%//Q10022
- 30 C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//1.40E-76// 388aa//32%//P46821
  - C-NT2RP3001580//Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds.//0//1730bp//85%//AF163665
- C-NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//2617bp//99%// U35832
  - C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.80E-18//91aa//38%//Q92609
  - C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.80E-09//132aa//31%//O22468
  - C-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1557bp//98%//AJ012449
  - C-NT2RP3001672//Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete cds.//0// 2836bp//99%//AF149046
  - C-NT2RP3001679//Homo sapiens rec mRNA, complete cds.//0//2495bp//99%//AB023584
  - C-NT2RP3001688//Homo sapiens DNA binding protein p96PIF mRNA, complete cds.//0//1869bp//99%// AF173868
  - C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.00000024//481aa//21%// P25386
  - C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.40E-33//161aa//32%//P54356
  - C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.//0//1788bp//99%//AF113534
  - C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58// 1138bp//63%//AF193613
- 50 C-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//1.10E-240//902bp//99%//AF054177
  - C-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.//6.90E-132//774bp//88%//AF008554
  - C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10E-132//294aa//84%//Q14141
- 55 C-NT2RP3001739//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//1.40E-15//190aa//32%// Q09701
  - C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.80E-117//462aa//55%//P52272

- C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.60E-11//348aa//27%//P24733
- C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.40E-18//249aa//30%//Q04652
- C-NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds.//
- 5 C-NT2RP3001855//HOMEOBOX PROTEIN PKNOX1 (HOMEOBOX PROTEIN PREP-1).//8.10E-125//302aa//60%//P55347
  - C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.20E-14//242aa//24%//Q00808 C-NT2RP3001898//Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds.//0//1587bp//100%//AB000624
- 10 C-NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA, complete cds.//4.30E-91//656bp//81%//AF177478
  - C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-22//227aa//33%//P08458 C-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//3.10E-92//314aa//51 %//Q09251
- 15 C-NT2RP3001969//TRICHOHYALIN.//2.70E-11//442aa//23%//P37709
  C-NT2RP3002004//H.sapiens mRNA for FAST kinase.//1.50E-192//475bp//94%//X86779
  C-NT2RP3002007//SAP1 PROTEIN.//1.1 OE-68//474aa//32%//P39955
  C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III.//5.30E-25//139aa//
- 48%//Q09232
  C-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA
  - C SUBUNIT.//1.00E-299//397aa//94%//P18484
    C-NT2RP3002056//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//2.00E-48//475aa//35%//P29374
    C-NT2RP3002062//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0//
  - 3764bp//99%//AF095195
    C-NT2RP3002081//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//4.10E-233//1896bp//69%//AF111423
    - C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%//Q12387

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- C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//2.80E-253//474aa//93%//P15170
- C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.90E-151//223aa//91%//Q02614 C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28%//P45978
  - C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE).//8.60E-49//243aa//43%//Q58767
- C-NT2RP3002330//Homo sapiens eRFS mRNA, complete cds.//0//2443bp//99%//U87791
  C-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.20E-70//590bp//76%//X16396
  - C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR MCM4 (CDC21 HOMOLOG) (P1-CDC21).//8.60E-79//416aa//34%//P33991
- 40 C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16) (THREONINE DEAMINASE).// 3.70E-43//318aa//37%//P05792
  - C-NT2RP3002529//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS45.//8.90E-95//542aa//38%//P38932
- C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III.//5.80E-40//161aa// 52%//Q10010
  - C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//173aa//28%//P11598 C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//
    - 90aal/42%//P38660
- 50 C-NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds.//0//1703bp//99%//AF111109 C-NT2RP3002650//Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds.//0//2109bp//87%// AF165163
  - C-NT2RP3002663//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//8.10E-263//1243bp//
- 55 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%//P13060
  - C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.//0//1596bp//98%//AF151903
  - C-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.10E-93//1205bp//69%//D17577
  - C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.J/1.00E-07//70aa//

41%//P17564

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- C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL83 PROTEIN).//2.50E-55//187aa//39%//Q24371 C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%//Q31125
- C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%// P51026
  - C-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.50E-232//1282bp//85%//AF030430 C-NT2RP3002876//Drosophila melanogaster eyelid (eld) mRNA, complete cds.//1.30E-29//805bp//61%// AF053091
  - C-NT2RP3002909//P53-BINDING PROTEIN 2 (53BP2) (BCL2-BINDING PROTEIN) (BBP).//1.50E-125//512aa//47%//Q13625
  - C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2.00E-111//551aa//42%//Q04652 C-NT2RP3002953//Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds.//0//2388bp//99%//
  - C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2722bp//99%//D89053
- 15 C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.//3.90E-52//899bp//64%//AB029333 C-NT2RP3002988//Homo sapiens lkB kinase-b (IKK-beta) mRNA, complete cds.//1.80E-292//1325bp//99%// AF080158
  - C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mR-NA, complete cds.//0//2656bp//99%//AF084555
- 20 C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp// 82%//U78090
  - C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%//Q02357
  - C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.10E-05//258aa//24%//P23645
  - C-NT2RP3003078//Rattus norvegicus mRNA for ischemia related factor NYW-1, complete cds.//2.60E-112//633bp//88%//AB027149
  - C-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//3.60E-83//807bp//72%// D88315
  - C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds.//0//1998bp//91%//AB011414
- 30 C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%// AF071592
  - C-NT2RP3003145//Mus musculus metallocarboxypeptidase CPX-1 mRNA, complete cds.//0//2251bp//81%//AF077738
  - C-NT2RP3003185//TROPOMYOSIN1, FUSION PROTEIN 33.//2.80E-06//402aa//23%//P49455
- 35 C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.30E-98//269aa//62%//P52742
  - C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I.//5.70E-09//169aa// 31%//Q09674
  - C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//2.00E-210//1851 bp//76%//AF110267
- 40 C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//4.30E-187//1750bp//75%//U20286
  - C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds.//0//2350bp//99%//AB030656
  - C-NT2RP3003242//Homo sapiens stanniocalcin-related protein mRNA, complete cds.//0//2366bp//99%//AF098462
- 45 C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//
  4.20E-86//366aa//48%//P19474
  - C-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//0//2596bp//98%//L36983
  - C-NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.5e-310//1468bp//82%//AB033922
- 50 C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.10E-170//
  585aa//54%//064948
  - C-NT2RP3003313//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mR-NA, complete cds.//0//2476bp//99%//AF117657
  - C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52).//1.30E-35//178aa//44%//Q62191
  - C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//2.80E-07// 161aa//28%//P40084
  - C-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//0//2133bp//85%//U09874

- C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45//782bp//65%//U90653
- C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//743bp//90%//AF071317
- 5 C-NT2RP3003490//Homo sapiens mRNA for putative phospholipase, complete cds.//4.50E-81//649bp//67%// AB019435
  - C-NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.//5.60E-36//842bp//62%//AF091624
  - C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%//P53009
- 10 C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30//
  191aa//40%//P40529
  - C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0//3131bp//94%//AF106681
  - C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%//P35843
- 15 C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%//AB013885 C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//2.20E-13//146aa//42%//P14209
  - C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%//P35446
  - C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%//P24014
- 20 C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%//
  - C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds.//9.00E-238//1529bp//84%//U71294 C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//924bp//89%//AF130457
- 25 C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%//Q07590
  - C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%//P02720
  - C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete cds.//2.2e-316//1436bp//99%//AB020523
- 30 C-NT2RP3003846//Homo sapiens mRNA for putative phospholipase, complete cds.//4.80E-277//1255bp//99%// AB019435
  - C-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//4.50E-147//874bp//87%//U19181 C-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//2.20E-20//76aa//64%//Q09332
- 35 C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0//2191bp//99%// AF086628
  - C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%//X84692 C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%//Q13263
- 40 C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0//1806bp//99%//X76091
  - C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-229//1560bp//78%//AF126747
  - C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-DASE) (1.4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%//P08640
- 45 C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%//AF098948 C-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808 C-NT2RP3004206//CROOKED NECK PROTEIN.//1.40E-220//567aa//67%//P17886
  - C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%// AJ245820

C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-

- 50 C-NT2RP3004209//Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds.//0//2320bp// 99%//AF126736
  - CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.70E-13//118aa//33%//P52734
  - C-NT2RP3004258//Homo sapiens ZIS1 mRNA, complete cds.//0//1861bp//99%//AF065391
- 55 C-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//2.40E-248//1126bp//100%// AF088982
  - C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61%//AF007871 C-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%//

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- C-NT2RP3004378//Drosophila melanogaster separation anxiety protein (san) mRNA, complete cds.//3.90E-38//462bp//70%//AF225902
- C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1.00E-66//364bp//93%//AJ007798

  5 C-NT2RP3004428//CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 (CHD-4) (MI-2 AUTOANTIGEN 218 KD PROTEIN) (MI2-BETA).//5.20E-09//212aa//25%//Q14839

  C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.60E-61//170aa//40%//Q01820
  - C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.30E-113//466aa//
    42%//P34110
- 10 C-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//4.00E-303//1385bp//99%//AB012851
  C-NT2RP3004498//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//2.00E-249//
  1777bp//80%//U83176
  - C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.90E-295//893bp//92%//Y08260 C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.70E-37//190aa//39%//P40484
- 15 C-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//0//2075bp//87%//L11316
  C-NT2RP3004544//THYROID RECEPTOR INTERACTING PROTEIN 10 (TRIP10) (FRAGMENT).//1.00E-22//1.3aa//53%//Q15642
  - C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%//P51523
- C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//3.80E-08//
  150aai/28%.//Q01484
  - C-NT2RP3004572//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//0// 1853bp//99%//AF040701
  - C-NT2RP3004578//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//5.50E-12//396aa//23%//P39922
- C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%//AJ006266
   C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.20E-75//464aa//35%//Q02084
   C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%//
  - AF093097
  - C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.70E-72//254aa// 45%//P54352
    - C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferas e (GlcNAc6ST), complete cds.//0//2393bp//99%//AB014679
    - C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.60E-98//239aa//64%//P35526

KD SUBUNIT).//0//728aa//99%//Q10568

- C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65.//4.90E-51//335aa//37%//Q64375
- C-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//2160bp//99%//AJ012449
  C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%//AB011538
  C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100
  - C-NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.//1.40E-28//296bp//75%//
  - C-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//4.30E-188//1543bp//78%//U35776
  - C-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.00E-71//396aa//36%//P22579
  - C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.90E-15//104aa//40%// P15287
  - C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%//AJ006470 C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.70E-84//208aa//76%//Q03173
  - C-NT2RP4000259//GLUTATHIONE PEROXIDASE.2 (EC 1.11.1.9).//5.50E-29//153aa//43%//O23968
  - C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.50E-297// 1024aa//55%//P87115
    - C-NT2RP4000312//ADENYLATECYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//1.50E-26//237aa//28%//Q01631
    - C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//3.00E-07//101aa//32%//P26372
- 55 C-NT2RP4000367//Homo sapiens lkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0// 4782bp//99%//AF044195
  - C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.60E-77//262aa//54%//075570

- C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%//AJ238243 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.90E-110//435aa//50%//P52738
- C-NT2RP4000415//Drosophila melanogaster fumble (fumble) mRNA, complete cds.//6.20E-19//902bp//57%//AF221546
- 5 C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113)(MAN(9)-AL-PHA-MANNOSIDASE)(FRAGMENT).//2.60E-51//438aa//33%//P45701
  - C-NT2RP4000449//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds.//0//3143bp//99%//AF083106 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//3.00E-07//175aa//27%//P09309
- C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THI10 OLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15).//
  2.50E-37//291aa//38%//P50101
  - C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4).// 1.90E-67//721aai/29%//Q09475
  - C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.80E-50//214aa//50%//P40484
- 15 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.50E-106//495aa//45%//P45818
  - C-NT2RP4000524//Mus musculus Sec8 mRNA, complete cds.//0//3131bp//87%//AF022962
  - C-NT2RP4000528//NPL4 PROTEIN.//9.80E-86//515aa//37%//P33755

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90aa//42%//P38660

- C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.40E-14//233aa//31%//P40319
- C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.90E-188//863bp//99%//AF067730
- C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0.//3.70E-07//175aa//27%//P09309 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE.//1.10E-32//350aa//30%//P39625
- C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.10E-13//295aa// 27%//Q11073
- C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.20E-191//199aa//78%//P10267
  C-NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds.//4.60E-250//1462bp//84%//AF176524
  C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//
  0.000000032//67aa//31%//P53915
- C-NT2RP4000817//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN1,4-ALPHA- GLUCOSI-DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.80E-11//503aa//23%//P08640
  C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.30E-94//810bp//65%//Y18265
  C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.50E-21//271aa//28%//Q00808
  C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMI-
- 35 NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//5.70E-82//324aa//48%//O09175
  C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.10E-85//174aa//55%//P16415
  C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.20E-91//173aa//87%//O35682
  C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME EI (A1S9 PROTEIN).//9.60E-96//513aa//42%//P22314
  C-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//0//2127bp//86%//
  - C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.60E-26// 227aa//36%//Q06828
  - C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-ZYME 1).//1.50E-76//346aa//43%//Q61068
  - C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521
    - C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HEUCASE MJ1505.//1.40E-07//185aa//25%//Q58900 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.40E-26//
- 50 C-NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds.//2.30E-81//389bp//
  100%//AF094583
  - C-NT2RP4000989//UNC-47 PROTEIN.//8.20E-06//173aa//25%//P34579
  - C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700
- 55 C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.70E-16//401aa//26%//P39968
  - C-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//3.50E-257// 1377bp//91%//U67140
  - C-NT2RP4001029//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds.//0//2002bp//98%//

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- C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)//1.50E-92//443aa//44%//Q09996
- C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.70E-51//335aa//37%//Q64375
- 5 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.30E-123// 563aa//46%//P13586
  - C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0//1439bp//99%//AB023967
  - C-NT2RP4001086//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).// 2.30E-07//474aa//22%//P12036
- 10 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAM-INASE) (RNA EDITING ENZYME 1).//2.60E-17//121aa//36%//P51400
  - C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.90E-115//224aa//100%// P38378
  - C-NT2RP4001122/mPD PROTEIN.//1.40E-65//253aa7/41%//O15736
- 15 C-NT2RP4001126/TRICHOHYALIN.//2.90E-18//380aa//26%//Q07283
  - C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18) (SDAP).//2.10E-07//93aa//33%//P44514
  - C-NT2RP4001148//SOF1 PROTEIN.//1.30E-104//236aa//52%//P33750
  - C-NT2RP4001149//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//
- 20 4.40E-187//731bp//100%//AF037339
  - C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).// 3.40E-29//385aa//29%//P35331
  - C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//
    4.70E-29//227aa//35%//P52178
- 25 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.40E-104//1460bp// 65%//U95760
  - C-NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds.//0//2940bp//99%//AF111109 C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.70E-141//511aa//43%//Q99676
  - C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.20E-27//
- 30 90aa//42%//P38660

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- C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.80E-103//508aa//43%//Q04652
- C-NT2RP4001256//Homo sapiens mRNA for gamma tubulin ring complex protein (76p gene).//0//2006bp//100%// AJ249677
- C-NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%// AF174601
- C-NT2RP4001274//Human transporter protein (g17) mRNA, complete cds.//4.40E-58//1196bp//61%//U49082 C-NT2RP4001276//TRICHOHYALIN.//7.90E-09//126aa//32%//Q07283
- C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.90E-17//296aa//29%//P24391
- 40 C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.50E-213//1129bp//92%//
  AJ001119
  - C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//0.000016// 186aa//29%//O24076
  - C-NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.//9.20E-160//736bp//99%//AJ007014
- 45 C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7e-310// 1400bp//100%//AB017494
  - C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.40E-58//2425bp//59%//U53445
  - C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.60E-19//222aa//30%//Q08180
  - C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//9.20E-17//146aa//35%//P18160
  - C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I.//2.00E-53//436aa//30%//Q10085
- 55 C-NT2RP4001389//KESIPROTEIN.//1.70E-31//342aa//34%//P35844
  - C-NT2RP4001407//TRICHOHYALIN.//1.90E-05//298aa//21%//P22793
  - C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.70E-190//422aa//82%//Q14141
  - C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.20E-138//419aa//54%//Q99676

- C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cdsJ/2.70E-66//738bp//71%// AF129131
- C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE EI COMPONENT PRECURSOR (EC 1.2.4.2) (AL-PHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%//Q02218
- 5 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1.00E-27//374aa//29%//P39010 C-NT2RP4001529//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds.//0//2002bp//98%// AF198487
  - C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INTERGENIC REGION.//5.70E-54//242aa//38%//P25656
- 10 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mR-NA, complete cds.//0//3202bp//99%//AF152961
  - C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.70E-09//216aa//24%//P96902
  - C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//5.40E-07//213aa//26%//Q02453
  - C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.80E-10//109aa//36%//P35197

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- 15 C-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//0//874aa//
  96%//P53620
  - C-NT2RP4001575//Rattus norvegiqus mRNA for ARE1 protein.//0//1087bp//87%//AJ223830 C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS).// 1.70E-141//373aa7/47%//P73505
- 20 C-NT2RP4001634//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//2.80E-14//652aa//22%//Q02224
  C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.10E-46//234aa//32%//
  P40469
  - C-NT2RP4001644//MYOSIN UGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.40E--19//111aa//45%//P25323 C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN).//1.10E-45//310aa//27%// P12868
  - C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//4.00E-10//243aa//25%//Q10568
  - C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3.00E-10//128aa//32%//Q10282
- 30 C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//6.40E-170//1168aa//33%//Q09332
  - C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.90E-236//665aa//58%//P51523
  - C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//4.10E-16//263aa//27%//P98174
  - C-NT2RP4001790//Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds.// 0//3053bp//99%//AF170025
  - C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYC-OPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//241aa//30%//O35566
- 40 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.10E-19//77aa//54%//P55083 C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.30E-99//555bp//73%// AF155595
  - C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-85//489aa//43%//P55194 C-NT2RP4001861/HTUCHOHYALIN.//1.00E-35//307aa//34%//P37709
- 45 C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.40E-08//345aa7/25%//Q00808
  - C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.30E-38//258aa//32%//Q12024 C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.80E-60//303aa//38%//P49711
  - C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISO-
- ASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.50E-13//211aa//28%//Q43209
  C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.20E-13//356aa//27%//P13816
  C-NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds.//0//3203bp//87%//AF195418
  C-NT2RP4001975//Homo sapiens golgi membrane protein GP73 mRNA, complete cds.//0//3024bp//99%//
- 55 C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.90E-24//370aa//27%//Q04652 C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-168//601aa//52%//O67618 C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13)// 1.00E-137//679aa//40%//O43143

- C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.00E-150//722aa// 39%//Q05481
- C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND PI 9 SUBUNITS) (TFIIA-42) (TFIIAL).//6.70E-06//250aa//31%//P52655
- 5 C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.50E-63//159aa//53%//P38938
  - C-NT2RP4002791//NUCLEOPROTEIN TPR.//6.50E-05//659aa//23%//P12270
  - C-NT2RP5003461//RLR1 PROTEIN.//9.70E-22//177aa//27%//P53552

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- C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.50E-15//280aa//27%//Q00808
- C-NT2RP5003500//Mus musculus mRNA for heparan sulfate 6-sulfotransferase 2, complete cds.//1.30E-237//820bp//87%//AB024565
  - C-NT2RP5003506//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//0// 2289bp//99%//AF095448
  - C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.30E-23//219aa//40%//P37116
- 15 C-OVARC1000001//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp// 99%//AB029290
  - C-OVARC1000006//HISTONE H2A.1.//1.10E-55//117aa//99%//P02262
  - C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//4.20E-06//102aa//32%// O14727
- 20 C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cdsJ/2.60E-295//1393bp//97%//AF058922 C-OVARC100066//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//3.20E-07//60aa//45 %//P80022
  - C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//727bp//67%//AF156957
- 25 C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761
  - C-OVARC1000087//HISTONE MACRO-H2A.1.//1.60E-12//174aa//26%//Q02874
  - C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).// 8.40E-14//259aa//30%//P51610
  - C-OVARC1000106//TROPOMYOSIN 1, FUSION PROTEIN 33.//0.000032//165aa//27%//P49455
- C-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//120aa//32%//Q13107
  - C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Spl.// 2.50E-95//461bp//98%//AJ242975
- 35 C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.80E-32//511bp//65%// AF068332
  - C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.20E-120//351aa//54%//Q16665
- C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)(LEU40 CINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III)(AMINOPEPTIDASE YSCI).//5.40E-53//384aa//
  30%//P14904
  - C-OVARC1000304//PROTEIN MOV-10.//1.10E-249//519aa//87%//P23249
  - C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.70E-40//154aa//38%//P29363
  - C-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//9.20E-148//787bp//76%//U19614
  - C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.90E-14// 200aa//27%//P40004
  - C-OVARC1000437//TENSIN.//7.90E-181//340aa//84%//Q04205
  - C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.20E-25//227aa//25%//P11075
- 50 C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).//3.10E-10//125aa//35%//P51452
  - C-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//0//1872bp//89%//D87671
  - C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.20E-157//892bp//91%//AF051850
  - C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2) (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//Q15349
- 55 (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//Q15349
  C-OVARC1000564//Homo sapiens sorting nexin 5 (SNX5) mRNA, complete cds.//1.0e-310//1440bp//98%//
  AF121855
  - C-OVARC1000649//Human squamous cell carcinama of esophagus mRNA for GRB-7 SH2 domain protein, com-

plete cds.//0//1812bp//98%//D43772

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- C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888
- C-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).// 1.10E-209//293aa//95%//P39098
- 5 C-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//0//759bp//98%//AF038661
  - C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%//P25159
  - C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11//74aa//37%//P49596
- 10 C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.10E-46//121aa//79%//P08886
  - C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSE REGULATED PROTEIN) (GRP 75).//3.90E-46//78aa//98%//O35501
  - C-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//2.80E-258//1183bp//99%//Y17711
  - C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199
- 15 C-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//0//2095bp//99%//AF045584
  - C-OVARC1000862//M.musculus mRNA for FT1.//5.90E-226//1498bp//81%//Z67963
  - C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//2.20E-50//206aa//52%//P40484
  - C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.).//1.30E-32//170aa//34%//P37440
  - C-OVARC1000915//Homo sapiens histone deacetylase 5 mRNA, complete cds.//1.60E-121//591bp//97%// AF132608
  - C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP37).//0.0000054//135aa//28%//P03398
  - C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10//61aabp//49%//P32943
  - C-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//0//1961bp//82%//AB005549
- 25 C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.20E-17//127aa//33%//Q58343
  - C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-11//189aa//32%//Q06527
  - C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.50E-178//1113bp//86%//AF001533
  - C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%//AJ130978
  - C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN
- 30 EPS15) (AF-1P PROTEIN).//1.10E-08//216aa//23%//P42566
  - C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSORS.//1.90E-35//76aa//98%//P43490
  - C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1.00E-215//1027bp//98%//AF132946
  - C-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//0//1819bp//99%// AF082657
- 35 C-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))-//2.00E-214//769bp//97%//AJ005897 C-OVARC1001107//Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds.//6.10E-276//594bp//98%//AF167572
  - C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//5.1e-310//1588bp//93%// AF051782
  - C-OVARC1001154//Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds.//2.30E-296//1561bp// 93%//AF055008
  - C-OVARC1001171//Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds.//5.70E-151//436bp//92%//U94855
- 45 C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.10E-11//221aa//25%//P48510
  - C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%//AJ132192
  - C-OVARC1001232//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//5.10E-22//83aa//37%//Q10568
  - C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%// x62083
  - C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).// 0.0000014//224aa//26%//P25976
  - C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN.//0.00000073//247aa//27%//P18444
  - C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-110//207aa//99%//P09058
- 55 C-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.00E-252//1146bp//99%//AF034801
  - C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//6.00E-148//683bp//99%//AJ224819
  - C-OVARC1001417//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP170

- mRNA, complete cds.//0//1715bp//99%//AF135802
- C-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.90E-48//586bp//69%//U52426
- C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%//Q03111
- C-OVARC1001476//Mus musculus YGR163w mRNA homologue, complete cds.//1.80E-187//510bp//89%// AB017616
  - C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//0//1876bp//98%//AF016507
  - C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//0//777aa//91%//P98161
- 10 C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.40E-19//130aa//40%//P53081
  - C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%//AF031165
  - C-OVARC1001610//Homo sapiens choline/ethanolaminephosphotransferase (CEPT1) mRNA, complete cds.//0// 1870bp//99%//AF068302
- 15 C-OVARC1001703//Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds.//3.50E-16//399bp// 61%//AF133670
  - C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//2.80E-10//106aa//38%//Q62267
  - C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DI-AZEPAM BINDING INHIBITOR) (MA-DBI).//4.40E-40//195aa//41%//P07106
  - C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.30E-16//116aa//43%//Q13796
  - C-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.//4.00E-122//282aa//85%//P08942
  - C-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//6.40E-85//514aa//34%//P12945
  - C-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.// 0//963bp//99%//U97670
  - C-OVARC1001809//Mus musculus sphingosine kinase (SPHKla) mRNA, partial cds.//2.70E-190//1624bp//76%// AF068748
- 30 C-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMI-NO, ACETYLTRANSFERASE 1).//3.10E-81//497aa//35%//P12945
  - C-OVARC1001943//Mus musculus DEBT-91 mRNA, complete cds.//0//2035bp//87%//AF143859
  - C-OVARC1001987//Homo sapiens protactin regulatory element-binding protein (PREB) mRNA, complete cds.// 0//1083bp//99%//AF203687
- 35 C-OVARC1002050//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//0//1019bp//99%// AB029290
  - C-OVARC1002112//HISTONE MACRO-H2A.1.//3.00E-174//371aa//90%//Q02874
  - C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRI-ER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.40E-52//306aa//35%//
  - C-OVARC100213 8//SAP1 PROTEIN.//7.60E-60//128aa//59%//P39955
  - C-OVARC1002156//Danio rerio uridine kinase mRNA, complete cds.//6.00E-16//262bp//64%//AF195851
  - C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%//P31213
- 45 C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-09//207aa//30%//Q91854
  - C-PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.//0//2365bp//99%//AB019602
  - C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN-
- 50 ZYME).//1.60E-81//212aa//70%//P34547

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- C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.40E-17//185aa//32%//P08643
- C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.90E-54//190bp//94%//L22154
- C-PLACE1000066//SSU72 PROTEIN.//1.10E-39//206aa//43%//P53538
- C-PLACE1000081//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//0//2077bp//99%//U63127
- 55 C-PLACE1000133/TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//
  1.80E-62//158aa//81%//P20290
  - C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.80E-29// 134aa//43%//P52046

- C-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.30E-305//1417bp//98%//AF058291
- C-PLACE1000185//Homo sapiens mRNA for N-Acetylglucosamine kinase.//4.90E-258//1183bp//99%//AJ242910 C-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSI-
- 5 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%//P08640 C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%//AJ224979
  - C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.70E-30//352aa//31%//P15151
- C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.20E-132//334aa//72%//P23246
- 10 C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).// 2.80E-06//134aa//29%//P53368
  - C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//2041bp//87%// U35245
  - C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-241//1124bp//98%//AF135421
  - C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%//P51522
  - C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//1.60E-270//437aa//86%//P32455
- 20 C-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1540bp//99%//AJ012449 C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%//P52918
  - C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.00E-55//779bp//67%//AF044201
  - C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.20E-39//261aa//27%//Q08891

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- 25 C-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1992bp// 99%//AF180371
  - C-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLC110F1857Q7 (RZPD Berlin)).//2.10E-277//1260bp//99%//AJ005896
  - C-PLACE1000706//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//0//1366bp//99%//AF119043
  - C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds.//4.60E-250//1189bp//97%//AB028449 C-PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.//0//1985bp//98%//AF132952
  - C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%//P52734
- 35 C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.70E-07//251aa//24%//P23645 C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W.//2.50E-49//181aa//54%//P32899
  - C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.60E-19//404aa//26%//P39010 C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.40E-22//129aa//35%//Q03070
- 40 C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-153//326aa//64%//P52742
  - C-PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds.//5.90E-278// 1476bp//92%//AF110195
  - C-PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial.//0//1988bp//99%//AJ131721
    C-PLACE1001054//Homo sapiens mRNA for RuvB-like DNA helicase TIP49b, complete cds.//4.00E-300//
    1355bp//100%//AB024301
  - C-PLACE1001062//Homo sapiens mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase, partial CDS.//1.60E-207//742bp//99%//AJ007714
  - C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%//AF065485
- C-PLACE1001104//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//6.80E-18// 529aa//23%//Q99323
  - C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%//P52742
  - C-PLACE1001171//MYOTUBULARIN.//7.10E-84//198aa//73%//Q13496
  - C-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.00E-202// 1333bp//80%//D14336
- 55 C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.30E-54//257aa//46%//Q04652
  - C-PLACE1001294//Mus musculus XY body protein (Xybp) mRNA, complete cds.//6.20E-223//1092bp//78%// AF120207
  - C-PLACE1001304//Homo sapiens C2H2 (Kruppel-type) zinc finger protein mRNA, complete cds.//0//2145bp//

99%//AF159567

- C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//5.90E-228//827bp//99%//
- C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQ-UIEM).//3.00E-33//138aa//42%//Q61103
- C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.30E-61// 132aa//46%//Q12929
- C-PLACE1001517//Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete cds.//4.60E-112//392bp//87%//AB002137
- 10 C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.70E-130//244aa//99%//Q60809
  C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-118//429aa//48%//
  PS1523
  - C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.30E-66//174aa//45%//P91408 C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//4.00E-81//263aa//56%//P08635
- (THIOESTERASE II).//4.00E-81//263aa//56%//P08635

  C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HEUCASE PL10.//3.50E-75//439aa//41%//P16381

  C-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//2602bp//99%//AF061243

  C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//2900bp//99%//AJ006276
- 20 C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.40E-63//427aa//35%//Q57290
  - C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.// 0//1995bp//99%//AF058953
  - C-PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.//3.30E-31//925bp//62%//AF159159
- 25 C-PLACE1001869/L-RIBULOKINASE (EC 2.7.1.16).//2.00E-27//270aa//31%//P94524
  C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%//AF099935
  C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-GRPE INTERGENIC REGION.//7.50E-16//
  319aa//26%//P37908
  - C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091
- 30 C-PLACE1002046//UGATIN (FRAGMENT).//1.70E-240//560aa//80%//Q61211
  - C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE),//5.30E-07//188aa//29%//P49606
  - C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.50E-58//112aa//100%// O76094
- 35 C-PLACE1002140//Rattus norvegicus apelin mRNA, complete cds.//1.40E-43//425bp//74%//AF179679 C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%//P32591
  - C-PLACE1002395//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//7.90E-100//966bp//75%//AB030505
- 40 C-PLACE1002433//CHROMOSOME ASSEMBLY PROTEIN XCAP-E.//5.10E-05//278aa//24%//P50533
  - C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%//P41233
  - C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//4.20E-06//133aa//29%//Q13105
  - C-PLACE1002450//Human zinc finger protein mRNA, complete cds.//0//2565bp//99%//U69274
  - C-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//0//2092bp//84%//U69262
- 45 C-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//1.70E-113//545bp//98%//AF042273
  - C-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.90E-58//465bp//80%// U50927
  - C-PLACE1002532//HOMEOBOX PROTEIN DLX-5.//1.20E-152//289aa//96%//P70396
- C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5.00E-99//386aa//48%//P45890
  C-PLACE1002583//GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUR-6) (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMENT).//5.60E-34//76aa//98%//
  - P39087 C-PLACE1002591//CORONIN-UKE PROTEIN P57.//4.40E-70//208aa//66%//P31146
- 55 C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//5.50E-17//76aa//56%//P45340
- C-PLACE1002655//ADSEVERIN (SCINDERIN) (SC).//2.50E-278//543aa//92%//Q28046
  - C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%// AF079765

- C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0// 1750bp//99%//AF068180
- C-PLACE1002714//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//9.40E-13//500aai/21%//Q99323
- 5 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9.00E-45//305aa//33%// Q15391
  - C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-13//272aa//28%//P55201
  - C-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.80E-43//385bp//77%// U50927
- 10 C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-48//217aa//46%//P53973
  C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.50E-203//396aa//86%//
  P51522
  - C-PLACE1002908//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds.//0//1654bp//99%// AB028600
- C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.40E-78//496aa//37%//Q49091
  C-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//8.50E-44//225bp//100%//AF032387
  C-PLACE1003045//POLYCYSTIN 2 (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE TYPE II PROTEIN) (POLYCYSTWIN) (R48321).//1.70E-05//150aa//24%//Q13563
- C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.60E-79//253aa//60%//Q13268
  C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.80E-37//143aa//51%//P42743
  C-PLACE1003176//Homo sapiens clone pHN1868 tyrosyl-DNA phosphodiesterase protein (TDP1) mRNA, partial cds.//1.70E-148//687bp//99%//AF182003
- 25 C-PLACE1003190//SOF1 PROTEIN.//1.90E-110//325aa//48%//P33750 C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//4.90E-76//309aa//47%//

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- C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//7.90E-22//70aa//47%//P21541
- C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.90E-206//396aa//86%// P51522
- C-PLACE10033537/Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%//U92715
- C-PLACE1003366//Homo sapiens otoferlin (OTOF) mRNA, complete cds.//1.40E-78//542bp//67%//AF107403
  C-PLACE1003394//Homo sapiens RAB14 protein (RAB14) mRNA, complete cds.//2.60E-139//648bp//99%//AF152463
- 35 AF152463
  C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//1.30E-40//278aa//36%//P40556
  C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//1.70E-23//322aa//26%//Q13201
  C-PLACE1003519//H.sapiens hnRNP-E2 mRNA.//5.10E-218//905bp//99%//X78136
  - C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.0000011//101aa//32%//
    - C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-NENT).//7.70E-68//404aa//33%//P32802
  - C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//2.60E-93//270aa//66%// P46975
    - C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.90E-278//1275bp//99%//D83200
    - C-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//0.00000023//82aa//35%//Q02516
    - C-PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//6.20E-169//683bp//99%//AF191338
- 50 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.20E-10//380aa//25%//P18824 C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30%//P22793
  - C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8.00E-19//209aa//34%//Q08170
  - C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA complete cds.//6.20E-282// 1316bp//98%//AF053305
  - C-PLACE1003738//ZINC FINGER PROTEIN 135.//9.60E-118//350aa//46%//P52742
  - C-PLACE1003760//Homo sapiens tetraspanin TM4-A mRNA, complete cds.//5.20E-289//1313bp//97%// AF133423

- C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANS-FERASE).//3.70E-222//651aa//66%//P25500
- C-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//6.70E-113//501aa//46%// P10895
  - C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP-AMMONIA LIGASE) (CTP SYNTHETASE).//1.40E-243//584aa//74%//P17812
  - C-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE-TRNA UGASE) (ARGRS).//2.40E-108//581aa//40%//Q05506
- 10 C-PLACE1003923//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//0// 1670bp//99%//AF033120
  - C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).// 2.40E-124//326aa//73%//P80385
  - C-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//0//2384bp//86%//AF032666
- 15 C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4),//6.10E-181//340aa//96%//P29387
  - C-PLACE1004149//Rattus norvegicus GERp95 mRNA, complete cds.//3.30E-41//452bp//65%//AF195534
  - C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%//AJ010071
  - C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.50E-10//208aa//27%//Q62556
- 20 C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.// 0//1882bp//99%//AF069493
  - C-PLACE1004256//Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.//2.00E-93//960bb//76%//AF115778
  - C-PLACE1004258//Homo sapiens vanilloid receptor-like protein 1 (VRL-1) mRNA//0//1144bp//98%//AF129112
- 25 C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.70E-36//389aa//31%//O15393 C-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//0//1498bp//99%// AF084830
  - C-PLACE1004302//SOF1 PROTEIN.//1.90E-110//325aa//48%//P33750
  - C-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//0//1767bp//99%//Y11588
- 30 C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0// 2512bp//99%//AF100153
  - C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.20E-39//385aa//33%//Q63448
  - C-PLACE1004437//Human NAD\*-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//985bp//99%//U49283
- 35 C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%//P25823
  - C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1)7/2.90E-56//276aa//41%//P51522
  - C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds.//2.10E-16//402bp//62%//U90878
- 40 C-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.// 3.40E-227//1037bp//99%//AF040701
  - C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.//3.50E-274//1305bp//97%//AF132954 C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%//Q10568
- 45 C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.70E-18//264aa//32%//Q13438

- C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.40E-42//985bp//59%//X66277
- C-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.30E-195//982bp//96%//AF035606
- 50 C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPONENT) (N- RECOGNIN).//4.40E-35//578aa//27%//O60152
  - C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds.//7.10E-224//790bp//98%//AB022918
  - C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.90E-32// 259aa//32%//P30337
  - C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN.//5.20E-47//577aa//25%//P10267 C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//4.70E-65//695aa//29%//Q01631

- C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.90E-19//196aa//36%//Q08170
- C-PLACE1004868//MALE STERILITY PROTEIN 27/3.90E-39//261aa//27%//Q08891
- C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE
- 5 SPAC10F6.02C.//9.30E-11//94aa//47%//O42643

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- C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A).//4.90E-48//198aa//44%// P06151
- C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds//0//1853bp//98%//AF099936 C-PLACE1004937//SEL-10 PROTEIN.//6.30E-125//357aa//58%//Q93794
- 10 C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2.00E-14//205aa// 26%//Q11073
  - C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6e-313//1413bp//99%//AF132950 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.60E-56//565aa//30%//Q04652
  - C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//
  - C-PLACE1005187//APAG PROTEIN.//3.80E-13//122aa//36%//P05636
  - C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.30E-27//349aa//32%// Q01577
  - C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.30E-13//269aa//28%//P53352
- 20 C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111// 226aa//92%//P08760
  - C-PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds.//1.20E-226//748bp//95%//AF209931
    C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYN-
  - THASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.60E-09//194aa//27%//033335
  - C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4\* (PBP 4\*) (PBP 4A).//1.10E-09//93aa//31%//P32959
    C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//
    AJ006276
    - C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.60E-52//173aa//57%//Q09251
    - C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.// 7.60E-97//1287bp//67%//AJ010046
    - C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-11//60aa//48%//P46288
    - C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPQ (P135 PROTEIN) (IER 2.9/ER2.6).//
- 6.80E-09//267aa//30%//P29128
  C-PLACE1005611//Mus musculus mRNA for mDj10, complete cds.//2.00E-33//379bp//66%//AB028860
  - C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//AF083255
  - C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLE-OTIDE REDUCTASE).//2.10E-148//321aa//83%//P31350
    - C-PLACE10057277/Homo sapiens STRIN protein (STRIN) mRNA, complete cds.//2.00E-118//378bp//98%// AF162680
    - C-PLACE1005739/INTERFERON-GAMMA INDUCIBLE PROTEIN MG11///1.30E-237//585aa//72%//Q60710
      C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14)
  - (THIOESTERASE II).//2.50E-79//209aa//53%//P08635
    C-PLACE1005803//Homo sapiens mRNA for transcription factor (SMIF gene).//0//1985bp//99%//AJ275986
    C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.10E-217//994bp//99%//
    - C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482
- 50 C-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//730aa//99%//Q10568
  - C-PLACE1005890//BEM46 PROTEIN (FRAGMENT).//9.90E-42//224aa//43%//P54069
  - C-PLACE1005921//AIG1 PROTEIN.//3.00E-31//284aa//31%//P54120
  - C-PLACE1005951//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.// 1.10E-264//661bp//99%//AF203687
  - C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.70E-30//198aa//37%//P43636
    - C-PLACE1005955/VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)//5.40E-54//455aa//32%//P14904

- C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90)7/1.40E-07// 254aai/25%//P38129
- C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.//2.40E-177//829bp//99%//AF151852
- C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%//AJ236876
- 5 C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.70E-161//744bp//99%//X99906
  - C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.50E-148//681bp//99%//
  - C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//2.00E-28//236aa//30%//P98110
  - C-PLACE1006167//PAF1 PROTEIN.//7.30E-15//437aa//24%//P38351
  - C-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.70E-169//373aa//88%//P17427
- 15 C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.70E-116//496aa//48%//Q09747 C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2.00E-16//244aa//31%// P28675
  - C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMA-LEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM).//
- 20 4.60E-117//147aa//80%//P21796

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- C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds.//3.00E-07//376bp//59%//U76374
  C-PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds.//0//1649bp//99%//AF155112
  C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//
  1.30E-18//460aai/24%//Q00547
- C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//o//1168bp//99%//AF062085
   C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.50E-45//122aa//43%//P49910
   C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.20E-83//313aa//49%//P27550
   C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.70E-55//142aa//85%//Q90595
- 30 C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.10E-229//367aa//96%//Q00004
  - C-PLACE1006492//Homo sapiens transmembrane protein 2 (TMEM2) mRNA, complete cds.//0//2618bp//99%// AF137030
  - C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.//0// 2170bp//99%//AF191338
    - C-PLACE1006531//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//1967bp//99%// AF093097
    - C-PLACE1006534//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41)(PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE)(UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAM-
- INYLTRANSFERASE) (GALNAC-T1).//8.30E-08//100aa//41%//Q10472
  C-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.20E-09//426aa//21%//P39922
  C-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//
  0//1464bp//99%//U97670
  - C-PLACE1006626//Homo sapiens mRNA for Helicase-MOI, complete cds.//0//1760bp//99%//AB028449
- 45 C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.80E-24//734bp//62%//AB015630
  - C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.90E-13//177aa//33%//Q59263
  - C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).// 6.20E-63//191aa//43%//P13688
    - C-PLACE1006819//UNE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.80E-213//232aa//80%//P08547
      C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTE-RASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUI-
- TOUS NUCLEAR PROTEIN).//2.00E-15//188aa//29%//P35123

  C-PLACE1006878//TRNA-SPLICING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDONUCLEASE).//1.90E-08//122aa//36%//P16658
  - C-PLACE1006917//HSH49 PROTEIN.//5.50E-12//97aa//35%//Q99181
  - C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.70E-48//278aa//41%//

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- C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.30E-86//522aa//36%//P97998
- C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%// AR023421
- 5 C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.20E-35//180aa//33%//Q14542
  - C-PLACE1007105//Homo sapiens muskelin (MKLN1) mRNA, complete cds.//0//2449bp//98%//AF047489 C-PLACE1007140//TRICHOHYALIN.//1.30E-25//816aa//22%//P37709
  - C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-)
- 10 (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1.00E-42//370aa//31%//P54304
  - C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.50E-216//1068bp//96%//D50495
    - C-PLACE1007243//UNC-47 PROTEIN.//1.70E-07//211aa//27%//P34579
    - C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%//Y15908
- 15 C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.10E-17//1037bp//56%// AF117649
  - C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%//AF096870
  - C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa// 30%//P27715
  - C-PLACE1007409//WHTTE PROTEIN.//1.10E-64//428aa//32%//Q17320
  - C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.80E-25//140aa//35%//P27487
  - C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FA-
- 25 CIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.40E-53//426aa//33%//P52734
  - C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.40E-85// 385aa//45%//P08728
  - C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316// 1485bp//98%//AF159164
- 30 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1.00E-49//361aa// 36%//P34537
  - C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.60E-143//666aa//44%//Q99676
  - C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//1.00E-07//228aa//31%//P32506
  - C-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSI-
- 35 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%//P08640
  - C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//
    8.70E-09//279aa//28%//Q26457
  - C-PLACE1007697//GCN20 PROTEIN.//7.60E-119//717aa//38%//P43535
  - C-PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//82%//
  - C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%//AF061243 C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.50E-44//231aa//42%//P10265
    - C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%//AB019602
    - C-PLACE1007897//Homo sapiens FLASH mRNA, complete cds.//0//2145bp//99%//AF154415
- 45 C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.60E-14// 370aa//25%//Q99323
  - C-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION.//6.70E-13// 168aa//31%//P38226
  - C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//
  - C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0//2300bp//99%//AF079529
  - C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.10E-36//202aa//48%//P52272
- 55 C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSYN-110) (SYNAPTIC DEN-SITY PROTEIN PSD-93).//6.10E-14//128aa//39%//Q63622
  - C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NU-CLEOPORIN) (P105).//4.6e-318//613aa//94%//P52590

- C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179
  C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.).//3.00E-25//208aa//37%//Q03326
  C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.30E-24//395aa//31%//Q09531
- 5 C-PLACE1008177//TRICHOHYALIN.//2.30E-29//487aa//26%//P37709
  C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077
  C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808
  C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.30E-283//671aa//77%//P53620
- 10 C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.30E-18//162aa//37%//P12689 C-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//5.20E-137//672bp//77%//AF078779
  - C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PROTEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN-10).//2.20E-23//94aa//47%//Q05315
- 15 C-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds.7/1.90E-170//780bp//100%//AF036144
  - C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.30E-26//309aa//30%//Q04652 C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.30E-114//243aa//87%//P05432
  - C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRAN-SCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%//P41541
  - C-PLACE1008426//RESTIN (CYTOPLASMIC LINKER PROTEIN-170) (CLIP-170).//1.80E-11//365aa//25%// O42184
  - C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.10E-11//189aa//32%//Q06527

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- C-PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).//6.60E-243//1102bp//99%//AJ277275
- 25 C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.10E-09//62aa//48%//P22620
  - C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NU-CLEOPORIN) (P140).//7.80E-236//453aa//96%//P37199
  - C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591
- 30 C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (III HEAVY CHAIN H2).//5.20E-90//483aa//38%//O02668 C-PLACE1008650//PRL1/PRL2-LIKE PROTEIN.//2.00E-127//354aa//62%//O13615
  - C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF03 8406
- 35 C-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//0//1670bp//99%//AF060543 C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein radlA.//2.30E-269//1225bp//99%// AJ004974
  - C-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//8.80E-268//1171bp//90%//AF032668 C-PLACE1009020//NIFS PROTEIN.//3.90E-55//279aa//41%//P12623
- 40 C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112 C-PLACE1009060//BRO1 PROTEIN.//6.70E-19//567aa//24%//P48582 C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.90E-44//480aa//
  - 30%//P30432 C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.10E-179//452aa//67%//P51814
- 45 C-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds.//
  0//2529bp//99%//AF035586
  - C-PLACE1009130/UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2.00E-68//181aa//43%//Q05086
  - C-PLACE1009158//Mus musculus mRNA for death inducer-obliterator-1 (Dio-1).//5.40E-200//1790bp//75%//
    AJ238332
  - C-PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.//9.60E-255// 1179bp//98%//AF150105
  - C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%//P29675
  - C-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//2.00E-78//262aa//43%//
  - C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%//P14922
    C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.10E-132//1229bp//75%//AF107295

- C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX27/2.50E-10//151aa//29%//Q12067
- C-PLACE1009398//ZINC FINGER PROTEIN 135.//6.20E-97//361aa//51%//P52742
- C-PLACE1009404/HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//4.70E-08//165aa// 33%//Q09820
- 5 C-PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds.//1.00E-173//1367bp//77%// AF176523
  - C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.80E-71//82aa//89%//P42356
  - C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.10E-289//550aa//93%//P54319
- 10 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//3.90E-40//
  179aa//37%//P34580
  - C-PLACE1009477//Homo sapiens ubiquitin-fusion degradation protein 2 (UFD2) mRNA, complete cds.//6.60E-147//592bp//99%//AF043117
  - C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR)7/8.10E-99//228aa//75%//Q99418
  - C-PLACE1009571//Homo sapiens PTD002 mRNA, complete cds.//5.90E-185//857bp//99%//AF078857
    - C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.10E-54//291aa//40%//Q00808
    - C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.30E-60//209aa//41%//P25159
  - C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.50E-285//538aa//99%// P55161
    - C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp//100%//AF062534
      C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN
    - CHROMOSOME I.//7.00E-33//166aa//43%//Q09876 C-PLACE1009721//MSF1 PROTEIN.//1.70E-22//176aa//33%//P35200
- 25 C-PLACE1009731//AIG1 PROTEIN.//1.60E-22//274aa//28%//P54120
  - C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds.//4.30E-294// 1329bp//100%//AB012190
  - C-PLACE1009798//RLR1 PROTEIN.//1.60E-18//270aa//23%//P53552
  - C-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.30E-59//405aa//33%//
  - C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-).//6.50E-28// 209aa//38%//P43510
    - C-PLACE 1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION.//1.90E-108//277aa//43%//P53145
- 35 C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds.//0//1730bp//99%//AF038963 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.60E-59//450aa//34%// P28175
  - C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.20E-70//736bp//73 %//U48288
- C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//6.00E-279//1402bp//94%//X84692
   C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%//AF065482
   C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.40E-268//506aa//98%//Q62671
  - C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.30E-114//537aa//44%//Q04652
- C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR
- SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.70E-20//156aa//42%//P22082
  C-PLACE1010148//CYUCIN I (MULTIPLE-BAND POLYPEPTIDE I).//4.60E-07//431aa//23%//P35662
  - C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPUCING COMPONENT, 35 KD) (PR264 PROTEIN).//9.80E-11//95aa//49%//Q01130 C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).//
  - 5.1 OE-27//371aa//28%//Q14246
    - C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.60E-77//214aa//62%//P25722
    - C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.20E-18//467aa//30%//P46804 C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//
- 55 1.10E-09//350aa//22%//P52178

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C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).//2.00E-09//126aa//29%//P34024 C-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds//0//2082bp//91%//AF003927

- C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.// 0//1981 bp//99%//AB022718
- C-PLACE1010529//Homo sapiens TANK binding kinase TBK1 (TBK1) mRNA, complete cds.//0//1750bp//99%// AF191838
- 5 C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//1.20E-07//616aai/24%// P25386
  - C-PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.//8.80E-300//1359bp//99%// AF191771
- C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//
  1904bp//99%//AB017546
  - C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.00000016//120aa//28%//P02642 C-PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.//7.50E-08//324bp//64%//AF109907
  - C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS 13.//5.70E-75//423aa//39%//Q01755
- 15 C-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//1.80E-222//808aa//52%//Q09332
  - C-PLACE1010702//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//5.20E-151//427aa//55%//P28160 C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4.00E-299//1091bp//99%//AB019987
- 20 C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.90E-91//668bp//82%// AF020267
  - C-PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.//0//1448bp//99%//AB034205
  - C-PLACE1010771//M.musculus HCNGP mRNA.//7.40E-168//966bp//89%//X68061
- 25 C-PLACE1010811//Rattus norvegicus mRNA for protein encoded by bdeight gene, partial.//1.60E-217//858bp// 87%//AJ010392
  - C-PLACE1010833//CALTRACTIN(CENTRIN).//0.0000001//154aa//28%//P41209
  - C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.30E-143//407aa//58%//005481
- 30 C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.50E-25//583aa// 23%//P35580
  - C-PLACE1010926//HYPOTHETICAL 72.2 KD PROTEIN C12C2.05C IN CHROMOSOME II.//7.60E-23//103aa//53%//Q09746
  - C-PLACE1010942//Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds.//0//1440bp//99%//AF114487
    - C-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//5.30E-98//297aa//48%//P45890
    - C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha protein, complete cds.//0//1701bp//97%//AB015019 C-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC
  - 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).//0//646aa//97%//P10894
- 40 C-PLACE1011056//HISTONE HI, GONADAL.//6.80E-13//154aa//37%//P02256

- C-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEFG).//1.50E-22//63aa//88%//Q07803
- C-PLACE10111114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//2.90E-71//190aa//44%//Q03532
- C-PLACE1011160//Homo sapiens HFB30 mRNA, complete cds.//0//1691bp//99%//AB022663
- 45 C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.//1.30E-89//167aa//100%//P03830
  - C-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.).//3.20E-12//212aa//29%//Q03326
  - C-PLACE1011229//Homo sapiens ubiquitin-specific protease homolog (UPH) mRNA, complete cds.//2.30E-152//701bp//99%//AF153604
  - C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//3.50E-20//496aa//25%//P10587
- 50 C-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//7.20E-151// 697bp//99%//AF102265
  - C-PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.//1.20E-74//380bp//97%//AB019602
  - C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.70E-78//383aa//39%//Q61703
- 55 C-PLACE1011399//Homo sapiens CGI-72 protein mRNA, complete cds.//3.20E-90//427bp//99%//AF151830
  - C-PLACE1011433//TRANSCRIPTION FACTOR IIIA (FACTOR A) (TFIIIA).//3.00E-10//236aa//25%//P34695
  - C-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2040bp//99%//AF065482
  - C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//

4.90E-11//147aa//32%//P52178

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- C-PLACE1011576//Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds.//0//1791bp//82%//
- C-PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds7/4.10E-259//1538bp//87%//AF177476
  - C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (3OST3B1) mRNA, complete cds.//0//1559bp//99%//AF105377
  - C-PLACE1011664//CROOKED NECK PROTEIN.//1.60E-187//505aa//64%//P17886
- C-PLACE1011858//Homo sapiens BAG-family molecular chaperone regulator-2 mRNA, complete cds.//1.30E-255//1179bp//99%//AF095192
  - C-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%//U61969
  - C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//1.30E-15//409aa//27%//P35580
  - C-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//0//2782bp//99%//AF059617
- 15 C-PLACE101-2031//Homo sapiens sorting nexin 13 (SNX13) mRNA, partial cds.//0//1701bp//100%//AF121862 C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.60E-42//104aa//49%// O09475
  - C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//1.10E-116//364aa//45%//P42566
- 20 C-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds.//2.70E-107//981bp//74%//AF082556
  - C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//2.20E-29// 212aa//35%//P10586
  - C-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//6.10E-293//388aa//99%//P38650
- 25 C-PLACE2000062//Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type lectin, complete cds, clone:HP01347.//6.30E-166//656bp//94%//AB015629
  - C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0//3174bp//99%//AF027219 C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33%//O15736
  - C-PLACE2000216//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//6.60E-115//226aa//99%//Q01082
  - C-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//6.00E-57//239aa//34%//Q04652
  - C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E-167//880aa//37%//P23098
  - C-PLACE2000341//Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds.//0// 1554bp//99%//AF069307
- 35 C-PLACE2000371/TENSIN.//2.90E-78//561aa//37%//Q04205
  - C-PLACE2000373//F-SPONDIN PRECURSOR.//8.60E-16//371aa//28%//P35446
  - C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).//6.30E-37//90aa//98%//P10586
  - C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//1.60E-14//180aa//39%//P14209
  - C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS).//9.90E-229//821aa//54%//Q09996
  - C-PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds.//3.80E-271//642bp//99%//AF062085
  - C-PLACE2000427//PROBABLE HELICASE MOT1.//1.20E-26//200aa//27%//P32333
- C-PLACE2000438//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOS-AMINYLTRANSFERASE) (GALNAC-T1).//2.10E-86//348aa//41%//Q10472
  - C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//2.50E-25// 165aa//40%//P33450
- 50 C-PLACE2000477//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.//6.70E-127//671bp// 94%//AF072733
  - C-PLACE3000009//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1)(FRAG-MENT).//3.50E-30//400aa//30%//P11414
  - C-PLACE3000020//Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds.//0//2253bp//99%// AF033861
    - C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//1979bp//90%//Y17267
    - C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC157/1.90E-08//281aa//22%//P22224
    - C-PLACE3000145//TENSIN.//1.00E-108//277aa//75%//Q04205

- C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type 1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds.//0//2043bp//99%//AF170084
- C-PLACE3000169//ZINC FINGER PROTEIN 135.//2.50E-90//358aa//47%//P52742

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- C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds.//0// 1862bp//98%//AF105020
  - C-PLACE3000242//Human trophinin mRNA, complete cds.//0//2290bp//99%//U04811
  - C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//0//1435aa//92%//P53995
  - C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds.//0//4583bp//83%//AF143946
- 10 C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.60E-08//359aa//23%//P08640
  - C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULU (EC 2.7.1.-).//1.00E-54//418aa//38%// P46549
  - C-PLACE3000416//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//1.80E-141//565bp//98%//AB029290
  - C-PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.//0//3012bp//98%//AF153085
  - C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.90E-54//626aa//29%//P35580
  - C-PLACE4000014//X-LINKED HEUCASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.10E-111//348aa//41%//
  - C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.//0//4661bp//99%//AF165281
  - C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%//P08640
- 25 C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%// AF146689
  - C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//1.60E-86//190aabp//88%//AF091234
  - C-PLACE4000156//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.40E-235//516aa//
  - C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654).//7.00E-22//369aa//25%//P52746
    C-PLACE4000211//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0//5709bp//96%//AB032254
  - C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0//2567bp//88%//AF030430
- 35 C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protem.//0//5143bp//90%//Z70200
  - C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%//P55201
    - C-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//0//2034bp//89%//AF032667
    - C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1).//8.10E-24//319aa//31%//P30771
- 40 C-PLACE4000369//Homo sapiens thyroid homone receptor-associated protein complex component TRAP240 mRNA, complete cds.//1.40E-185//1135bp//67%//AF117754
  - C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME).//7.20E-22//54aa//62%//Q01576
  - C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5142bp//90%//Z70200
- 45 C-PLACE4000450//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zinc finger domain 2A, complete cds.//0//5709bp//96%//AB032254
  - C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)7/5.70E-60//254aa//44%//P13002
  - C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN).// 2.40E-191//828aa//48%//P21783
  - C-PLACE4000548//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.70E-13//784aa//21%//P08640
  - C-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN).//1.50E-26//252aa//35%//P55824
- 55 ZYME FAF) (FAT FACETS PROTEIN).//1.50E-26//252aa//35%//P55824
  C-PLACE4000581//FIBROPELLIN | PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1)
  (UEGF-1).//9.30E-70//226aa//52%//P10079
  - C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.90E-17//201aa//34%//

### P49816

- C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//6340bp//87%//Y17267
- C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//431aa//29%//O60100
- 5 C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochondrial protein, complete cds7/0//2384bp//99%//AF047690
  - C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%//AF034800 C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEU-
- TRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%//P17655

  C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%//

  AB021663
  - C-THYRO1000034/TRICHOHYALIN.//9.40E-10//176aa//30%//P37709
  - C-THYRO1000072//MYOSIN UGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%//P11799
- 15 C-THYRO1000085//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B.//2.00E-72//155aa//92%//Q06710 C-THYRO1000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//0//1737bp//87%// U49055
  - C-THYRO1000132//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.10E-159//824bp//95%//U97018
- 20 C-THYRO1000173//Homo sapiens AP-mu chain family member mulB (HSMU1B) mRNA, complete cds.//0//
  1713bp//99%//AF020797
  - C-THYRO1000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%//AJ005698
  - C-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%// P51523
- 25 C-THYRO1000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%//AB016068 C-THY-RO1000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//0//1567bp//99%//AF124145
  - C-THYRO1000343//ATROPHIN-1 (DENTATORUBRAL-PALUDOLUYSIAN ATROPHY PROTEIN).//4.90E-06// 280aa//31%//P54259
- 30 C-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%//P17563
  - C-THYRO1000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299// 1325bp//99%//AF072864
  - C-THYRO1000395//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%//AF156857 C-THYRO1000401//Human TcD37 homolog (HTcD37) mRNA, partial cds.//1.10E-90//430bp//99%//U67085
- 35 C-THYRO1000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%//AB022663
  - C-THYRO1000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)).// 4.20E-98//408aa//42%//P19474
  - C-THYRO1000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%//AF118566
- 40 C-THYRO1000585//Homo sapiens protein associated with Myc mRNA, complete cds.//0//1901bp//99%//
  AF075587
  - C-THYRO1000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%// AF140360
- C-THYRO1000662//Homo sapiens XPV mRNA for DNA polymerase eta, complete cds.//0//2341 bp//99%//
  45 AB024313
  - C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%//AJ132889
  - C-THYRO1000684//Homo sapiens BAG-family molecular chaperone regulator-5 mRNA, complete cds.//0// 3347bp//99%//AF095195
  - C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%//
  - C-THYRO1000756//ALPHA-N-ACETYLGALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACIII)(STY).//1.80E-55//243aa//42%//Q64686
  - C-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.// 2.40E-157//1656bp//70%//U37373
- 55 C-THYRO1000852//Human branched-chain amino acid aminotransferase (ECA40) mRNA, complete cds.//1.40E-137//689bp//96%//U62739
  - C-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//0// 2387bp//99%//AF079529

- C-THYRO11000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//7.50E-57//315aa//43%//P32322
- C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5.00E-83//566aa//37%//P43550
- 5 C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%//P35132 C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN

UGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%//P52491

C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%//P31948

C-THYRO1001100//ZINC FINGER X-UNKED PROTEIN ZXDA (FRAGMENT).//1.20E-67//245aa//62%//P98168

C-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds.//1.30E-110//1947bp//65%//AF053700

C-THYRO1001134//Homo sapiens CGI-78 protein mRNA, complete cds.//0//1898bp//99%//AF151835

C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa//

- 62%//Q05481
  C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTSZ) gene, exons 4, 5, and 6 and complete cds; and TH1 gene partial sequence.//3.80E-100//478bp//99%//AF136276
  - C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%//P45701
- C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%//AF121861
  C-THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.//2.00E-263//3101bp//68%//
  AF064729
  - C-THYRO1001374//CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE (EC 3.1.2.2) (LONG CHAIN ACYL-COA THIOESTER HYDROLASE) (CTE-II).//1.80E-13//361aa//22%//O00154

C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%//P30427

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- 25 C-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//1.10E-131//219aa//81%// O70503
  - C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMMHC-B).//2.70E-171//559aa//59%//P35580
  - C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//99%//AJ002190
  - C-THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//4.10E-273//1947bp//82%//AF175968
  - C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//0//1820bp//99%// AJ225089
- 35 C-THYRO1001703//NIFR3-LIKEPROTEIN.//2.90E-32//282aa//32%//P45672
  - C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%//Q04652
  - C-THYRO1001738//TUBULIN--TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.40E-20//217aa//30%//P38584
  - C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.40E-74//158aa//89%//P42128
  - C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81%//
  - C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%//AF126484
  - C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.40E-30//80aa//60%//P25916
  - C-Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIPL1) gene, complete cds.//0//980bp//96%//AF180472
- 45 C-Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.//0//1858bp//99%//AF132936 C-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds.//7.10E-71//345bp// 100%//AF081192
  - C-Y79AA1000231//Homo sapiens nucleolar protein NOP5/NOP58 mRNA, complete cds.//0//1515bp//99%// AF123534
- 50 C-Y79AA1000268//Mus musculus Nip21 mRNA, complete cds.//2.10E-50//648bp//64%//AF035207
  - C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%//Q02910
  - C-Y79AA1000328//SEL-10 PROTEIN.//0.000000067//219aa//25%//Q93794
  - C-Y79AA1000342//Homo sapiens Ciz1 mRNA, complete cds.//0//2644bp//81%//AB030835
  - C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%//AF157833
  - C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//0//2048bp//93%//X84692
  - C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.00E-20//261aa//27%//P25343
  - C-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete

cds.//8.30E-252//1207bp//85%//U41736 5

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- C-Y79AA1000540//CELL POLARITY PROTEIN TEA1.//2.10E-12//211aa//33%//P87061
- C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT)7/0//652aa//98%//P17427
- C-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.40E-27//216aa//34%//P28320 C-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds.//2.00E-287//2031bp//82%// AF060503
- C-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//5.80E-254//1477bp//84%//X69942
- C-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//0//1594bp// 10 99%//AF093670
  - C-Y79AA1000748//Rattus norvegicus clone C42 CDK5 activator-binding protein mRNA, complete cds.//6.60E-286//1832bp//84%//AF177477
  - C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).// 4.90E-91//200aa//64%//Q61990
  - C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//3.00E-37//469aa//27%//P49902 C-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//1.10E-236//1076bp//99%// AF098799
  - C-Y79AA1000794//Homo sapiens actin-associated protein 2E4/kaptin (2E4) mRNA, 2E4-1 allele, complete cds.// 0//1610bp//99%//AF105369
  - C-Y79AA1000800//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds.//1.60E-284//1288bp// 99%//AF072733
  - C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//5.00E-173//220aa//79%//P05209
  - C-Y79AA1000962//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II)7/4.20E-17// 430aa//27%//Q99323
  - C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%//AF100757 C-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//3.90E-248//1468bp//87%//U38253
  - C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.//4.70E-151//985bp//87%//U52962 C-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD).//3.10E-138//583aa//47%//P45953
    - C-Y79AA1001211//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.//0//1435bp// 99%//AF139658
    - C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HY-DROXYSTEROID DEHYDROGENASE 1).//7.70E-50//228aa//42%//P51657
      - C-Y79AA1001236//Homo sapiens cell division protein mRNA, complete cds.//0//1612bp//99%//AF063015 C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//996bp//99%//AJ011738
      - C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46).//0.000000023//193aa//30%// Q03309
- C-Y79AA1001323//Mus musculus mRNA for GSG1, complete cds.//3.30E-172//1171bp//83%//D87325 40 C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0// 4708bp//99%//AF055084
  - C-Y79AA1001391//HOMEOBOX PROTEIN HOX-A13 (HOX-1J).//1.20E-58//178aa//66%//P31271
  - C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-).//1.20E-13//230aa//32%//O83746
- C-Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.//8.50E-45 65//784bp//62%//AF083115
  - C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18//151aa//38%//P35132
  - C-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//4.50E-193// 1333bp//80%//D14336
  - C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KI-NASE) (PI4K-ALPHA).//7.50E-76//85aa//90%//P42356
    - C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- AC-TIVATING ENZYME).//1.90E-40//482aa//27%//P27550
- C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).// 55 2.50E-14//410aa//24%//Q00547
  - C-Y79AA1001603//POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGALACTOS-

- AMINYLTRANSFERASE) (GALNAC-T1).//1.70E-84//313aa//48%//Q07537
- C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.80E-91//209aa//41%//P52740
- C-Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.//3.4e-310//1430bp//98%//AF077049 C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gc1) mRNA, complete cds.//1.40E-78//
- 5 227aa//40%//Q01820

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- C-Y79AA1001705//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//3.40E-47//626bp//68%//AF033120
- C-Y79AA1001711//Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds.//1.20E-258//1185bp//99%// J04137
- 10 C-Y79AA1001827//Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds.// 0//1689bp//98%//AF177145
  - C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//AF192913
  - C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTI-
- 15 VATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489
  - C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149
  - C-Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds.//7.10E-52//279bp//97%// AF174602
  - C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.00E-10//94aa//47%//O42643
  - C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743
  - C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5.00E-163//752bp//99%//X86018
  - C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415
- 25 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133
  - C-Y79AA1002204//COMPLEXIN 2 (SYNAPHIN 1) (921-L).//7.50E-09//131aa//35%//Q13329
  - C-Y79AA1002208//ANKYRIN.//8.10E-34//188aa//38%//Q02357
  - C-Y79AA1002209/TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//1.60E-72//437aa//39%//P00952
- 30 C-Y79AA1002210//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//0.0000018//140aa//25%//Q13829
  - C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17// 146aa//35%//O16264
  - C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//7.10E-17//213aa//31%//P30620
- 35 C-Y79AA1002246//SYNAPTOTAGMIN V.//1.60E-28//286aa//32%//O00445

NA, complete cds.//0//1545bp//96%//AF152961

- C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384
- C-Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.//0//1209bp//99%//AF116574
- C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.90E-186//1130bp//82%// X67877
- 40 C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%// Y18208
  - C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879
  - C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp// 86%//U49385
- 45 C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725 C-Y79AA1002433//Homo sapiens chromatin- specific transcription elongation factor FACT 140 kDa subunit mR-
  - C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.50E-136//472aa//49%//Q05481
- 50 C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa// 51%//Q05481
  - C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-311// 1444bp//98%//AF129534

### Claims

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1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set

forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.

- 2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, wherein said oligonucleotide comprises at least 15 nucleotides.
- 3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence 3'-end nucleotide sequence is selected from the group consisting of:

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NO: 16216, SEQ ID NO: 16163 / SEQ ID NO: 16217, and SEQ ID NO: 16164 / SEQ ID NO: 16218

4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.

	5.	A polynucleotide comprising a coding region in the polynucleotide of claim 4.
10	6.	A substantially pure protein encoded by polynucleotide of claim 4.
	7.	A partial peptide of the protein of claim 6.
	8.	An isolated polynucleotide selected from the group consisting of
15		(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following SEQ ID NOs:
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     SEO ID NO: 10553, SEQ ID NO: 10555, SEQ ID NO: 10556, SEQ ID NO: 10557, SEQ ID
     NO: 10558, SEQ ID NO: 10560, SEQ ID NO: 10562, SEQ ID NO: 10564, SEQ ID NO: 10566.
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     SEQ ID NO: 10584, SEQ ID NO: 10586, SEQ ID NO: 10588, SEQ ID NO: 10590, SEQ ID
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20 (b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence set forth in any one of the following SEQ ID NOs:

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SEQ ID NO:19008, SEQ ID NO:19010, SEQ ID NO:19015, SEQ ID NO:19017, SEQ ID NO:19019, SEQ ID NO:19021, and SEQ ID NO:19023

(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences of (b);

(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence of (a).

9. A substantially pure protein encoded by the polynucleotide of claim 8.

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10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.

- 11. A vector comprising the polynucleotide of claim 5 or 8.
- 12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
- 5 13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
  - 14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.
- 15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.
  - 16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.
- 15 17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.
  - 18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.
  - 19. A method for synthesizing a polynucleotide, the method comprising:
    - a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
    - b) recovering the synthesized product.
- 25 20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.
  - 21. The method of claim 19, wherein the complementary strand is obtainable by PCR.
  - 22. A method for detecting the polynucleotide of claim 8, the method comprising:
    - a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
    - b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.
- 23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium on which the database is stored.

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Figure 1

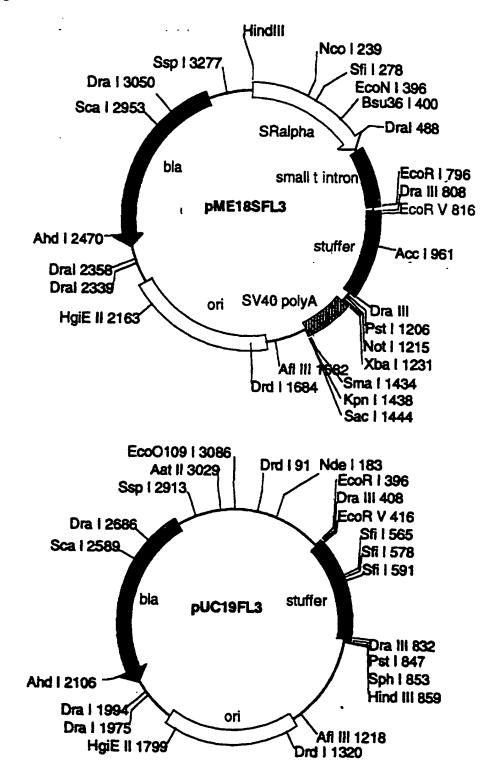


Figure 2

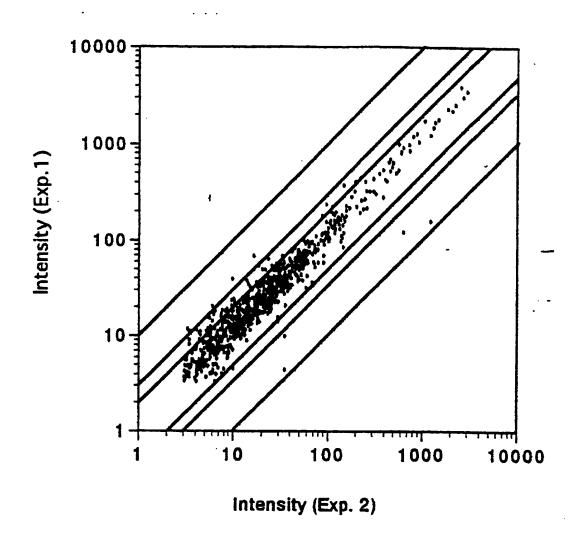
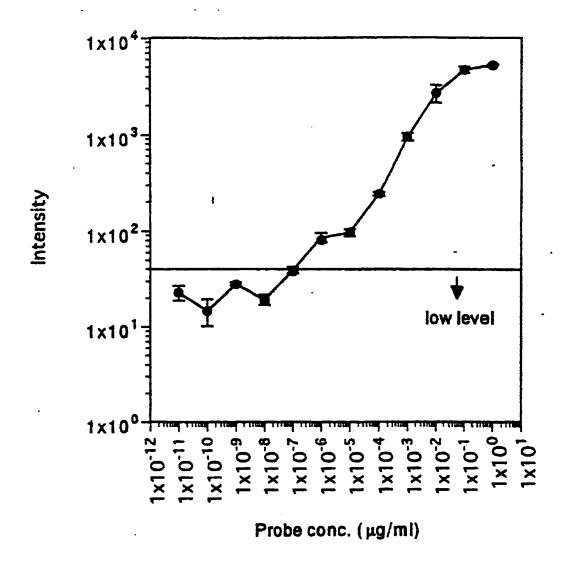


Figure 3



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